



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: Lynn A Doucette-Stamm and David Bush
- (ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
AND THERAPEUTICS
- (iii) NUMBER OF SEQUENCES: 5206
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 - (B) STREET: 100 Beaver Street
 - (C) CITY: Waltham
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02354
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: CD-ROM ISO9660
 - (B) COMPUTER:
 - (C) OPERATING SYSTEM:
 - (D) SOFTWARE:
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/ 085131
 - (B) FILING DATE: May 12, 1998
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/051553
 - (B) FILING DATE: July 2, 1997
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ariniello, Pamela Deneke
 - (B) REGISTRATION NUMBER: 40,489
 - (C) REFERENCE/DOCKET NUMBER: GTC-011
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (781)893-5007
 - (B) TELEFAX: (781)893-8277

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACACCTTGTT CATTATCATT ATCCACTAAA ACTCAAAGAA AGGATAGAAG CAAAACGTCA	60
GCTTTATTCA GTTCTGAACA ATTTGCCTCA AGTGTCCTATA TGACTAACAT TGACCGCCGT	120
ATCAGCAAAA CCAAAAAAGC CATCTATCAA GCTTTTATAC AACTTTTGAA TGCTAAGGGC	180
TACGAGGCCA CTA CTGTTCA GGATATCATT GATCTCGCAG ATGTGGGACG ATCCACCTTT	240
TACTGTCACT ATGAGAGATA G	261

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGAGCTGTT CAAGTCAACA TTATGGACTA TATTTAAAAG AGGAGATCGT TATGTCGATT	60
AATGTATTTT AAGCGATTTT AATTGGATTA TGGACAGCTT TCTGTTTTAG TGGAATGCTG	120
TTAGGAATTT ACACCAATAG ATGTATTGTT CTGTCATTTG GTGTCGGAAT TATTCTAGGT	180
GATCTGCCTA CTGCTCTTGC AATGGGAGCT ATTGGTGAAT TGGCTTATAT GGGATTCCGT	240
GTTGGTGCTG GAGGTACTGT TCCACCAAAC CCCATCGGAC TGATAATGCG CGGTATCCAC	300
NNGAGTTGA	309

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTGATTCGTT CACATTCTAT TACAATCTAC TATAATAAAA TGATGAGAGT TATTACAAAT	60
TATAGGTTTG AAAAATCATT AATTTCTTTT TCGAGTATTT TAACTAATGC CTCTTCTTTG	120
GTTAGTCGTA ATAAAGTTAT TCCTTTATCA ATCAAATCGG AGTTATGTTG TAGTATTCCC	180
AAGCGTACTT GA	192

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 903 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTCTAGTT CATTTGTGGT CATTTTTTGT ACTCATATAC CTTTAAAATA TAAAAGGAGG	60
TTGTACATGT ATCGAATTCT AAATCCAATG AATCACAATG TCTCGTTTGT CAGAAATGAT	120
AAGGGAGAAAG AGGTGATTGT AATTGGTAAG GGGATTGCAT TCGGAAAGAA GAAGGGGGAT	180
TTGATTGCTG AAAATCAGGT TGAGAAAATC TTTCGGATGA AGACCGAAGA GTCCAGAGAA	240
AACTTTATGG CTCTTCTCAA AGATGTTCCG CTTGATTTTA TCACAGTGAC CTATGAAATC	300
ATTGATAAGC TATCAAAGAA ATATCATTAT CCGATTCAAG AGTATCTCTA TGTAACCTTG	360
ACAGATCATA TTTACTGTTC TTATCAAGCT CTAACCTCAAG GAAGGTACAA GGATAGTAAT	420
CTGCCAGATA TTTCCTGCTAA GTATCCTGTC GCCTTTTCAAA TCGCAAATGA AGCTTTTGAA	480
ATTTACCGTC AGAAGCTAGC AGATCATTTT CCTGAGGACG AAATTATTCTG GATTGCTTAT	540
CATTTTATTA ATGCTGAAGG TGAAAATGAA GTGGAACCTG TGGAGTCGAT TGATAAGAGG	600
AAAGAAATTC TCAGGAATGT TGAAGAAGTT TTAACGGACT ATGCAATTCA ACGAACTAAA	660
AAGAATAACC ATTTCTATGA TCGCTTTATG ATCCATTTGA ATTATTTCTT GGATTATTTA	720

GACAGATCTA	GAGATGATAA	CCAATCACTT	CTGGATATGG	AAGATCATAT	TAAACAATCC	780
TATCCAAAAG	CCTTCGAGAT	TGGTTCCAAG	ATCTATGATG	TGATTACGCA	ACATACGGGT	840
CTTGATTTGT	ATAAAAGTGA	ACGAGTTTAT	CTAGTTCTAC	ATATCCAACG	TTTATTGTCA	900
TAA						903

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TATAATAGTT	CTATGAGATT	AGATAAATTT	TTAGTTGCCT	GTGCGGTGGG	AAGTCGGACT	60
GAGGTCAAAA	ACTTGCTCAA	GGCTGGGCGC	GTGACTGTAA	ATGGTAAAAA	AGAAAAATCA	120
GCTAAATTGC	AGATTGATGA	AAAAATAGAT	GAGATTCGCT	TTGATGGGCA	AGTGTTGGAG	180
TATGAAGAGT	TTGTCTACTA	CATGATGAAC	AAGCCCAAAG	GAGTTATATC	AGCGACTGAG	240
GATCCCAAGC	ACAGAACCGT	TCTGGACTTG	TTGGATGACT	TGGCGCGGAG	TAAGGAAATT	300
TTCCCAGTAG	GACGCTTGGA	TATTGACACG	CATGGTCTTT	TGCTCTTGAC	CAATGATGGT	360
CAGCTGGCTC	ATGTTCTTCT	TTCGCCCAAG	CGTCATGTGG	ACAAGACTTA	TCTGGCACAA	420
GTCAAGGGAA	TCATGACCCA	AGAAGATGTG	GAGATATTTG	CTGAGGGTAT	TCCTCTCAAA	480
GACTTTACCT	GTCAACCCGC	TATACTGGAG	CTTGTATCCA	TAGATACAGA	AAAGAATCAA	540
AGCCAAATCC	GTGTGACCAT	TGCAGAAGGG	AAGTTTCATC	AGATCAAGCG	TATGGTGGGC	600
TACTGTGGCA	AGGAAGTGGT	GGACTTGCAA	CGATTGACTA	TGGGAACTTT	AGTATTAGAT	660
GAGAACCTGG	AACGAGGGGG	AAGTGGCGTC	GCTTGA			696

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TATAATAGTT	CTATGTTAAA	ATCAGAAAAA	CAATCACGTT	ATCAAATGTT	AAATGAAGAA	60
TTGTCCTTCC	TATTGGAAGG	CGAAACCAAT	GTTTTGGCTA	ATCTTTCCAA	CGCCAGTGCT	120
CTCATAAAAAT	CACGTTTTCC	TAATACCGTA	TTTGCAGGCT	TTTATTTGTT	CGATGGAAAG	180
GAATTGGTTT	TAGGCCCTT	CCAAGGAGGT	GTTTCCTGCA	TCCGTATTGC	ACTAGGCAAG	240
GGTGTGTTTG	GTGAGGCAGC	TCACTTTCAG	GAAACTGTTA	TTGTTGGAGA	TGTGACGACC	300
TATCTCAACT	ATATTTCTTG	TGATAGTCTA	GCTAAAAGTG	AAATTGTGGT	GCCGATGATG	360
AAGAATGGTC	AGTTACTTGG	AGTTCTGGAT	CTGGATTCTT	CAGAGATTGA	GGATTACGAT	420
GCTATGGATC	GAGATTATTT	GGAACAAATT	GTCGCTATTT	TGCTTGAAAA	GACAGCATGG	480
GACTTTACGA	TGTTTGAGGA	AAAATCTTAA				510

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGACCAGTT	CACAGAGTGT	CACTCCTGTT	CTTCAAACAA	ATTACTACAT	CGACACGCCT	60
GATTTTGAAC	TGCGAGAAAA	GAAAGTCGCT	ATGCGCATTC	GAACCTTTGA	AGACTGGGCT	120
GAGTTGACAC	TCAAAGTCCC	GCAGAGTGTT	GGAAACATGG	AATACAACCA	AAAATTGCAA	180
CTAAAAGATG	CTGAGAACTA	TCTGAGTAAG	GAAGAACTTA	CTCAAGGGCT	AGTACTAGAT	240
GACTTAGCGA	CACATGGTAT	CCAAAGTAAG	AACTAG			276

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGAGAAGTT	CAAAATTTGG	TATTATCCCT	GAGTTGATTG	GACGCTTGCC	TGTTTTTGCG	60
GCTCTTGAGC	AATTGACCGT	TGATGACTTG	GTTGCGCATCT	TGAAAGAGCC	AAGAAATGCC	120
TTGGTGAAAC	AATACCAAAC	CTTGCTTTCT	TATGATGATG	TTGAGTTGGA	ATTTGACGAC	180
GAAGCCCTTC	AAGAGATTGC	TAATAAAGCA	ATCGAACGGA	AGACAGGGGC	GCGTGGACTT	240
CGCTCCATCA	TCGAAGAAAC	CATGCTAGAT	GTCATGTTTG	AGGTGCCGAG	TCAGGAAAAT	300
GTGAAATTGG	TTCGCATCAC	TAAAGAAACT	GTCGATGGAA	CGGATAAACC	GATCCTAGAA	360
ACAGCCTAG						369

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 924 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGGAGAGTT	CAATGAGTAA	GCATCAGGAA	ATTCTAAGCT	ATTTGGAGGA	ATTACCAGTA	60
GGTAAAAGGG	TCAGTGTTTC	TAGCATTTTC	AATCATCTAG	GAGTTAGTGA	TGGAACAGCC	120
TATCGGGCTA	TTAAAGAAGC	TGAAAACCGT	GGAATTGTGG	AGACCCGTCC	TAGAAGTGGA	180
ACAATTCGTG	TTAAATCCCA	GAAAGTTGCT	ATAGAGAGAT	TAACGTTTGC	TGAAATTGCA	240
GAAGTGACTT	CTTCTGAGGT	TCTGGCTGGG	CAAGAAGGTT	TAGAGAGAGA	ATTTAGTAAG	300
TTTTCAATTG	GTGCCATGAC	TGAACAAAAT	ATCTTGCTTT	ACCTTCATGA	TGGGGGGGCTC	360
TTGATTGTCG	GAGACCGAAC	CCGTATTCAG	TTGCTAGCCT	TGGAATATGA	AAATGCAGTT	420
CTGGTTACAG	GGGGATTTC	GGTTCATGAT	GATGTGCTTA	AACTGGCCAA	TCAAAAAGGG	480
ATTCTGTGTC	TAAGAAGTAA	GCATGATACC	TTTACCGTCG	CGACCATGAT	CAATAAAGCC	540
TTGTCAAATG	TCCAAATCAA	GACTGATATT	CTGACAGTTG	AGAAACTTTA	TCGCCCTAGT	600
CATGAGTATG	GTTTTCTGAG	AGAGACAGAT	ACAGTTAAAG	ATTATTTGGA	CTTGGTTCGT	660
AAGAATCGTA	NCAGCCGTTT	CCCTGTTATC	AATCAACATC	AGGTCGTTGT	TGGCGTTGTA	720
ACCATGAGAG	ACGCTGGTGA	TAAATCACCA	AGCACGACAA	TTGATAAGGT	TATGTCTCGT	780
ANTCTATNTT	TGGTTGGATT	ATCGACAAAT	ATTGCCAATG	TGAGTCAACG	GATGATCGCA	840

AAAACTTTG AATTGGTACC ATTTTGTCCG AANCAATCAA ACTTTGCTTG GCGTTGTGAC	900
GCAACAAAAT GTCTGAGAAA ATGA	924

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAAGGGAGTT CATCTATCGT GTGGAAAAAG AAGAAAGTTA AGGCAGGTGT TCTCCTCTAC	60
GCAGTCACCA TAGCAGCCAT CTTTAGTCTT TTGTTGCAAT TTTATTTGAA CCGACAAATC	120
GCCCACTATC AAGACTATGC TTAAATAAAA GAAAAATTGG TTGCTTTTGC CATGGCTAAA	180
CGAACCAAAG ATAAGGTTGA GCAAGAAAGT GGGGAACAGT TTTTAAATCT AGGTCAGGTA	240
AGCTATCAAA ACAAGAAAAC TGGCTTAGTG ACGAGGGTTC GTACGGATAA GAGTCAATAT	300
GAGTTTCTGT TTCCTTCAGT CAAAATCAAA GAAGAGAAAA GAGATAAAAA GGAAGAGGTA	360
GCGACCGATT CAAGCGAAAA AGTGGAGAAG AAAAAATCAG AAGAGAAGCC TGAAAAGAAA	420
GAGAATTCCT AG	432

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCCGGTGGTT	CCGTATGGAA	GGGCCATCGC	TCAACGGATA	AAAGCTACCC	TGGGGATAAC	60
AGGCTTATCT	CCCCCAAGAG	TTCACATCGA	CGGGGAGGTT	TGGCACCTCG	ATGTCGGCTC	120
GTCGCATCCT	GGGGCTGTAG	TCGGTCCCAA	GGGTTGGGCT	GTTCGCCCAT	TAAAGCGGCA	180
CGCGAGCTGG	GTTTCAAGAC	TCGTGAGACA	GTTCGGTCCC	TATCCGTCGC	GGGCGTAGGA	240
AATTTGAGAG	GATCTGCTCC	TAGTACGAGA	GGACCAGAGT	GGACTTACCG	CTGGTGTACC	300
AGTTGTCTTG	CCAAAGGCAT	CGCTGGGTAG				330

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCGGTGGTT	CCGTATGGAA	GGGCCATCGC	TCAACGGATA	AAAGCTACCC	TGGGGATAAC	60
AGGCTTATCT	CCCCCAAGAG	TTCACATCGA	CGGGGAGGTT	TGGCACCTCG	ATGTCGGCTC	120
GTCGCATCCT	GGGGCTGTAG	TCGGTCCCAA	GGGTTGGGCT	GTTCGCCCAT	TAAAGCGGCA	180
CGCGAGCTGG	GTTTCAAGAC	TCGTGAGACA	GTTCGGTCCC	TATCCGTCGC	GGGCGTAGGA	240
AATTTGAGAG	GATCTGCTCC	TAGTACGAGA	GGACCAGAGT	GGACTTACCG	CTGGTGTACC	300
AGTTGTCTTG	CCAAAGGCAT	CGCTGGGTAG				330

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCCGGTGGTT	CCGTATGGAA	GGGCCATCGC	TCAACGGATA	AAAGCTACCC	TGGGGATAAC	60
AGGCTTATCT	CCCCAAGAG	TTCACATCGA	CGGGGAGGTT	TGGCACCTCG	ATGTCGGCTC	120
GTCGCATCCT	GGGGCTGTAG	TCGGTCCCAA	GGGTTGGGCT	GTTGCCCCAT	TAAAGCGGCA	180
CGCGAGCTGG	GTTCAGAACG	TCGTGAGACA	GTTTCGGTCCC	TATCCGTCGC	GGGCGTAGGA	240
AATTTGAGAG	GATCTGCTCC	TAGTACGAGA	GGACCAGAGT	GGACTTACCG	CTGGTGTACC	300
AGTTGTCTTG	CCAAAGGCAT	CGCTGGGTAG				330

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCCGGTGGTT	CCGTATGGAA	GGGCCATCGC	TCAACGGATA	AAAGCTACCC	TGGGGATAAC	60
AGGCTTATCT	CCCCAAGAG	TTCACATCGA	CGGGGAGGTT	TGGCACCTCG	ATGTCGGCTC	120
GTCGCATCCT	GGGGCTGTAG	TCGGTCCCAA	GGGTTGGGCT	GTTGCCCCAT	TAAAGCGGCA	180
CGCGAGCTGG	GTTCAGAACG	TCGTGAGACA	GTTTCGGTCCC	TATCCGTCGC	GGGCGTAGGA	240
AATTTGAGAG	GATCTGCTCC	TAGTACGAGA	GGACCAGAGT	GGACTTACCG	CTGGTGTACC	300
AGTTGTCTTG	CCAAAGGCAT	CGCTGGGTAG				330

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAGAAGGTT	CTTTTGGGAT	TTTTAAAGGA	AATAATATGA	AAAAATATAT	TTTTATGCGT	60
GTTTTGCGGT	CATTGGTTTC	GATTTTCTTA	GTAACGACTT	TGACCTACAC	GATTATCTAT	120
ACCTTG GTTC	CTCGAAAAAT	GATTTTCAAG	CAGGATCCTA	ACTATAATAA	AATTGCGACA	180
ACGGCTGATA	AACGTGATAA	CTATGAAAAT	ACTGTGTTTG	AGCGTATGGG	CTACATTGAG	240
TATTACGATA	CTAGAGAGTT	GCAAGAAAAG	GCAAGTAGCA	TGGATTCTTC	TGTAACAGTA	300
GAAGCAAATG	CGACCAATAA	AGCTATTTAT	GAAAAGTACA	TCAATCAATT	AGGTCATGGT	360
TGGACTTTGG	GAGAATTTAC	TGAAAGTGGT	CAATTCATG	CTACTCGTGA	AATTCCAATT	420
TTTGAACGTG	TTTTTCACTT	CTATGCTAAC	TTGATTGACA	TTGACCATAC	AAATAAAATC	480
CAAGACCCTG	AAAATCCAGA	CTTGAAACGC	TACCTTCGTT	TTGAAAATGA	TCCAGCTATC	540
GGATGGTCAT	TGGTCGGTTC	AGGAACTAAA	CATAAATATC	TCTTGTACTT	TAACAGTCAG	600
TTCCCATTTG	TTCATCAAAA	CTTTGTGAAC	TTGAATTTAG	GTGACTCTTA	CCCAACCTAT	660
GCTAATACAC	CAGTTCTTCA	GGTTATTACT	CAAGGTCAAG	GACAAACCAA	AACTGCCCCA	720
GTTTCAGTTC	CAACAGGTAA	GAAAAACGCT	TCTGTAAATA	TTTACTCAAG	AACCTACAAG	780
TCACCTAGTC	AGGCTGACTC	TCGTGAAGTA	GCTAGCTATG	GGAAAGATGA	TCCTTATACA	840
GCGACTGAAA	GTAATTACCA	ATATCCATCT	ATGATTGTCA	GCTCTGCTAT	TACTGGTTTG	900
ATTGGTTTGG	TTCTTGCCTA	TGCTCTTGCC	GTGCCACTTG	GTTTCAGCCAT	GGCTCGTTTC	960
AAGAACACTT	GGATTGATAG	CCTCTCAACA	GGGACTTTGA	CCTTCTTGCT	TGCTCTTCCA	1020
ACGATTGCCT	TGGTTTACAT	CGTTCGATTG	ATTGGATCAT	CTATTGCCCT	TCCAGATTCA	1080
TTCCCTATCT	TGGGAGCTGG	AGATTGGCGT	TCTTACGTTT	TACCAGCAGT	CATCCTTG GT	1140
TTGTTGGGTG	CTCCTGTTAC	AGCCATTTGG	ATTTCGTCGT	ACATGATTGA	CTTGCAATCT	1200
CAAGACTTTG	TTCGTTTCGC	TCGTGCAAAA	GGTTTGTCTG	AAAAAGAAAT	TTCAAACAAA	1260
CACATCTTTA	AAAATGCCAT	GGTTCCGCTG	GTTTCAGGAA	TTCCCTGGTGC	CATTATTGGG	1320
GTTATCGGTG	GTGCAACCCT	TACTGAAACA	GTCTTCGCCT	TCCCAGGTAT	GGGTAAAATG	1380
TTGATTGACT	CTGTAAAAGC	ATCTAATAAC	TCTATGGTCG	TTGGTCTTGT	CTTCATCTTT	1440
ACATGTATTT	CTATCTTCTC	ACGTCTTTTG	GGAGATATTT	GGATGACTAT	TATTGACCCA	1500
CGTATTAAAT	TGACTGAGAA	AGGAGGCAAA	TAA			1533

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAAGGAGGTT	CTACCATGAA	ACAAGAATGG	TTTGAAAGTA	ATGATTTTGT	AAAAACAACA	60
AGCAAGAACA	AGCCTGAAGA	GCAAGCTCAA	GAGGTTGCAG	ACAAGGCTGA	AGAAACGATA	120
GCCGATCTCG	ATACACCAAT	TGGAAAAAAT	ACTCAAGTAG	AGGAGGAAGT	CTCTCAAGCT	180
GAAGTCGAAT	TGGAAAGCCA	GCAAGAAGAG	AAAATTGAAA	CTCCTGAAGT	CGGTGAAGCG	240
AGAACAGAAA	TAGAAGAAAA	GAAGGCATCT	AATTCTACTG	AAGAAGAGCC	AGACCTTTCT	300
AAAGAAACAG	AAAAAGTCAC	TATAGCTGAA	GAGAGCCAAG	AAGCTCTTCC	TCAGCAAAAA	360
GCAACCACGA	AAGAGCCACT	TCTTATCAGT	AAATCTTTAG	AAAGTCCTTA	TATCCCCGAC	420
CAAGCTCCAA	AATCTAGGGA	TAAATGGAAA	GAGCAAGTGC	TTGATTTTTG	GTCTTGGCTA	480
GTGGAAGCGA	TCAAATCTCC	TACAAGTAAG	TTGGAAACAA	GTATCACACA	CAGTTACACA	540
GCCTTTCTCT	TGCTCATTCT	GTTTTCTGCA	TCTTCCTTTT	TCTTTAGTAT	CTATCACATC	600
AAACATGCTT	ACTATGGACA	TATAGCAAGC	ATTAACAGTC	GCTTCCCTGA	GCAGCTAGCT	660
CCTTTAACTC	TTTTTTCTAT	CATCTCTATC	CTAGTAGCGA	CAACACTCTT	CTTCTTTTCA	720
TTCTCTTGG	GTAGTTTCGT	TGTGAGACGA	TTTATCCACC	AGGAAAAGTA	CTGGACGCTA	780
GACAAGGTTT	TCCAACAATA	TAGTCAACTC	TTGGCAATTC	CAATCTTCCT	CACTGCTATT	840
GCTAGTTTCT	TTGCTTTCTT	TGATAGCCTA	CGATTTACAG	CCCTCTTGTG	TGTGATTAGC	900
ATTGGAATCA	TTCTGCTTGC	CAGTCTCCAT	ATCATTACAA	GACCAAGTCA	AGCAAGTGAA	960
ACCGACTCCT	TCTATCAATT	ATTCTTGTCT	GTCTTGTGA	ACGGAGTTAT	TATCCTCCTC	1020
TTCTTTGTAG	CTGAAGTGGC	ACTGATTGGA	GATTATCTTC	GTATCTTGGC	CTTTCTTTAA	1080

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTTTTTCT	CGTTGTAAAC	ATCAAGGCTT	GCTGTTATCT	CATCTAAGAT	CAATATCGGC	60
GCATCTTTTA	AGAAGGCTCT	GGCTATTGAT	AATCTTTGTC	TTTCTCCTCC	TGATAGCTCA	120
GCTCCGTTTT	CACCAATAAC	TGTATCGAAA	CCTTTATCCA	TTTTTTCTAT	AAAATCTGTG	180
CAATTTGCAA	GTTTTGCTGC	TCTTTTAACC	TCTTCGTCAC	TTGCATCTTG	CTTACCGATT	240
CTAATATTTT	CCATAACGCT	TTGA				264

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AACATTCTCT	CAACTACAAG	TACCAAGGGG	ATTTCCTCAGT	ATGAGATTAA	GAAGCGACTG	60
GAAATTACAG	CTAGAATCGC	CCATCAGTTG	GATGAAGAAA	TGGGTGAAAT	TCGTGATGAT	120
ATCCAAGAGG	CCCAGGCACT	TTTGTATCCT	TTGAGTAGAA	AATTAAATGA	CGGTGTAGGA	180
AACAGTGACG	ATACAGATGA	AGAATACAGG	TAA			213

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACTCTTATCT	CATTGCTAT	TGCCATTGTC	ATCGGAATTA	TCTTCGGTAT	GTTTAGCGTT	60
AGCCCATACA	AATCTCTTCG	CGTCATCTCT	GAGATTTTCG	TTGACGTTAT	TCGTGGTATT	120
CCATTGATGA	TTCTTGCAGC	CTTCATCTTC	TGGGGAATTC	CAAACCTCAT	CGAGTCTATC	180
ACAGGCCAAC	AAAGCCCAAT	TAACGACTTT	GTAGCTGGAA	CCATTGCCCT	CTCACTCAAT	240
GCGGCTGCTT	ATATCGCTGA	AATCGTTCGT	GGTGGTATTC	AGGCCGTTCC	AGTTGGCCAA	300
ATGGAAGCCA	GCCGAAGCTT	GGGTATCTCT	TATGGAAAAA	CCATGCGTAA	GATTATCTTG	360
CCACAAAGCA	ACTAA					375

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...996
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTGCAAATCT	CCATGATAAG	ATCCGTGAAA	AAATGGGATT	TGCCCCATCTG	GCTGACTAGG	60
AGGAAGGAAA	TGTCTGAAAA	ATTAGTAGAA	ATCAAAGATT	TAGAAATTTT	CTTCGGTGAA	120
GGAAGTAAGA	AGTTTGTGCG	GGTTAAAAAT	GCTAACTTCT	TTATCAACAA	GGGAGAAACT	180
TTCTCGCTTG	TAGGTGAGTC	CGGTAGTGGG	AAAACAACTA	TTGGTCGTGC	TATCATCGGT	240
CTAAATGATA	CAAGTAATGG	AGATATCATT	TTTGATGGTC	AAAAGATTAA	TGGTAAGAAA	300
TCGCGTGAAC	AAGCTGCGGA	ATTGATTCGT	CGAATCCAGA	TGATTTTCCA	AGACCTGCC	360
GCAAGTTTGA	ATGAACGTGC	GACTGTTGAT	TATATTATTT	CTGAAGGTCT	TTACAATCAC	420
CGTTTATTTA	AGGATGAAGA	AGAACGTAAA	GAGAAAGTTC	AAAATATTAT	CCGTGAAGTA	480
GGTCTTCTTG	CTGAGCACTT	GACTCGTTAC	CCTCATGAAT	TCTCAGGCGG	TCAACGTCAA	540
CGTATCGGTA	TTGCCCCGTG	CTTGGTTCATG	CAACCAGACT	TTGTTATTGC	AGATGAGCCA	600
ATTTTCAGCCT	TGGACGTTTC	TGTACGTGCC	CAAGTCTTGA	ACTTGCTCAA	AAAATTCCAA	660
AAAGAGCTCG	GCCTGACCTA	TCTCTTCATC	GCCCATGACT	TGTCGGTTGT	TCGCTTTATT	720
TCAGATCGTA	TCGCAGTTAT	TTACAAGGGT	GTTATTGTAG	AGGTTGCAGA	AACAGAAGAA	780
TTGTTTAACA	ATCCAATTCA	CCCATATACT	CAAGCCTTGC	TTTCAGCGGT	ACCAATCCCA	840
GATCCAATCT	TGGAACGTAA	GAAGGTCTTG	AAGGTTTACG	ACCCAAGTCA	ACACGACTAT	900
GAGACTGATA	AGCCGTCTAT	GGTAGAAATC	CGTCCAGGTC	ACTATGTTTG	GGCGAACCAA	960
ACCGAATTGG	CACGTTATCA	AAAAGGACTA	AAC TAG			996

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTGTCCTCCT	CTAGGGCCTC	TATTCGGGTG	AAGAAGGGCG	ATGTTTTTTGA	CTCCAACGAA	60
GCCATGTCCA	CTAAGATAAA	GCAGGGTGGA	ACGACCTACG	ATATTGCCAT	TCCAAGTGAA	120
TACATGATTA	ACAAGATGAA	GGACGAAGAC	CTCTTGGTTC	CGCTTGATTA	TTCAAAAATT	180
GAAGGAATCG	AAAATATCGG	ACCAGAGTTT	CTCAACCAGT	CCTTTGACCC	AGGTAATAAA	240
TTCTCCATCC	CTTACTTCTG	GGGCGACTCA	CTTTGTGGAG	AAACTTTCAG	ACACGGAACA	300
ACTCAATAA						309

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTAACTCCT	CTAAAATTAG	TTGTTTACGT	TCTGTTTTTA	ACACTGAATC	ACCTCCTGTT	60
ATCGTTTACA	CTATTCATTC	TATCATACTT	TCTTTCGAAG	TCAAGCATTT	TTTATCATTT	120
TCTTTCAAAA	TCTATCATTT	TTTCTTATTT	CTAGAATTTT	TATTGCAAGA	TAAGAGCCTT	180
TATGGTAGAC	TATTTGAGTA	A				201

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAAAACACCT	CTGTGCTATA	CTTGTTGTTT	ACCACAAACA	CAAGGAAAGG	CACAGAGATG	60
CAAGAACATT	ATACCCCAAA	AGGGAAACAT	TTGACAATAG	ATAACCGTCG	CTTGATTGAG	120
CGGTGGAAGA	ATGAAAATAA	GTCCAATCGT	GAAATTGCAG	GCTTGTTAGG	AAAGGCGCCT	180
CAAACGATTC	ATAATGAAGT	CAAAAGAGGT	ACAACTTTAC	AACAAGTGAG	AAAAGGGCTA	240
TACAAAAAGG	TCTATTCTGC	CGATTACGCA	CAAACGTGTT	ACCAATTCAA	TCGAAAACGG	300
TCGGTGAAAA	AGTTAATTTT	AACAAAGGAA	ATCAGAGAGA	AGATCTTACA	CTATCATAAG	360
CACATAAGCA	AAAAATTTTCG	CCTGAAATGA				390

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAAACACCT	CTGTGTTATA	CTTGTTGTTT	AACCACAAAC	ACAAGAAAGG	CACAGAAATG	60
CAAGACAATT	ATACTACAAA	AGGTAAACAT	TTGACAATCG	ATAGCCGTCG	CTTAATCGAA	120
AGATGGAAAA	AAGAAGGAAA	ATCAAATAGA	GAAATTGCCCT	CTCTACTTGG	AAAAGCTCCT	180
CAAACATATC	ACACTAAAAA	CAAGCGTAGG	ACAGTCCGAA	AATGTCTTGG	AAAAGGGCGC	240
TTCAAAGAGG	TTTATTCTGC	CGACTATGCT	CAACAGTCTT	ATGAAAACAA	TCGCAAGCGC	300
TCGGTCAAGA	AATCAAGCTT	GACCAAGGAA	CTAAAGGAAA	AGATTCTCCA	CTATCATAAC	360
CAAAAATTTT	CGCCTGAAAT	GATGGTGATG	GCTAAAGGGG	TTAACGTGGG	AATTTCAACC	420
ATTTACTATT	GGATTCATCA	TGGAAAATTG	GGGTTAAGCA	AGCAGGATCT	GCTTTACCCT	480
AGAAAAGGAA	AAGTGCTTAA	GAAACAGGCT	AGCACCAACT	TTAAACCTGC	TGGTCAATCC	540
ATCGCACAGC	GGCCTGAAGC	TATCAATCTT	CGCTTGGAGA	ATGGGCATTA	TGAGATTGAT	600
ACGGTTTTAC	TTACGAGATC	GAAAAACTAC	TGCTTGCTTG	TCTTGACGGA	TCGAAAGAGT	660
AGACATCAGA	TCATCCGATT	GATTCCAAAT	AAAAGTGCTG	AGGTGGTCAA	TCAGGCTCTA	720
AAACTCATCT	TAAAAACAAC	CAAGATTCTT	TCCATCACGG	CAGATAATGG	AACGGAATTC	780
AATCGCTTGT	CTGATGTATT	TTCTGAGGAG	CACATTTATT	ATGCGCACCC	CTATGCCCTCT	840
TGGGAAAGGG	GAACATAATG	GAATCACAAC	AGGCTCATTC	ATAGATGGTT	ACCTAAGGGA	900
ACCAAGAAAA	TGACTCCCAA	AGAAGTCGCA	TTCATCGAAA	AGTGGATTAA	CAACTATCCT	960
AAAAAATGCT	TGAACTACAA	GTCACCCAGA	GAAGACTTCT	TGATGGCTAA	CTTGAACCTG	1020
AAATTTAGCG	TCAGAAACAA	ATCACGAAAT	CGATTCAAAT	TTTGCAGGTC	GTTTAAATAT	1080
CCTGCGCGCA	GGTGTCTTGT	GTGCTAA				1107

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAAAACACCT	CTGTGCTATA	CTTGTTGTTT	ACCACAAACA	CAAGGAAAGG	CACAGAGATG	60
CAAGAACATT	ATACCCCAAA	AGGGAAACAT	TTGACAATAG	ATAACCGTCG	CTTGATTGAG	120
CGGTGGAAGA	ATGAAAATAA	GTCCAATCGT	GAAATTGCAG	GCTTGTTAGG	AAAGGCGCCT	180
CAAACGATTC	ATAATGAAGT	CAAAAAGAGT	ACAACTTTAC	AACAAGTGAG	AAAAGGGCTA	240
TACAAAAAGG	TCTATTCTGC	CGATTACGCA	CAAACTGTTT	ACCAATTCAA	TCGAAAACGG	300
TCGGTGAAAA	AGTTAATTTT	AACAAAAGAA	ATCAGAGAGA	AGATCTTACA	CTATCATAAG	360
CACATAAGCA	AAAATTTTCG	CCTGAAATGA				390

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAAAACACCT	CTGTGTTATA	CTTGTTGTTT	AACCACAAAC	ACAAGAAAGG	CACAGAAATG	60
CAAGACAATT	ATACTACAAA	AGGTAAACAT	TTGACAATCG	ATAGCCGTCG	CTTAATCGAA	120
AGATGGAATA	AAGAAGGAAA	ATCAAATAGA	GAAATTGCCT	CTCTACTTGG	AAAAGCTCCT	180
CAAACTATCC	AACTAAAAAT	CAAGCGTAGG	ACAGTCCGAA	AATGTCTTGG	AAAAGGGCGC	240
TTCAAAGAGG	TTTATTCTGC	CGACTATGCT	CAACAGTCTT	ATGAAAATAA	TCGCAAGCAC	300
TCGGTCAAGA	GATCAAGCGT	GACCAAGGAA	CTAAAGGAAA	AGATTCTCCA	CTATCATAAC	360

CAAAAATTTT TGCCTGAAAT GATGGTTATG GCTAAAGGGG TTAACGTGGG AATTTCAACC	420
ATTTACTATT GGATTCATCA TGGAAAATTG GGGTAA	456

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...528
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGTCGACCT CGCTCAGTCC ATGCTTACCT TACCTTGCTA AAAGGAGTTA CATTATTATG	60
AATAAATCAG AACACCGCCA CCAACTTATA CGCGCTCTTA TCACAAAAAA CAAGATTCAT	120
ACACAGGCTG AGTTGCAAGC CCTTCTTGCT GAGAACGACA TTCAAGTAAC CCAGGCAACC	180
CTCTCACGCG ACATCAAAAA TATGAACCTA TCAAAAAGTCC GCGAAGAAGA TAGCGCTTAT	240
TATGTTCTTA ACAATGGTTC CATCTCAAAA TGGGAAAAAC GTCTCGAACT CTACATGGAA	300
GACGCCCTTG TCTGGATGCG CCCAGTTCAA CACCAAGTCC TACTAAAAAC CCTTCCTGGA	360
CTGGCTCAAT CCTTTGGTTC TATCATTGAT ACTTTGAGCT TCCCTGACGC TATCGCTACC	420
CTTTGTGGTA ATGATGTCTG TCTTATCATC TGTGAAGATG CAGATACTGC TCAAAAAGTGC	480
TTTGAAGAAC TGAAAAAATT CGCCCCACCA TTTTCTTTG AAGAATAA	528

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCTTCTGCCT	CTTCTGGTTG	TCAATTGACC	AGCCTTGAGC	AATTCATTAA	CCAAGGAATG	60
ATCGCTCGTC	AACTGATGGT	ATTCTTCTCC	ACGAATCAAG	CCGATACGCG	AATCACCAAT	120
ATGAGCATAG	ATAGCCTGAT	TATCAATAAT	AGCAAGGACT	TCCAAAGTAG	TTCCCATGCC	180
TCTGTAAGCT	TCATCCTGAC	CAAGCTGGTG	AATCTTTTGA	TTTTCAATTT	CTAG	234

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTATTGGCCT	CAGGTTTCCA	TTTGCAATCA	GAAAGGGATT	TTATGTCCAT	TATTCAAAAA	60
CTTTGGTGGT	TTTTCAAGTT	AGAAAAACGC	CGTTATCTAG	TCGGAATTGT	GGCCCTGGTC	120
TTGGTTTCCG	TCCTCAATCT	CATTCCTCCT	ATGGTTATGG	GGCGGGTTAT	TGATGCCATC	180
ACATCGGGGC	AATTAACCCA	GCAGGACCTC	CTTCTTAGCC	TATTTTACTT	GCTACTTGCA	240
GCCTTTGGTA	TGTACTATTT	GCGCTATGTG	TGGCGTATGT	ATATCCTTGG	GACCTCTTAT	300
TGCTTGGGAC	AGATCATGCG	GTCTCGCTTG	TTTAAGCATT	TCACAAAAAT	GTCGTCAGCC	360
TTTTATCAAA	CCTATCGGAC	GGGTGATCTG	ATGGCACACG	CAACCAATGA	TATCAATGCC	420
TTGACTCGTT	TAGCAGGTGG	CGGTGTCATG	TCTGCGGTGG	ATGCCTCTAT	CACGGCTCTG	480
GTGACTTTGT	TGACCATGCT	CTTTAGCATC	TCATGGCAGA	TGACTCTTGT	TGCCATTCTC	540
CCCCTACCTT	TCATGGCCTA	TGCGACTAGT	CGCCTAGGGA	GAAAGACTCA	TAAGGCCTTT	600
GGCGAATCCC	AAGCTGCTTT	TTCTGAACTC	AATAACAAGG	TACAGGAGTC	CGTATCAGGT	660
ATCAAAGTGA	CCAAGTCTTT	CGGTTATCAG	GCAGACGAGT	TGAAGTCTTT	TCAGGCAGTC	720
AATGAATTAA	CCTTCCAAAA	GAACCTGCAA	ACCATGAAAT	ATGATAGTCT	CTTTGACCCT	780
ATGGTTCTCT	TGTTTGTTGG	TTCGTCCTAT	GTTTTAACGC	TTTTGGTTGG	CTCCTTGGTG	840
G TTCAGGAAG	GGCAGATTAC	AGTTGGGAAT	CTAGTCACCT	TTATCAGCTA	TTTGGATATG	900
CTGGTCTGGC	CTCTTATGGC	CATCGGCTTC	CTCTTTAATA	CTACTCAGCG	AGGGAAGGTT	960
TCTTACCAGC	GGATTGAAAA	TCTTTTGTCT	CAGGAATCTC	CTGTACAAGA	CCCGGAGTTT	1020
CCTCTGGATG	GTATTGAAAA	TGGGCGTTTG	GAGTATGCCA	TTGACAGCTT	TGCTTTTGAA	1080
AATGAGGAAA	CACTGACGGA	TATTCACTTT	AGTTTGCCAA	AAGGGCAAAC	ACTGGGCTTG	1140
GTTGGGCAGA	CAGGCTCTGG	GAAAACGTCC	TTAATCAAGC	TCCTCTTGCG	TGAATACGAT	1200
GTGGATAAGG	GCGCCATTTA	TCTAAACGGT	CACGATATTC	GGGACTATCG	TCTGACAGAC	1260
CTTCGCAGTC	TCATGGGCTA	TGTTCCCTCAG	GACCAGTTTC	TTTTTGCGAC	TTCAATCCTA	1320
GACAATATCC	GCTTTGGTAA	TCCTAACTTG	CCCCTTTCAG	CGGTGAGGGA	AGCTACTAAG	1380
CTAGCCCCGAG	TTTACCAAGA	TATTGTAGAC	ATGCCTCAAG	GATTTGATAC	GCTGATTGGT	1440
GAAAAAGGAG	TCAGTCTTTC	TGGTGGTCAA	AAGCAACGGT	TGGCTATGAG	TCGGGCTATG	1500
ATTTTAGACC	CTGATATCTT	GATTTTGGAT	GATTCCTTAT	CCGCCGTAGA	TGCCAAGACA	1560
GAGTATGCGA	TTATCGACAA	CCTCAAGGAG	ACGCGAAAAG	ACAAGACAAC	CATTATCACT	1620

GGCCATCGCC TCAGTGCAGT TGTCCATGCA GATTTGATTT TAGTCCTGCA AAATGGTCAA	1680
ATTATCGAAC GAGGCAGGCA CGAAGACTTG CTAGCTTTGG ATGGCTGGTA TGCCCAAACC	1740
TACCACTCTC AGCAGCTGGA AATGAAGGGA GAAGAAGATG CAGAATAA	1788

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTTTTCGAT TTACAACAAC TAATCCTGAG TTTCCTTCTA TGATTGAACT ATTTAGTATC	60
TTACCAGAAT ATCCATTAAA GAAGGACGGT CGAGAAATTC CCTTACATTT TGACCAAGAT	120
GCTAGTTTAT CAGCCTTATT ATTGGATGAA GATTATTATA ATATATTGGT GCATGAAAAA	180
GAAACCATT CAGGGGTATTC GGTATTGAGT AATTGTGGTC TATACTCTTC GAAAATCTCT	240
TCAAACCACG TCAGCTTCCA TCTACAACCT CAAAACAGTG TTTTGAGCAG CCTGCAGCTA	300
GCTTCCTAG	309

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTATACT	CTTCGAAAAAT	CTCTTCAAAC	CACGTCAGCG	TCGCCTTACC	GTATGTATGG	60
T TACTGACTT	CGTCAGTTTC	ATCTACAATC	TCAAAACCAT	GTTTTGAGCT	GACTTCGTCA	120
GTTTCATCTA	CAACCTCAAA	ACCATGTTTT	GAGCTGACTT	CGTCAGTTTC	ATCTACAACC	180
TCAGAACCAT	GTTTTGAGCT	GACTTCGTCA	GTTTCATCTA	CAACCTCAAA	ACCATGTTTT	240
GAGCTGACTT	CGTCAGTTTC	ATCTACAACC	TCAAAACTGT	GTTTTGAACA	ACCTGCGGCT	300
AGCTTCCTAG	TTTGCTCTTT	GATTTTCATT	GAGTATTAA			339

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGAGCTCACT	CGAGGTTTAT	GCCCCTGTCC	TTTCGCTACC	AAGTGCTGCT	TCTGGATTAT	60
ATTGATAAGG	CCCTTTCGGC	AGAGGAGTTT	GAATCTCGTA	TCGAGACAGC	CCTCCTCTAT	120
GCCAATGGTC	AAGACAGTAA	AAGTCTAGCG	GAAGATTGCT	TTTACTTTAA	ATCAAAATTT	180
GCTCAATTCC	AGTATCCTTT	TAAAGAGGTT	TACTATCTCG	AAACGTCCAC	AAGACCCCAT	240
CGTGTTATTC	TCTATACCAA	GACAGACAGG	CTGGAATTTA	CAGCGAGTCT	AGAGGAGGTT	300
CTCAAGCAGG	AGCCTCGTTT	CTTGCACTGC	CATCGCTCTT	TTCTCATCAA	TCCTGCCAAT	360
GTGGTGCAAT	TAGATAAGAA	AGAAAAACTG	CTTTTCTTTC	CCAATGGTGG	AAGTTGTCTA	420
ATCGCGCGTT	ATAAGGTCAG	GGAAGTGCTC	GAGGCTATTA	ATAACTTACA	CTGA	474

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 771 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTGCTGCCTT	TATCAATACA	AAAGGGAAAA	GGCTTCCTAC	GAATCATTCC	ATTCCTCTTT	60
GCCATTATCG	GTGGTTACCT	TTTCGCACTA	ACTCTTGGCT	TGGTTGACTT	TACACCAGTT	120
CTTAAAGCCA	ACTGGTTCGA	AAGTCCTGGT	TTCTACTTGC	CATTTAGCAC	AGGTGGTGCC	180
TTTAAAGAGT	ACAATCTTTA	CTTTGGTCCA	GAAGCCATCG	CTATCTTGCC	AATCGCTATC	240
GTAACAATTT	CTGAACATAT	CGGAGACCAT	ACTGTTTTGG	GTCAAATCTG	TGGCCGTCAA	300
TTCTTAAAAG	AACCAGGTCT	TCACCGTACT	CTTATTGGTG	ACGGTATCGC	AACCTCTGTT	360
TCTGCCTTCC	TTGGTGGACC	AGCCAATACA	ACTTACGGAG	AAAATACAGG	GGTTATCGGT	420
ATGACTCGTA	TCGCTTCTGT	CTCAGTTATC	CGTAACGCTG	CCTTCATCGC	GATTGCCCTC	480
AGCTTCCTTG	GTAAATTCAC	TGCCCTTGATT	TCAACTATTC	CAAACGCTGT	ACTTGGTGGT	540
ATGTCAATCC	TTCTCTATGG	GGTTATCGCC	AGCAATGGTT	TGAAAGTCTT	GATTAAAGAA	600
CGTGTGATT	TCGCTCAAAT	GCGAAACCTC	ATCATCGCAA	GTGCTATGTT	GGTTCTTGGA	660
CTTGGAGGAG	CTATCCTTAA	ACTTGGTCCA	GTTACACTTT	CAGGTACTGC	CCTTTCAGCC	720
ATGACAGGAA	TCATCTTGAA	CTTGATCTTG	CCATACGAAA	ATAAAGACTA	A	771

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AATATAAACT	CAATGAAAAT	CAAAGAGCAA	ACTAGGAAGC	TAGCCGCAGG	TTGCTCAAAA	60
CACAGTTTTG	AGGTTGTAGA	TAAGACTGAC	GAAGTCAGCT	CAAAACATGG	TTTTGAGGTT	120
GTAGATGAAA	CTGACGAAGT	CAGTAATCAT	ATCTACGGCA	AGGCGACACT	GACGAAGTTT	180
GAATTGGATT	TTCGCAGAGT	GTAA				204

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTACCAA	ACT	CAAGGA	AGAA	TACGG	AGAGG	AGAGAG	CAAA	AGCCAT	C	TTT	GAAAG	CCTGT	60
AGTCTG	CGAA	ACAAAG	CCAG	TATTC	GTGTA	ACAGAC	CTAA	GTCGAA	AAAG	GGAAAT	CCAA	120	
GCCTTG	T	TGG	AGGCG	AATGA	TTCCCT	TTTTA	GCAACC	ACTC	GTCTG	GT	TAA	GGAGCA	180
CATTTT	GCAG	GGCATA	AATTT	GTTTG	CGGAT	GGAGCC	ATTA	CCATCC	AAAG	CGAGT	CCAGT	240	
CAGCTG	GT	TG	CTCCG	ACGCT	TGATTT	TACAA	GGTGAT	GAGC	GAGTG	C	TTGA	TCCTGT	300
CTCCAG	GT	TG	AAAAC	AGCCC	ATATAG	CCCTC	TTATCT	TACG	ACAGGT	CAGG	TTACTG	CTCT	360
GGACTT	GTAC	GACCACA	AGT	TGGATT	TTAAT	TCAAGAAA	AAT	GCCCAAC	GC	TGGGAG	TTGC	420	
AGATCG	GGGT	CAAACT	CAAA	AATTGG	ATGC	CAGAAA	AGGTG	CATGA				465	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 768 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAGAAA	ACT	CAGCTA	TCTC	ATGTAAA	ATG	CAGAG	AGTTG	AGTTTT	TTTTT	AAGGCA	AATT	60
TGGTATA	AATA	GTTTTA	AATAA	GGAGG	AGTTT	CTCAT	GATAA	AAATC	TTATT	GGTTG	AGGAT	120
GACCTAG	GTC	TGTCAA	ATTC	AGTAT	TTTGAC	TTTTT	AGACG	ATTTT	GCGGA	TGTTAT	GCAG	180
GTATTT	GATG	GAGAAGA	AGG	TCTTT	TACGAA	GCTG	AGAGTG	GTGTCT	TATGA	CTTGAT	TTTG	240
CTGGATT	TGA	TGTTGCC	CAGA	AAAAA	ATGGT	TTCCA	AGTCT	TAAAAG	AATT	GCGTGA	AAAAG	300
GGAATT	TACG	CACCA	GTCT	GATTAT	GACT	GCCA	AGGAAA	GTTTGG	ATGA	CAAGGG	GACAT	360
GGATT	TGAAC	TGGGAG	CGGA	TGATT	TCTG	ACCAA	ACCTT	TCTAC	CTAGA	AGAACT	TAAA	420
ATGCGG	ATTC	AGGCC	CTTCT	CAAAC	GTTCA	GGGAA	GT	TTA	ATGAAA	ACAC	CTTGAC	480
GGGAAT	ATCG	TGGT	TAAATTT	ATCAAC	CAAT	ACCGT	TAAAG	TTGA	AGATAC	TCCTGT	TCGAA	540
TTGCTG	GGGGA	AAGAG	TT	CGA	TTTACT	AGTT	TATTT	CC	TTT	AAAAT	CAAAA	600
CCTAAG	ACGC	AGATTT	TTTGA	CCGTC	TATGG	GGATT	TGATA	GTGAT	ACAAC	GATTT	CGGTT	660
GTCGA	AGTCT	ATGTTT	TCAAA	AGTCC	GTAAG	AAATT	AAAAG	GAACC	ACTTT	TGCAG	AGAAT	720

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATCATGAACT	CTATTTCGAAA	AACCTTTGAAC	AAGAACCAGA	ACAAAAAAAA	GAAAGACGCA	60
AGTATATCCC	TCCACAAACC	CATCCGTGGA	AACTCACATC	TTTCAAACAA	TATCTTCATA	120
AAAATAAAAA	GGATTATGAA	GAGTTTAAAG	GAGGATTTTT	CAGTACGTGC	TGAAAAATAT	180
GAGAACTATC	AGGAGACATT	TCAAGGGCCT	AACAGTTTTT	CCAAAACCGA	TCCAGATGCC	240
ACTTTTATGC	GGATGAAGGA	AGATCATATG	AAAAATGGTC	AACTCAAGGC	TGCTTATAAT	300
CTTCAAATCG	CTACGGAAAA	CCAATTTGTT	CTTCACTATG	ATGTCTTTTC	AAATCCGACA	360
GATACCAAGA	CTCTTCTGCC	ATTCTTTGAA	ACCTATCCGC	ATGACTTGAA	GACAGTTGTC	420
GCAGATGCTG	GATATGGAAG	TGAAGAGAAC	CTCCTTCGTT	TAGATGAAAA	GGAGGTAAAC	480
CATCTGATTA	AATATGCCAT	GTTTGATAAG	GAACAGAAGA	GAGGCTATAA	ACAGTCAGCT	540
AGAAACTTAG	CGAATTGGCA	CTATAATGAC	AAGGAGGATA	GCTATACACA	TCCTGATGGC	600
TGGTATTATC	GTTTTACCA	TACCAACAT	CAGAAAACAC	AGACAGACTT	TCAACAAGAA	660
ATCAAGGTTT	ACTACGCCGA	CGAACCTGAA	TCAGCCCCTC	AAAAGGGACT	GTATATGAAC	720
GAAGGCTATC	AAAACCTGAA	GGCGAAAGAA	TGTCAAGCGC	TTTTATCTCC	CCAAGGTAGA	780
CAGATTTTCG	CTCAACGCAA	GATTGATGTG	GAACCTGTCT	TTGGGCAGAT	AAAGGCTTGT	840
TTGGGTTACA	AGAGATGTAA	TCTGAGGGGC	AAGCGTCAAG	TGAGAATTGA	CATGGGATTG	900
GTACTTATGG	CCAATAACCT	CCTAAAATAC	AATAAGAGAA	CGACTCAAAA	TTAA	954

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTCAGAACT	CTCTACTTCT	ATCCTCTATC	CTCCTCTACA	ATGTCAAAAC	AAGAACAATG	60
ACTGTAGCTA	TTTATACAGA	GGTTCTCAGA	GGAAATTACG	GTGTAGCCGC	AGCCTTGTC	120
ACTATCCTGA	CTGTTCTAAC	AGTAGGTTCC	TTGCTCTTGT	TTATGAAAAT	CTCTAAAAGC	180
AATAGCATT	CACTTTAG					198

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1764 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCGTTACGAT	TGTTTCAAGT	AAAAAAGGAG	TTTGATATGT	CTAATGGACA	ACTAATTTAT	60
TTAATGGTTG	CAATTGCAGT	CATTTTAGTT	CTGGCTTATG	TAGTGGCAAT	CTTTCTACGT	120
AAGCGAAACG	AGGGGAGATT	AGAGGCGCTA	GAAGAAAGAA	AAGAAGAACT	ATACAATCTT	180
CCAGTAAATG	ATGAAGTAGA	AGCTGTAAAA	AATATGCACT	TGATTGGACA	AAGTCAAGTG	240
GCTTTCCGTG	AATGGAATCA	AAAATGGGTC	GATTTATCTC	TCAACTCTTT	TGCCGATATT	300
GAAAATAATC	TCTTTGAAGC	AGAAGGTTAT	AACCATTGAT	TTCGTTTTCT	CAAGGCCAGT	360
CATCAAATTG	ACCAAATTGA	GAGTCAAATT	ACTTTGATTG	AAGAAGATAT	TGCGGCAATT	420
CGCAATGCTT	TGGCAGACTT	AGAGAAGCAA	GAATCTAAAA	ATAGTGGTCG	TGTTCTTCAT	480
GCTTTGGATT	TATTTGAGGA	ACTTCAGCAT	AGAGTTGCTG	AAAATTCAGA	ACAGTATGGT	540
CAAGCCTTGG	ATGAAATTGA	AAAACAATTA	GAAAATATCC	AATCTGAATT	TTTACAATTT	600
GTAACCTTGA	ATTCATCGGG	TGACCCTGTG	GAAGCCGCAG	TGATTTTGGG	TAATACAGAA	660
AATCACATTT	TGGCCTTAAG	TCATATTGTG	GATCGTGTTC	CAGCCTTGGT	TACGACGCTT	720
TCTACAGAA	TGCCAGATCA	ATTACAGGAT	TTGGAAGCCG	GTTATCGTAA	ACTAATTGAT	780
GCTAATTATC	ATTTTGTTGA	AACGATATT	GAAGCGCGTT	TCCACTTGCT	TTATGAAGCA	840
TTCAAGAAAA	ACCAAGAGAA	TATTCGTCAG	TTGGAATTGG	ATAATGCCGA	ATATGAGAAT	900
GGACAGGCAC	AAGAGGAAAT	CAATGCCTTG	TATGATATTT	TACTCGAGA	AATTGCTGCT	960
CAGAAAGTAG	TGGAAAATCT	ACTTGCAACT	CTTCCAACCT	ACCTTCAACA	TATGAAAGAG	1020
AATAATACTT	TATTGGGAGA	AGATATTGCA	CGTTTGAACA	AGACCTATTT	ACTTCCTGAG	1080
ACAGCTGCAA	GCCATGTTTC	TCGTATTTCAG	ACAGAATTAG	AGAGTTTTGA	GGCAGCTATT	1140
GTTGAGGTAA	CTTCAAATCA	AGAAGAACCA	ACCCAAGCTT	ATTCAGTTCT	TGAAGAAAAT	1200

CTTGAGGATT	TACAAACTCA	ACTAAAAGAT	ATTGAAGATG	AGCAAATTTTC	AGTTAGTGAG	1260
CGCCTGACAC	AAATTGAGAA	AGATGATATT	AATGCACGTC	AAAAGGCCAA	TGTTTATGTC	1320
AATCGTCTCC	ATACTATCAA	GCGATACATG	GAAAAACGCA	ATCTGCCAGG	TATTCACAA	1380
ACTTTCTTGA	AGTTATTCTT	TACGGCAAGC	AATAATACCG	AGGATTTAAT	GGTTGAGTTA	1440
GAACAAAAAA	TGATTAACAT	TGAATCTGTT	ACCCGAGTTC	TTGAAATTGC	AACGAATGAT	1500
ATGGAAGCTT	TAGAAACGGA	AACTTATAAT	ATTGTACAAT	ATGCAACTTT	GACAGAGCAA	1560
CTCTTGCAAT	ATTCTAACCG	CTATCGCTCA	TTTGATGAAC	GCATTCAAGA	AGCATTTAAC	1620
GAAGCTTTAG	ATATTTTGA	AAAAGAATTT	GATTATCACG	CTTCATTTGA	TAAGATTTCT	1680
CAAGCATTTG	AAGTGGCAGA	GCCTGGTGTA	ACCAATCGCT	TTGTTACCTC	ATATGAGAAA	1740
ACACGTGAAA	CGATTTCGTTT	TTAA				1764

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTGCCTTGCT	CGATGATATT	TCCATCTTTC	ATGACCAAGA	TCAAGTCTGC	ATTTCCGGATG	60
ATTGACAAGC	GGTGGGCAAT	GACAAAGGAT	GTGCGTCCTT	CCATCAAACG	GTCCATGGCT	120
TTTTGGATCA	ATTCCCTCTGT	CCGTGTGTCA	ACAGAAGAAG	TCGCCTCATC	CAAAATCAAA	180
AGCGATGCAT	CCTTAAGAAG	GGCACAAGCA	ATAGTCAATA	GTTGTTTTTTG	TCCTACAGAC	240
AAGGTCACGG	TGTCATCCAA	GATGGTATCA	TAG			273

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCA	TTGCT	CCCAA	ATCAG	AGGAT	TGTGG	GTCG	CAATAA	TAAT	GGTCCG	ATTC	GGATTT	60
TTTA	GAGATT	CTAG	GATGGA	AAGTA	AATTCC	TCAG	AGTTTT	TGGG	GTCTAG	TGA	AGCGGT	120
GGTT	CATCTG	CGAGA	AATCAA	AGGT	GGATCC	TTTA	AAATTA	TCTT	CGCTAA	TGCA	ACACGT	180
TGTG	CTTCTC	CTCCT	GATAA	CTCAA	ATATA	GGTT	GCTTCA	AATC	CAAATA	A		231

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAAAA	ATGCT	CTGAA	ATGAC	AAGTA	ATCAT	TTCAG	AGCAC	GCAAAA	AGCA	CAAAT	TATACT	60
TTTAT	CTTCT	TTCAT	CCAGA	CTATA	CTGTC	GGCTT	TGGAA	TTTCA	CCAAA	TCAT	GCCTTT	120
CGGCT	CGTGG	GCTAT	ACCAC	CGGT	AGGGAA	TTGC	ACCCTG	CCCT	GAAAT	AGTT	TATCAA	180
TTACA	GATGA	TTATA	GTACT	TAATT	TTTGAA	TATGT	CAACA	GATAA				225

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCATGGTGCT	CTGGGTGCCA	AGATGAGCGG	TGGTGGGCTA	GGAGGTTGTA	TCATAGCCTT	60
GGTAACCAAT	TTGACACACG	CACAAGAACT	AGCAGAAAAG	TTAGAAGAGA	AAGGAGCTGT	120
TCAGACATGG	ATAGAGAGCC	TGTAACAGTA	CGTTCCTACG	CAAATATTGC	TATTATCAAA	180
TATTGGGGAA	AGAAAAAAGA	AAAAGAGATG	GTGCCTGCTA	CTAGCAGTAT	TTCTCTAACT	240
TTGGAAAAATA	TGTATACAGA	GACGACCTTG	TCGCCCTTAC	CAGCCAATGT	AACAGCTGAC	300
GAATTTTACA	TCAATGGTCA	GCTACAAAAT	GAGGTCGAGC	ATGCCAAGAT	GAGTAAGATT	360
ATTGACCGTT	ATCGTCCAGC	TGGTGAGGGC	TTTGTCCGTA	TCGATACTCA	AAACAATATG	420
CCTACGGCAG	CGGGCCTGTC	CTCAAGTTCT	AGTGGTTTGT	CCGCCCTGGT	TAAGGCTTGT	480
AATGCTTATT	TCAAGCTTGG	ATTGGATAGA	AGTCAGTTGG	CACAGGAAGC	CAAATTTGCC	540
TCAGGCTCTT	CTTCTCGGAG	TTTTTATGGA	CCACTAGGAG	CCTGGGATAA	GGATAGTGGA	600
GAAATTTACC	CTGTAGAGAC	AGACTTGAAA	CTAGCTATGA	TTATGTTGGT	GCTAGAGGAC	660
AAGAAAAAAC	CAATCTCTAG	CCGTGACGGG	ATGAAACTTT	GTGTGGAAAC	CTCGACGACT	720
TTTGACGACT	GGGTTCGTCA	GTCTGAGAAG	GACTATCAGG	ATATGCTGAT	TTATCTCAAG	780
GAAAAATGATT	TTGCCAAGAT	TGGAGAATTA	ACGGAGAAAA	ATGCCCTGGC	TATGCATGCT	840
ACGACAAAGA	CTGCTAGTCC	AGCCTTTTCT	TATCTGACGG	ATGCCCTCTA	TGAGGCTATG	900
GACTTTGTTC	GCCAGCTTCG	TGAGAAAAGGA	GAGGCCTGCT	ACTTTACCAT	GGATGCTGGT	960
CCCAATGTTA	AGGTCTTCTG	TCAGGAGAAA	GACTTGAGAC	ATTTATCAGA	AATTTTCGGT	1020
CAGCGTTATC	GCTTGATTGT	GTCAAAAACA	AAGGATTTGA	GTCAAGATGA	TTGCTGTAA	1080

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTCAAAAGCT	CTATGGAAAA	TCCTCTGAGA	AAAGTGTTTG	CCCCCTCTGA	CAACTCAACC	60
TTTTTGAGGA	AGAGTCTCCA	TCTGAGGAAG	ATGGAGATGT	TCCCAGTTGA	AACAGAGGAA	120
ATTACCTACA	AACGTAAGAA	ATCTAAAGGG	AAACGCCAAG	CTCTTCTTGC	CCAATTTGAT	180
TCAGAAGAAG	TTCATCATCA	AGTAGAAGAG	AGGATTTGCC	CTGATTGTCA	GGGAGATCTA	240
AAAGAGATTG	GAGGGAGTCT	TCAAGGACAA	GAATTGGTCT	TTATTCCTGC	GCAATTAAAA	300
CGCATAGATC	ATATCCAACA	CGCTTACAAA	TGCCAAGCAT	GCAGTGATAA	AAATCCGAGT	360
GATAAAATCG	TGAAAGCTCC	TATTCCTAAA	GCCCCCTTAT	AA		402

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

NGCNNAAGCT CGCATATTAT CCTGTACGTC TCCGACATGT ATGGTGCGAC CATCTTGGTA	60
CCATTGATTT TGGGAATGCC TGTATCTGTT GCCCTTTTGT CTCAGGTGT TGGAACACTC	120
ATCTACATGA TTGCTACTGG TTTTAAAGTT CCAGTTTATC TAGGTTCTTC ATTTGCCTTT	180
ATCACAGCTA TGTCACTGGC TATGAAAGAA ATGGGGGGGG ATGTATCTGC TGCCCAAACA	240
GGGGTTATCT TGACTGGTNT GGTCTATGTC CTTGTTGCTA CCAGCATCCG ATNTGTANGA	300
ACAAAATGGA TTGATAAACT CTNN	324

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 918 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACACACGGCT CCCCCTTTGG GCATTTTAT GCTAAAATAG TAGCTATGGA TAAAATTATT	60
AAACTATAT CAGAAAGCGG AGCCTTTCGT GCTTTTGTC TTGATAGCAC GGAAACCGTC	120
CGCACTGCTC AAGAAAAACA TCAAACCAA GCTAGCTCAA CTGTAGCGCT TGGTCGAACT	180
CTTATCGCCA GCCAGATTCT CGCAGCCAAT GAAAAAGGAA ATACCAAAC TACAGTTAAG	240
GTGTTGGGAT CTAGCTCTCT AGGTGCTATT ATCACCGTCG CTGATACCAA GGGGAACGTC	300
AAAGGCTACG TTCAAATCC TGGTGTGAC ATCAAAAAGA CTGCGACTGG TGAAGTCCTA	360

GTCGACCTT	TTGTTGGAAA	TGGTCAATTC	CTCGTTATCA	CAGACTACGG	TACTGGAAAT	420
CCTTACAATT	CTATAACTCC	CCTCATCTCT	GGAGAAATCG	GTGAAGACCT	TGCCTTTTTAC	480
CTTACTGAAA	GCCAACAAAC	GCCTTCAGCG	GTCGGCCTCA	ATGTCCTTTT	GGACGAGGAA	540
GACAAGGTCA	AGGTTGCAGG	TGGTTTCCTA	GTTCAAAGTCT	TGCCAGGAGC	CAAGAAAGAA	600
GAGATTGCTC	GCTTTGAAAA	ACGCATCCAA	GAAATGCCAG	CTATCTCTAC	TCTTCTCGAA	660
AGCGACGACC	ATATCGAAGC	CCTCCTCAAG	ACTATCTACG	GGGACGAAGC	CTACAAGCGT	720
CTTTCTGAAG	AAGAAATCCG	TTTCCAATGT	GACTGTAGCC	ATGAACGCTT	TATGAACGCT	780
CTTGCCAGCC	TTCCAAGCTC	AGACTTACAG	GAAATGAAAG	AGGAAGACCA	CGGGGTAGAA	840
ATCACTTGTC	AATTCTGCCA	AACTACTTAC	AACTTTGATG	AAAAGGACCT	GGAGGAACTC	900
ATTCTGTGACA	AATCTTAA					918

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...606
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TTTTTAGGCT	CTGTCTTTAA	ACGTTTCTTT	TTAGGGATGA	TTGCGACAGC	CTTCTTTTGG	60
CTATTAACTT	TAGCAGGAGG	GATTATCCTT	GGTCTAGCGC	CGGCTAGTGC	CACCTTGATG	120
AGCTTATATG	CAGAACATGG	TTATAGCTTT	CGGGAATACA	GTTTGAAGGA	GGCTTGGTCT	180
CTTTACAAGC	AAAAATTTGT	CTCAAGCAAC	CTGATTTTCT	ATAGCTTTT	AGGTGTGGGT	240
CTAGTTTTGA	CCTATGGTTT	GTATCTATTG	GTGCAATTGC	CTCATCAGAC	CATTGTTTCAT	300
TTGATTGCGA	CCCTTTTGAA	TGTCCTAGTA	GTTGCCCTGA	TCTTTTTTGGC	TTATACAGTA	360
TCTTTAAAAAT	TACAAGTTTA	TTTTGCCTTG	TCCTATCGAA	ATAGTCTCAA	ATTATCCTTG	420
ATTGGCATCT	TTATGAGTCT	AGCAGCTGTG	GCCAAGGTTT	TCCTTGGGAC	TGTGCTACTT	480
GTAGCAATTG	GTTACTATAT	GCCTGCCCTG	CTATTTTTTG	TAGGAATTGG	GATGTGGCAT	540
TTCTTTATCA	GTGATATGTT	GGAACCTGTC	TATGAAATCA	TCCATGAAAA	ATTGGCGACA	600
AAATAG						606

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACACAGCCTT	TAAAACAGTG	TTTAAGTGGG	AAGTATAAGT	CCTGGAGGTT	AATTGTGGAG	60
AAAATCATT	AAGAAAAAAT	TTCTTCCTTA	CTTAGTCAAG	AAGAAGAAGT	CCTCAGTGTT	120
GAACAAC	GTGGAATGAC	CAATCAAAAC	TATTTGGCCA	AAACAACAAA	TAAGCAATAC	180
ATTGTTAAAT	TCTTTGGTAA	AGGGACAGAA	AAGCTTATCA	ATCGACAAGA	TGAAAAAGTAC	240
AATCTTGAAC	TACTAAAGGA	TTTAGGCTTA	GATGTAAAAA	ATTATCTTTT	TGATATTGAA	300
GCTGGCATCA	AAGTAAATGA	GTATATCGAA	TCTGCGATTA	CGCTTGATT	AACGTCAATC	360
AAGACCAAGT	TCGACAAAAT	TGCTCCAATA	TTACAAACTA	TTCATACATC	TGCTAAGGAA	420
TTAAGAGGAG	AATTTGCTCC	TTTTGAAGAA	ATCAAAAAAT	ACGAATCCTT	GATTGAAGAA	480
CAAATTCCTT	ATGCCAACTA	TGAATCTGTT	AGAAATGCAG	TCTTCTCCTT	AGAGAAAAGA	540
CTGGCTGACT	TAGGTGTTGA	CAGAAAATCT	TGTCATATCG	ATTTGGTGCC	TGAAAACCTT	600
ATCGAATCAC	CTCAAGGACG	ACTTTATTTG	ATTGACTGGG	AATATTCATC	AATGAATGAT	660
CCAATGTGGG	ATTTGGCTGC	CCTCTTTTTA	GAGTCTGAAT	TCACTTCCCA	AGAGGAAGAA	720
ACTTTCCTTAT	CTCACTATGA	GAGTGACCAA	ACACCGGTTT	CTCATGAAAA	GATTGCTATT	780
TATAAAATTT	TACAAGATAC	TATTTGGAGT	CTATGGACTG	TCTATAAGGA	AGAGCAAGGT	840
GCAGATTTTG	GTTACTATGG	TGTGAATCGT	TACCAAAGAG	CTGTTAAAGG	TTTGGCTTCT	900
TATGGAGGAT	CAGATGAAAA	GTAA				924

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AACGATAGAT	TTTTGAATAG	GAATAAGATC	ATGTTTGGAT	TTTTTAAGAA	AGATAAGGCT	60
GTGGAAGTAG	AGGTTCCGAC	ACAGGTTCCCT	GCTCATATCG	GCATCATCAT	GGATGGCAAT	120
GGCCGTTGGG	CTAAAAAACG	TATGCAACCG	CGAGTTTTTG	GACATAAGGC	GGGCATGGAA	180
GCATTGCAAA	CCGTGACCAA	GGCAGCCAAC	AAACTGGGCG	TCAAGGTTAT	TACGGTCTAT	240
GCTTTTTTCAT	ACGGAAAACT	GGACCCGTCC	AGATCAGGAA	GTCAAGTTTA	TCATGAACTT	300

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CACACCAGAT	TGTGGCTCTG	GCATGCGTGG	GTTCGATCCC	CATCACTCGC	CTATTTTATA	60
TTGGGGTATA	GCCAAGCGGT	AAGGCAAGGG	ACTTTGACTC	CCTCATGCGT	TGGTTCGAAT	120
CCAGCTACCC	CAGTTACTAT	TTGCCGGCGT	GGCGGAATTG	GCAGACGCGC	TGGACTCAAA	180
ATCCAGTGTC	CGCAAGGACG	TGCCGGTTCG	ACCCCGGCCG	CCGGTATAGT	ATAG	234

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGCTAAGAT	TCAGCGGATT	GAGGCAAGCG	ATGAAGATGA	ATAAGAAATC	AAGCTACGTA	60
ATCAATCGTT	TACTTTTAGT	CATCATAGTA	CTGATTTTAG	GTA CTCTGGC	TCTAGGAATC	120
GGTCTAATGG	TAGGTTATGG	AATCTTGGGC	AAGGGTCAAG	ATCCATGGGC	TATCCTGTCT	180
CCAGCAAAAT	GGCAGGAATT	GATTCATAAA	TTTACAGGAA	ATTAG		225

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGTGATTTAT CCATGTTTCAC AGGAATAATT GAAGAAATCG GAAAAGTTGA AAGAATACAG	60
AAAGACTCTC GTAATTGTAA ACTATCAATT AAAGCCTCAA AAATATTAAC GGATATCCAT	120
TTAGGTGATA GTATAGCAGT AAATGGTATC TGTCTTACAG TTACTCATTT CAATCATCAA	180
TCCTTTACAG TTGATGTAAT GAATGAAACA TGGAGTCGAA CAGCTCTTAC TCTATTAAAA	240
CATGGAAGTG AGGTGAATCT AGAAAGAGCC TTATCTGTCA ACGGTCGACT TGGGGGTCAC	300
GTCGTTACAG GACACATTGA TGGTACAGGA AAAATCTCGT CAATAAAAAA AGATGATAAT	360
GCTGTATGGT ATCAAATCAA CACACAAAAA GAAATTTTAG ATTTAATAGT TGAAAAAGGA	420
TCTATTACAA TTGACGGCAT TAGTCTGACT GTCGCTAAAG TCTCCAAAGT AACTTTTTCA	480
GTATCTGTTA TCCCTCATAC CTTGGAACAA ACCATTCTTA AGAGTAAACA AGTCGGGAGT	540
ACAGTAAATC TTGAAAATGA TATCTTAGGT AAATATGTGC AAAAACTGAT GGATAACTCT	600
CCAAAATCAG AAATATCTAA GGAAC TATTA TATCAAAATG GATTTTAG	648

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACGAGTTTAT	CTAGTTCTAC	ATATCCAACG	TTTATTGTCA	TAAAAATTTA	TTTAAACTA	60
TATAAGGAGA	ATTCTATCAT	GAATAGAGAA	GAAGTAACAT	TGTTAGGTTT	TGAAATCGTA	120
GCCTATGCTG	GCGATGCTCG	TTCAAAACTA	TTGGAAGCCT	TGAAGGCTGC	TGAAGCTGGT	180
GATTTTGAAA	AAGCGGACGC	TCTGGTAGAG	GAAGCTGGTA	GCTGTATTGC	AGAGGCTCAC	240
CACGCGCAAA	CAAGTCTATT	GACTAAGGAA	GCTTCTGGTG	AGGACTTAGC	GTATAGTGTG	300
ACCATGATGC	ATGGTCAAGA	TCACTTGATG	ACAACATATCT	TGTTAAAAGA	CCTAATGCAC	360
CATTTAATTG	AACTTTACAA	GAGAGGAGTT	AAATAA			396

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AAGCCCTTAT	CCGTTTCTAC	AAAGACTGGA	ACCTATATTG	GTAGGAGGAG	AAATATGACA	60
ATGCCAAATA	TTATTATGAC	CCGTATCGAT	GAACGGTTGA	TTCATGGACA	AGGACAACCTT	120
TGGGTAAAAAT	ACCTAGGTTG	TAATACGGTC	ATTGTTGCCA	ATGACGAAGT	AAGCACGGAC	180
AAGATGCAAC	AAACTCTGAT	GAAAACAGTT	GTGCCAGACT	CAGTTGCCAT	GCGTTTCTTC	240
CCTTTGCAAA	AGGTGATTGA	TATCATTCAC	AAGGCTAATC	CTGCTCAAAC	GATCTTTATC	300
GTTGTAAAGA	ATGTGAAGGA	TGCTTTAACC	TTGGTAGAAG	GTGGTGTCCC	TATCAAAGAA	360
ATCAATATTG	GGAACATTCA	CAATGCTACT	GGTAAAGAGC	AAGTGACACG	CTCCATCTTC	420
CTAGGTGAAG	AGGACAAGGT	GGCCCTCAAG	GAATTGAGCC	AAACTCATCA	AGTAACATTT	480
AATACGAAAA	CAACTCCAAC	AGGAAATGAT	GGAGCTGTTC	AAGTCAACAT	TATGGACTAT	540
ATTTAA						546

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GACAGCTTAT	CTGCTCAGTG	CTGGTATCCA	GTCTTTTGGG	ATTGGGGATT	CTCTGGTATC	60
AAGGTGCCTT	GTTTATGGCA	ACGGTGCAAC	TGGTCATCAT	TGCTCTTCTA	CTTTATGGAT	120
TGCACCTTGG	CAGGGATTTC	TACCTTACTA	AGTGTCGTCT	ATCTACTTGG	TTTACAGGAA	180
AATAGTCTGG	TGGATCTATT	GAAAGGGAAA	CTCCCTCTCA	AACGTATGAT	GACATTGATG	240
ATGGTGGGGC	AACTCTTAGC	TGTATTGGTG	GTCCGATCGA	GTGCGACACG	TCTCCTACCC	300
CACTACCGTG	AAATGCAGGA	AATGGAGAGA	GCTAGCAATA	AATGGAGCCA	GTCCCTCAGAC	360
CGTTACCGTC	TATCCTTTGG	TTGGTCTAGT	GCATTTGCCG	ATGAAGAAGG	AACGCGTAAG	420
GATAATCGTG	AGTGGCAGAC	ATTTACTGAA	GAACGGTTAG	CCAATACAGA	CTCTTTTTTAT	480
ATTATGAGCA	ATGTTGACAA	TTTCTCAGAT	GGAGCAGAAG	TGGACCTAGA	TGGCAATCGT	540
CTCAGTGACT	ACACACCGTC	AGGGAATGTT	ATCTATGTCT	CACCGCGCTA	TCTGATAGAA	600
GAAAAGATTA	CCGTTTCTTC	AGAGTTTATG	GACAAGATGC	AAAAC TTGTC	TGAGGGAGAG	660
TTTGGGCTGA	TCTTGCCTGA	GAGCTTGCGA	GAGCAGTCTA	TCTACTACCA	AGGATTGTTT	720
ACAGATTACC	TGCAAACTT	TTCATCTGAA	AGTGTAGAAG	TGACGAGTCA	GAAACACTAC	780
CTCCACAGG	TAAGGCTAGC	TTTTACAGAA	ATAGGACAGG	AACGTTTCCT	CTATAATGAT	840
GGGTACAAGA	CAACACGCCA	GTACCTAAAA	GATCCGATTA	TTGTAGTTCT	AACGCCGCAA	900
GCGACTGGAA	CAAGACCTGT	TGCAGGGATG	TTGTGGGGAA	CTACGGCTAA	TAGTGCCTTG	960
AAACTAGATC	GATATGGAGA	CAGCATCACA	GCTCTAAAAG	AGCAAGGTCT	GTATCACAAG	1020
GTTTCTTACT	TGGTAAAAAG	CCAGCTATTT	TTTGCCAAGG	TACTAAATGA	CAAACGGGTG	1080
GAGTTTACT	CTCTCCTTAT	TGGGACGATT	TTGACCCTGT	CTACGGCTAT	CTTGTTATTT	1140
GATTCCATGA	ATCTTCTCTA	TTTTGAGCAG	TTCAGACGGG	ATCTTATGAT	TAAACGTCTT	1200
GCTGGTATGA	CAATCTATGA	GCTTCATGGC	AAGTATTTAC	TGGCGCAAGG	AGGAGTTCTC	1260
TTGCTTGGCC	TAGTCCTATC	TAGTATTTTG	ACAAGAGATG	GTTTGATTAG	CGCTCTAGTT	1320
GTAGCTTTGT	TTACGCTTAA	CGCCCTCTTG	ATTTTAGTAA	GGCAGGACAA	AAAAGAAGAA	1380
GCTGGTAGCA	TGGCAGTATT	GAAAGGAAAA	TAA			1413

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CAGAAATTAT	CAGTCCCCTGT	CCTAGACACC	ATCAAGCCAG	ATCCCTTCCC	AGAACAATAT	60
TTCCTAGAAA	TTACCAGTCC	AGGCTTGGAA	CGTCCTTTGA	AAACCAAGGA	TGCCGTCGCT	120
GGAGCGGTTG	GAAAATACAT	CCATGTCGGA	CTCTACCAAG	CCATCGATAA	GCAAAAAGGTC	180
TTTGAAGGAA	CTTTGTTGGC	CTTCGAAGAG	GACGAGTTGA	CTATGGAATA	TATGGACAAG	240
ACGCGTAAGA	AAACCGTCCG	AATTCCATAC	AGTTTAGTAT	CAAAAGCACG	TTTAGCAGTT	300
AAATTATAG						309

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AAGAAATTAT	CGGAGGTTAG	CCATATGGCA	TTTGAAAAAA	TCATTCAAGTT	AAAAAATTGT	60
CGTTACGATT	ACACTCTTAG	CCCTTCTGTT	AAAAAATTCA	CCCTCAAAGA	TAACACCTTT	120
TTTGAAACTA	AGGTTGGTAA	CTATGAACTG	ACTCGCCTTT	TGGAAAAAGT	GCCAAACAGC	180
GGTGAAGGCT	TCCAAC TCAA	AATCATCATT	AACAAGGAAC	TTACAGGGGC	TAAAATCAAT	240
ATCACTGACA	AGTTTGGCCT	TCGTCTAGTT	GATATTTTCA	AATCAGAAGA	CCACCATATT	300
CATCAGGAAA	AATTCTACTT	CCTCATGGAT	AGCTTGGTAG	AACGTGGTAT	CTTTACAAAA	360
TCGGAAAGAT	AG					372

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGCGGATTAT	CACTGGCGGA	AAGACCCAGA	ATTAGGTTTT	TTCTCGCACA	TTGTTGGGAA	60
CGGTTGCATC	ATGCTAGGGT	AGGACCTGTT	GATAATGGTG	CCTGGGACGT	TGGGGGCGGT	120
TGGAATGCTG	AGACCTATGC	AGCGGTTGAA	CTGATTGAAA	GCCATTCAAC	TAAAGAAGAG	180
TTCATTAGAC	GGACTACCGC	CTTTATATCG	AACTCTTACG	CAATCTAG		228

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTCTGGTTAT	CCTATCAAAC	TTGCTTGCAA	GACGAGTCGA	TCCAAACTCA	GCTTTGTCTCT	60
AGAAAGGAGG	AGAATATGGC	AAAAAAGAAA	ATTAAAAAAG	AAAAAATTGA	TAATGTCGGC	120
ATTCACTCCT	TCAGTAAGAA	AGCAGATATC	TTCTTCAGTA	TCATTTCCGGG	TTTGATTGCC	180
CTCTCTTGTA	TCCTACCTTT	TGTATTCGTT	ATCATTATTT	CAGTGACAGA	CGAGAAAAGC	240
CTCCTCCAAT	ACGGCTATAG	CTTCTTCCCA	TCCCAATTTG	GCTTAGACGG	TTTTGAGTTT	300
TTGGCACAGT	TTAAGGATAA	AATCCTACAA	GCCCTCTTCA	TCTCTGTCTT	TGTAACCGTA	360
GTTGGGACAT	TGACAAATGT	CTTTATCACA	ACAACCTATG	CCTACGCTAT	TTCACGGACA	420
ACCTTTAAGT	ATCGCAGATT	CTTTACCATC	TTCGTTCTGC	TCAGTATGTT	GTTCAACGCT	480
GGTTTGGTAC	CAGGTTATAT	CATGGTGACT	CGTGTGCTTC	AGCTTGGGGA	TACTGTTTGG	540
GCCTTGATTG	TTCCAATGCT	TCTCTACCA	TTTAACATCA	TCTTGATGCG	TTCTTCTTTC	600
AAGAAGACCA	TTCCAGAAGC	CATTCTAGAA	TCCGCTCGTA	TCGATGGTGC	CAGTGAAGCC	660
CGGATTTTCT	TCCAAATCTG	TTTGCCATTG	TCACTACCAG	GTATCGCAAC	CATCACGCTC	720
TTAACAGCTC	TTGGTTTCTG	GAATGACTGG	TTCAACGCCC	TTCTTTACAT	CAAGAGTGAC	780
AACTTGATATC	CATTGCAATA	TTTGCTCATG	CAAAATCCAAC	AAAATATGGA	CTACATTGCC	840
AAAGCGGTCG	GCTTGACTGG	TCAACTGGGA	GTTGCTCTAC	CGAAAGAAAC	AGGTCGTATG	900
GCCATGGTTG	TGGTTGCAAC	CCTTCCAATC	GCGATTTTGT	ATCCATTTTT	CCAACGCTAC	960
TTTGTAAGAA	GTTTGACTAT	CGGTGGTGTG	AAAGAATAG			999

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...921
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TTATCTCTAT	CATTGTCATC	TCAATCTCTA	TGGTTGCATT	CAAGAAACTA	CACGCATTTG	60
ATATGGAGGA	CGTCTAAGAT	GAATAACTCA	ATTAAACTCA	AACGTAGACT	GACTCAAAGC	120
CTTACTTACC	TTTACCTGAT	TGGTCTATCA	ATTGTAATTA	TCTATCCACT	GTTGATTACC	180
ATTATGTCAG	CCTTTAAAGC	AGGTAACGTC	TCAGCCTTTA	AACTAGATAC	TAATATCGAC	240
CTCAATTTTG	ATAATTTTAA	AGGCCTCTTC	ACTGAAACCT	TGTACGGTAC	TTGGTACCTC	300
AACACTTTGA	TTATCGCCTT	AATTACCATG	GCTGTTCAAA	CAAGTATCAT	CGTACTTGCT	360
GGTTATGCTT	ACAGCCGTTA	CAACTTCTTG	GCTCGTAAAC	AAAGTTTGGT	CTTCTTCTTG	420
ATCATCCAAA	TGGTGCCAAC	TATGGCCGCT	TTGACAGCCT	TCTTCGTTAT	GGCGCTTATG	480
TTGAACGCCC	TTAACCACAA	CTGGTTCCTC	ATCTTCCTCT	ACGTGGGTGG	TGGTATCCCG	540
ATGAATGCTT	GGCTCATGAA	AGGCTACTTC	GATACAGTGC	CAATGTCTTT	AGACGAATCT	600
GCAAAACTAG	ACGGTGCAAG	ACACTTCCGC	CGCTTCTGGC	AAATTGTTCT	TCCACTTGTT	660
CGCCCAATGG	TTGCCGTACA	AGCTCTCTGG	GCCTTCATGG	GACCTTTCGG	GGACTATATC	720
CTCTCTAGTT	TCTTGCTTCG	TGAGAAAGAA	TACTTTACTG	TTGCCGTAGG	TCTCCAAACC	780
TTCGTTAACA	ATGCGAAAAA	CTTGAAGATT	GCCTACTTCT	CAGCAGGTGC	TATCCTCATC	840
GCCCTTCCAC	TCTGTATTCT	CTTCTTCTTC	CTACAAAAGA	ACTTTGTTTC	AGGACTTACA	900
AGTGGTGGCG	ACAAGGGATA	A				921

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1272
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TTGCAACTAT	CGAAGAGAAA	TTGTCAAAAC	GCTAAGGGGA	AGCCTATGTT	AGATGTAGAA	60
GCGATTTCGCA	AGGATTTTCC	AATTTTATAGAT	CAGATTGTCA	ATGATGAACC	TCTGGTCTAT	120
CTGGACAATG	CTGCGACGAC	ACAAAAACCA	CTAGTAGTTC	TGAAAGCTAT	TAACAGTTAC	180
TATGAGCAGG	ACAATGCCAA	TGTTCCACCGT	GGTGTCCATA	CCTTAGCGGA	ACGAGCGACA	240
GCTTCTTATG	AAGCTGCTCG	TGAAACCATT	CGTAAGTTTA	TTAATGCAGG	CTCTACAAAG	300
GAAATTCTCT	TTACCAGAGG	AACGACAACC	AGCCTTAACT	GGGTGGCAGC	CTTTGCTGAG	360
GAAATTCTCG	CTGAGGGAGA	CCGGGTCTTG	ATTTTCAGTAA	TGGAACACCA	TTCTAATATC	420
ATTCCATGGC	AGGAAGCTTG	TCGAAAGACT	GGAGCAGAGC	TTGTCTATGT	CTATCTTAAA	480
GACGGTGCCT	TGGATATGGA	GGATTTGCGA	GCTAAATTGA	CTGATAAGGT	TAAATTTGTT	540
TCCCTAGCTC	ATGCCCTCCAA	TGTTCTTGGT	GTGGTCAATC	CGATCAAGGA	AATCACTCAA	600
TTAGCCCACC	AAGTTGGGGC	AATTATGGTA	GTGGATGGTG	CTCAATCTAC	ACCTCATATG	660
AAGATTGATG	TCCAGGACTT	GGATCTGGAC	TTTTTCGCCT	TTTCGGGTCA	CAAGATGGCT	720
GGTCCGACTG	GTATCGGTGT	CCTTTACGGC	AAAGAAAAGT	ATCTTGAGCA	AATGTCTCCA	780
GTAGAATTTG	GCGGCGAGAT	GATTGATTTT	GTCTACGAGC	AATTTGCTAG	TTGGAAGGAA	840
TTGCCTTGGA	AATTTGAGGC	TGGAACGCCA	AATATGGCAG	GAGCTATTGG	ACTTGCGACT	900
GCAGTTGATT	ATCTGGAAAA	GATTGGTATG	GATGCCGTTG	AAGCTCATGA	ACAGGAATTG	960
ATTGCGTACG	TCTATCCAAA	ACTGCAGGCA	ATTGAGGGAT	TGACCATTTA	CGGTTCTCAG	1020
GATTTGGCTC	AACGTTCCGG	TGTTATTGCC	TTTAACCTAG	GTGATCTCCA	TCCTCACGAT	1080
CTTGCGACGG	CTCTGGATTA	TGAAGGAGTG	GCTGTTTCGTG	CTGGTCACCA	TTGTGCGCAA	1140
CCCTTGCTTC	AGTATTTGGA	AGTCCCAGCA	ACAGCTCGTG	CAAGTTTTTA	TATCTACAAT	1200
ACCAAGGCAG	ATTGCGACAA	ACTAGTCGAT	GCCCTACAAA	AGACAAAGGA	GTTTTTCAAT	1260
GGCACTTTCT	AA					1272

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGATGCTAT	CCGTGAATAC	TATTTTAGAA	AAATTTTATA	AAGAACACCA	AGTCAAACCC	60
TTCATATCGC	CTGAACGAGA	GTTGGATACT	TGGCTTCTAA	GTCCCAAGCC	CGTTCCCAAG	120
CGAAATATGG	ACTTATTAGT	AGATGATTCA	CTAGCAGGAG	ATATCATTTT	ACTATGGAGA	180
ATCCAGTTTG	GTACTTTTAC	CACTGAAACA	TGA			213

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACTCTTATAT CTAATTCATT CAACATTGAA GCAAGTGTGA GAGATGCTGA TGTGGTGATT	60
GGAGCCATTC TCATCCCTGG TGCAAAAGCA CCGGAATTGG TGACAGATGA GATGGTCAAA	120
CAAATGCGTC CAGGCTCTGT ATCGTTGACC TTGCTGTTGA CCAAGGTGGC CTTATCGAAA	180
CAGCTGACCG TGTGA	195

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TTGGAGAGAT TAGCAAAATC CCTTGGTATT GCCTATTTCA CTGCCAACCA GCTTGAAGTC	60
AAAGAAGGTC TTTTAACAGG AAAATTAGTT GGACAAATTA TAAGTCCCCA GGTCAAAAAA	120
GAAACTCTGG AAAAATGGAG AAAGAACTA AAACTTTCTA AAGAAAGAAC GGTGGCAATC	180
GGTGATGGGG TCAATAATCT ATTAATGTTG AAGTCGGCGG AGTTAGGAAT CGCCTTTTGT	240
GCCAAAGAAG TGCTCAAAAA AGAAATACCA CATCATGTTG ACAAGAGGGA TTTTTTAGAA	300
GTTCTTCCTT TGATTGACTG TTTAGAATGA	330

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCATCTGTAT CTGTAAAGTG GGTATCAATA GCGTCACGAG TTGTTCCAGC AACAGGACTG	60
GCAATAACAC GGTCTTCGCC CAAGATAGCA TTGATCAAGC TTGATTTTCC AACGTTTGGA	120
CGACCAATCA GGCTAAACTT AATGACATCT GGATTTTCTT CCTCATATTC ATTTGGAAGA	180
TTTTCTACGA TAGCATCTAG TACATCCCCT GTACCGATTG CATGGACAGA TGAGATAGGC	240
AGTGGTTCAC CCAAACCGAG AGCATAG	267

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 609 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...609
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAGGGAGTAT CCGCCATGAC AAGAACTGAA TACCTGACTC AGCTAGAACT CTATCTCAAG	60
AAACTACCTG AAGCTGACCG TATCGAAGCC ATGGACTATT TCAGAGAGCT CTTTGACGAT	120
GCTGGAGTCG AAGGAGAAGA AGAACTCATC GCTAGTTTGG GAACTCCCAA AGAAGTGGCC	180
CACGAAGTTC TATCCAATCT TCTCGATAAA AAAATCAATG AAGCACCCGC TCAAAAAAAT	240
AACCGACAAA TTTTACATAT CGCCTTGTTA GCCCTCCTTG CAGCACCTAT CGGCATTCCCT	300
CTGGGAATCG CCATCCTCGT GACCCTGTTT GCAATCCTTG TAGCCGCTTT GACTGTTCATT	360
CTGGCTTTCT TTGCAGTTTC CATACTGGGT ATCATCGGCG GATTCCTATT TTTAGTTGAA	420
AGTTTCACTG TCCTCGCCCA AGCCAAATCA GCCTTTATCT TGATTTTGG TTCTGGTTTA	480
CTGGCTATCG GTGCTTCTTC GCTAGTTTGA CTAGGCATTT CCTATGTAGC TCGCTTCTTC	540
GGTCTACTCA TTGTTCGTCT GGTACAATTT GTTCTTAAAA AAGGAAAGAG AGGTAATCAG	600

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AAATTGGTAT	CTTCTTGTC	GTCTGTGTAT	GCTACAAGAG	CTAGTTTCTT	GGATGGACAG	60
GGAATTACAG	TTGATGAGAT	GGCTTGGATA	ATTAGGGGCA	TTGTGAATGC	ATTGATTGGT	120
AGATACATAA	AATTAGGTAC	TTATGCGGCT	AAGTATGGTA	TTAGTATGGC	GCGTTCCTATC	180
TTAAATAGGG	CAGCTGCAAC	TGCGGCAGCA	AGAGTAGGAT	TATTGACTAA	GATTTTTTGA	240
TGGATTTTAC	GAATAGCTGT	GCTCGCAGCT	GATGTATATG	GTAATTTTGC	CAACAATATT	300
GCTGTAGCTT	GGGATGCACA	TGATAAAATC	CCTAACAATG	GTCGTATAAA	CTTTTAA	357

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AACGTGGTAT	CTTTACAAAA	TCGGAAAGAT	AGAGCCAAAA	TGTTTGAAC	TGTTTGAAC	GACCTATAAG	60
GACTGCTATC	ATGTAGAGCG	TACTCTCAAG	TATGAGGATC	ATGAGGCTCT	CATGTTGACT		120

TTGTCAGGAT GTTGTACACC TTACCNAGAT ACACTTTATG TGACTTCTCT GACTTTTAGG	180
GGCCAAAAAAG TTTATCAGGG TCTGTCGGAG ACCTCTACCG TTTTCTATCT C	231

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATAATTTTCAT CAAAATTATT ACCCAATGTT ATTTTACCTA GGTTAATTAT TTTTTCGGTG	60
ATGTACACCA ACTCCAAAGG AACGTTAATA AACATCTCTG TAAAACGGGT CATATTATCT	120
CTATTTTTGA GAAAAAACT TTTCTCAATA TCAATTGGAT TTACTTTATC TCCAGTTTTT	180
CTTCCAAAAG CTATTCCCCT TCCAAAAAGA AGAATATCGA TATCTTTTTT ACTTTGCGCA	240
ATTACGGCAT TGTGGTTTAG TATTCGTTTT ATGATCATAA AATTTCCTT TTAA	294

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCAATTTTCAT CACGGGTCAT CTTTTTCATCC GCATCATCGA ATGACATAGG AGTCAAATGG	60
CTCAAGAAAT TGGTCGAAGC AGCTAAAAGC CAAACAAAAG GACTGACTAG TTTTCCGATC	120

CCAATGATAA CCGGCGCTGT ACGAATTCGC AAGGCATCCT TTAGATTAAG AGCGATTCTC	180
TTAGGATATA ATTCCCCAAA AACGATGGAA ATATAG	216

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACATATTCAT CGTCTCAAGA AAAACAGTCT GATTGGAAAG TACAATACAC TCGTTGTCTT	60
GATATCATCT TTCCTGAGTT GGATAAAATC GTTGGAAAGC ATTCAGAATA TACCTACCAA	120
CTCTTGACAC GCTACCCTAA TCCTCAGAAA AGGATTGAGG CAGGATTTGA TAAGCTGATA	180
GAAATTAAGC GATTGACCGC TTCTAATTCA AGGGCTTTTT GCCGTGCTCT AAAATCATCG	240
CCAAATCATC AAATTGAAAT AAGAAATAGT TTAGATAAAA CTATTGACTT TTCTTATAGT	300
TTGTCTTTCT CTTAA	315

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TTCAATTCAT CATCTTTGCA CTTGGAGTTC TTCTATACAT TCCATTTATC AAAGTTAATG	60
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ACAAAGTTGT	TGAACAAGAA	ATGGAAGGTT	AAGATTATGA	AACAAATTTT	ATTAGTATGT	120
AATGCGGGAA	TGTCGACAAG	TATGCTTGTT	AAAAAATGC	AACAAAGTGC	GACTGAACGT	180
GGGATTGAAA	TCTCTATCCA	AGCAAAATCA	ATGACAGAAG	CTAAAAAGAA	TATCCATGAA	240
GCAGATGTCA	TTCTAATTGG	GCCACAAATT	CGTTATGAGT	TACTTGCTGT	GAAAGAAATT	300
GCAGGAAATA	TCCCTGTAGA	TACCATTGAT	ATGCGGGATT	ACGGAATGAT	GAATGGAGCA	360
AAAGTTCTGG	AACAAGCACT	TGCATGGATA	GGAGAAATAA	GATGA		405

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...702
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACTCTATCAT	CAAACTCTAG	ACTTAATCGA	TCATACTCAA	GAGGAGGTAA	TCCAATGAAC	60
ACTAGTCTTA	AACTCAGCAA	ACAACTCAGT	TTTGGAGAGG	AGATTGCTAA	TAGCGTGACC	120
CATGCTGTGG	GTGCAGTCAT	CATGCTTATC	TTGCTGCCTA	TTTCATCCAT	CTATAGTTAT	180
GAAGCACACG	GATTTTATC	CTCTATCGGC	GTTTCCATTT	TCGTCATCAG	TCTCTTTCTC	240
ATGTTCCAT	CATCCACCAT	TTATCACTCT	ATGGCCTATG	GTTTCGACCA	CAAATATGTC	300
TTGCGAATCA	TTGACCATTC	TATGATTTAC	GTTGCCATTG	CCGGCTCATA	CACGCCCGTT	360
GTCTTGACCT	TGATGAATAA	CTGGTTTGGC	TATCTGATTA	TTGTCATCCA	TTGGGGAACG	420
ACCATCTTTG	GTAATCTCTA	TAAATCTTT	GCTATAAATG	TCAATGATAA	ATTTAGCCTT	480
GCTCTTTACC	TGATTATGGG	CTGGTTGGTT	CTGGCTATCA	TTCTTGCCAT	TATCAATCAA	540
ACGACACCCG	TTTTCTGGAG	TCTCATGGTA	ACTGGCGGAC	TCTGTTATAC	AGTTGGAGCT	600
GGATTTTATG	CCAAGAAAAA	ACCTTATTTT	CACATGATTT	GGCATCTCTT	TATCCTAGCT	660
GCGTCCGTAC	TCCAATACAT	CGTATTGTT	TATTACATGT	AA		702

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGCAATCAT	CGCTTTATAT	TATTTTTTCAA	GGAGGAAGAA	TGAAAATTTT	ACCGTTTATA	60
GCAAGAGGAA	CAAGTTATTA	CTTGAAGATG	TCAGTTAAAA	AGCTTGTTCC	TTTTTTTAGTA	120
GTAGGATTGA	TGCTAGCAGC	TGGTGATAGT	GTCTATGCCT	ATTCCAGAGG	AAATGGATCG	180
ATTGCGCGTG	GGGATGATTA	TCCTGCTTAT	TATAAAAATG	GGAGCCAGGA	GATTGATCAG	240
TGGCGCATGT	ATTCTCGTCA	GTGTACTTCT	TTTGTAGCCT	TTCGTTTGAG	TAATGTCAAT	300
GGTTTTGAAA	TTCCGGCAGC	TTATGGAAAT	GCGAATGAAT	GGGGACATCG	TGCTCGTCGG	360
GAAGGTTATC	GTGTAGATAA	TACACCGACG	ATTGGTTCCA	TTACTTGTTT	TACTGCAGGA	420
ACTAATGTTT	ATGGTGCCCT	GGTGTCAAAG	TAA			453

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 843 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TCGTCGTCAT	CGCCGATTGT	GAGGAGTTTA	GGAGGAAATA	TGACCCAGGA	TTTACAGAAA	60
AGAACCTTGT	TTGCAGGGAT	TGCCCTGGCT	ATTTTCCTAC	CAATTTTAAT	GATTGGGGGC	120
CTCTTGCTTC	AGATAGCAAT	CGGAATCATA	GCCATGCTAG	CCATGCATGA	ACTTTTGAAG	180
ATGAGAGGTC	TAGAGACCAT	GACGATGGAG	GGCCTCTTGA	CCCTCTTTGC	AACCTTTGCA	240
TTGACCATTC	CCTTGAGAGAA	TTACCTGACT	TTTTTGCCAG	TTGATGGGAA	TGTGGTTGCC	300
TATAGTGTTT	TGATTTCAAT	CATGTTAGGA	ACGACCGTTT	TTAGCAAGTC	TTATACGATT	360
GAGGATGCGG	TTTTCCCTCT	TGCTATGAGC	TTCTACGTGG	GCTTTGGATT	TAATGCTTTA	420
CTAGATGCTC	GTGTTGCAGG	TTTGGACAAG	GCTCTCTTAG	CCTTGTGTAT	CGTCTGGGCG	480
ACAGACAGTG	GTGCCTATCT	TGTTGGGATG	AACTATGGGA	AACGAAAGTT	AGCACCAAGG	540
GTATCGCCTA	ATAAAACCCT	TGAGGGTGCC	TTGGGTGGTA	TTTTAGGAGC	AATTTTAGTA	600
ACCATTATCT	TTATGATAGT	TGACAGTACA	GTTGCTCTTC	CATATGGAAT	TTACAAGATG	660
TCAGTCTTTG	CTATTTTCTT	TAGCATTGCT	GGACAATTTG	GTGATTTACT	AGAAAGTTTCG	720
ATCAAACGTC	ATTTTGGTGT	TAAGGATTCT	GGGAAATTTA	TCCCTGGACA	TGGTGGTGTT	780
TTGGATCGTT	TCGATAGTAT	GTTGCTTGTA	TTTCCAATCA	TGCACTTATT	TGGACTCTTT	840
TAA						843

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AGCAATGGAT TGAAGCTCCA TGTGTCGGCG GTTCGATTCC GTCTCGCGCC ATTTATATAT	60
TTTGGAAGGG TAGCGAAGAG GCTAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTTCG	120
GGGGTTCGAA TCCCTCCCCT TCCATTTTAC GGGCATAGTT TAAAGGTAGA ACTAAGGTCT	180
CCAAAACCTT CAGTGTGGGT TCAATTCCTA CTGCCCCTGT TAATAGAATT ATGGCGGGTG	240
TGGTGA	246

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...420
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CCATTTCCAT CAATCCCCGC AATACCAACA ATCTCTCCAG CACGAACATC CAAGGACAGA	60
TTTTTAACAG CTGGAACACC ACGGTTTTCA TTGACCACCA AATCTTTGAT AGACAAAACC	120
ACTTCTTTTG GTTTAGAGGC TTGCTTCTCT GTTTTAAAGG AAACAGAACG TCCTACCATC	180
ATTTCCGCCA AATCAGCATT GGTAGCCCCCT GCAATTTCAA CGGTTTCAAT TGATTTCCCA	240

CGACGGATAA	CTGTAACACG	GTCAGAAACT	GCGCGAATTT	CATCCAATTT	GTGGGTAATC	300
AAGATAATTG	ATTTTCCTTC	TTTGACAAGA	TTTTTCATAA	TAGCCATCAA	CTCATCAATT	360
TCTGATGGAG	TCAAAACAGC	CGTTGGTTCG	TCAAAGATAA	GGATATCAGC	CCCCCTATAA	420

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...507
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACGCTGCCAT	CCGTGCAGTT	GTTTCGTCAAG	CAATTTTCAGA	AGGAATGGAA	GTGTTTGGTA	60
TCTATGACGG	ATATGCTGGT	ATGGTTGCCG	GTGAAAATTC	ATCCCCTAAA	TGCAGCTTCA	120
GTAGGGGACA	TCATTTCTCG	TGGTGGTACT	TTTCTTCACT	CAGCTCGTTA	TCCAAATTTT	180
GCTCAACTTG	AAGGGCAACT	TAAAGGGATT	GAGCAATTGA	AAAAACACGG	AATTGAAGGT	240
GTAGTTGTTA	TCGGTGGTGA	CGGATCTTAC	CACGGCGCTA	TGCGTTTGAC	TGAACATGGC	300
TTCCCAGCTA	TTGGTCTTCC	AGGTACAATC	GATAACGATA	TCGTTGGTAC	TGACTTTTACA	360
ATCGGTTTTG	ACACAGCGGT	TACTACTGCC	ATGGACGCTA	TCAATAAAAT	TCGTGATACA	420
TCATCAATTC	ACCGTCGTAC	TTTTGTAATC	GAATTTATGG	GACGTAACGC	TGGTGATATC	480
GCTCTTTGGG	CTGGTATTGC	AACTGGT				507

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AATACTACAT	CTGGAGGTAC	TCCCATGCTT	TATGTGGGCA	TTGATGTCGC	TAAAAATAAA	60
CACGATGTTA	CAGCCTTGAA	TGTTCCAGGA	AAAACCTGTC	TTAAACCACT	CACTTTTTTCA	120
AATAATAAAG	CTGGTTTTGA	ACTCTTAGAT	CTGTCTCTTC	GACAACTCAA	CCAAGACTGT	180
CTCATCGCTC	TTGAAAATAC	CGGACATTAT	GCCTTTAATC	TACTGAACTT	CCTGCATGAA	240
CAAGGATATA	AAGTTTACAC	CTACAATCCT	TTGCTCATCA	AGGAATTTGC	CAAATCATT	300
TCACTTCGCA	AGACTAAAAC	GGATAAGAAA	GACGCTCATG	GCATCGCTCT	TAAACTTCTT	360
TCTGACCCCA	ATCGTGAACA	ATTTC AACAC	GATAATCGGC	AAGTAGAACT	AAAAATACTG	420
GCTAGACATA	TTCATCGTCT	CAAGAAAAAC	AGTCTGATTG	GAAAGTACAA	TACACTCGTT	480
GTCTTGATAT	CATCTTTCCT	GAGTTGGATA	AAATCGTTGG	AAAGCATTCA	GAATATACCT	540
ACCAACTCTT	GA					552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGGAAAACAT	CAATGGTAGA	CATGCTTACA	GAGGATGACT	TTAAAGAATT	GACCAAAGTT	60
AAAACCTGTA	GAGAAATTTG	TTGTCGATTT	TTTGATTCAA	AAGGTAAAGA	AGTCTATGAA	120
AACTTACAGG	AAAGAACGAT	AGCAATCTCT	TTGGAAGATT	TAAAAAATAT	TCCTCAAAGT	180
TTAGCTGTTG	CTTACGGTGA	TACGAAAGTA	TCTTCGATTC	TTTCTGTCTT	GCGTGCTAAT	240
TTAGTAAATC	ATTTGATTAC	AGATAAAAT	ACAATTTTAA	AAGTTTGGGA	AGAAGATGGT	300
GATTTGACTT	TTAGAGAGAT	TCTAGGTGAG	TGA			333

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTTTGGGCAT	CAATTTCTTT	GATAATACGA	GCTGGAACAC	CTGCTACTAC	CACGTTTTCT	60
GGGACATCTT	GGGTAACAAT	AGCTCCTGCT	GCGACAACCTG	AACCACTACC	GATTTGGACT	120
CCTTCGATAA	CCACTGCATT	AGCACCGATA	AGAACATTGT	CTCCGACACG	GA CTGGTTCA	180
GCACTAGCTG	GCTCAATCAC	ACCTGCCAAA	ACTGCACATG	CACCAACGTG	GCTATTTTAT	240
CCAACGATGG	CACGGCCACC	AAGGATGGCA	CCCATGTCAA	TCATGGTTCC	AGCACCGATT	300
TCAGCACCGA	TATTGATAAC	AGCTCCCATC	ATGATAACAG	CATTGTCACC	AATTTCCACC	360
TGGTCACGGA	TAATAGCACC	TGGCTCGATA	CGAGCGTTGA	TAGCACGCTT	ATCTAGCAAA	420
GGAAGTGCAG	AATTACGAGC	ATCTTGCTCG	ACAACATAA			459

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 555 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

ATCAAAGGAT	TGATAAATCA	GAAAGAAGGT	GATTTTTTGC	GAACATACGA	AAATAAAGAA	60
GAAGTAAAAAG	CTGAGATAGA	GAAAACATTT	GAGAAAATATA	TTT TAGAATT	TGATAATATT	120
CCAGAAAAATT	TAAAAGATAA	GAGAGCTGAT	GAAGTTGACA	GAAGTCCAGC	AGAAAACCTT	180
GCTTATCAGG	TTGGTTGGAC	CAACTTGGTT	CTTAAATGGG	AAGAAGATGA	AAGAAAGGGG	240
CTTCAAGTAA	AAACACCATC	GGATAAATTT	AAATGGAATC	AACTTGGTGA	ATTATATCAG	300
TGGTTCACAG	ATACCTACGC	TCATTTATCT	CTGCAAGAGT	TGAAAGCAAA	ATTAAATGAA	360
AATATTCAAT	CTATCTCTGC	AATGATTGAT	TCGTTGAGTG	AGGAAGAATT	ATTTGAACCG	420
CATATGAGAA	AGTGGGCTGA	TGAAGCGACT	AAAACAGCGA	CTTGGGAAGT	GTATAAGTTT	480
ATTCATGTAA	ATACGGTTGC	ACCTTTTGGG	ACTTTCAGAA	CTAAAATCAG	AAAATGGAAG	540
AAGATAGTAT	TATAA					555

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GATATGGGAT	TATTTGACCG	TCTATTCGGA	AAAAAAGAAG	AACCTAAAAT	CGAAGAAGTT	60
GTAAAAGAAG	CTCTGGAAAA	TCTTGATTTG	TCTGAAGATA	TTGAGCCTGC	CTTCACAGAA	120
GCTGAGGAAG	TTTCTCAAGA	AGAAGCAGAG	GTTGAAAGTT	CTGAAGAATC	TGTGTTCCAA	180
GAAGAGGATA	GTCAAGACAC	AGTCGAAGAA	AATCTGGATT	TAGAGCCAGT	TGTAGAGGTT	240
TCTCAAGAAG	AAGTAGAAGA	ATTTCCAAAC	TCACAAGAAG	TCACAGAGGA	AGAGAAGCTT	300
GAGCACGAAG	GAACTGTAGA	AGAAAATAAT	TTTGAAGTGC	TTGAACCAGA	AGCTCCTCAA	360
ACAGAAGAAA	CTGTTCAAGG	AAAATATGAC	CGCAGTCTTA	AGAAAACTCG	CACAGGTTTC	420
GGTGCCCGCT	TGAATGCCTT	CTTTGCTAAC	TTCCGCTCTG	TTGACGAAGA	ATTTTTTCGAG	480
GAACTGGAAG	AACTGTTGAT	TATGAGTGAT	GTTGGTGTCC	AAGTCGCTTC	TAACCTAACG	540
GAGGAACTAC	GTTACGAAGC	CAAGCTTGAA	AATGCCAAGA	AACCTGATGC	ACTTCGTCGT	600
GTCATCATTG	AGAAATTGGT	TGAGCTTTAT	GAAAAGGATG	GTAGCTACGA	TGAAAGCATC	660
CACTTCCAAG	ATAACTTGAC	AGTTATGCTC	TTTGTTGGTG	TGAATGGTGT	TGGGAAAACA	720
ACTTCTATCG	GAAAAGTAGC	CCACCGCTAC	AAACGAGCTG	GTAAGAAGGT	CATGCTGGTT	780
GCAGCAGATA	CCTTCCGTGC	GGGTGCAGTA	GCTCAGCTAG	CTGAATGGGG	CCGACGAGTA	840
GATGTTCCAG	TAGTAACTGG	ACCTGAAAAA	GCTGATCCAG	CCAGCGTGGT	CTTTGATGGT	900
ATGGAACGTG	CCGTGGCTGA	AGGTATCGAT	ATTCTCATGA	TTGATACTGC	TGGTCGTCTG	960
CAAAATAAGG	ATAACCTTAT	GGCTGAGTTG	GAAAAGATTG	GTCGTATTAT	CAAACGTGTT	1020
GTGCCAGAAG	CACCACATGA	AACCTTCTTG	GCACTTGATG	CATCAACAGG	TCAAAATGCC	1080
CTAGTACAGG	CCAAAGAATT	TTCGAAAATC	ACACCTTTAA	CGGGAATTGT	TTTGACTAAG	1140
ATTGATGGAA	CTGCTCGAGG	AGGTGTGGTT	CTAGCCATTC	GTGAAGAACT	CAATATTCCT	1200
GTAATAATTGA	TTGGTTTGG	TGAAAAAATC	GATGATATTG	GAGAGTTTAA	CTCAGAAAAC	1260
TTCATGAAAG	GTCTCTTGA	AGGTTTAATC	TAA			1293

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TATGCGGGAT TACGGAATGA TGAATGGAGC AAAAGTTCTG GAACAAGCAC TTGCATGGAT	60
AGGAGAAATA AGATGACAGA AGAAATGGAA TATATCTGTT TTCAGCTCAT TGCCAATAGT	120
GGAGCAGCCA AATCATCCTT TATTGAAGCC ATCCAAC TAG CTAAGGCAGG AAATTTAAAA	180
GAAGCGAAAA TTAAAGTTGA AGAAGCGGAA GACTCCTTAG TAGAAGCGCA CAAGATTCAC	240
TCTAATCTCA TACAAAAAGA AGCTACTGGA GAAAAAATAG GATTCTCCTT GCTATTTATG	300
CATGCAGAAG ACCAAATGGC TTCAACAGAG ATTATTCAGT TGCTATCTAA AGAATTCATC	360
GATCTCTATC AAAATAAATA G	381

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CACCTCAAAT CAAGCAATCT GCTAACTATG ACAAGGAAAA TTTTCAAAAC CGTCAACAAA	60
TCCGTAGAAG CCGGCTTTTA CCAAGCTATC TTAGATGCTG TATCTGACTT GCTTGCAAGC	120
TCAAAAATA CCATAACAAT TTTGGATATC GGTTGTGGTG AAGGATTCTA TTCTCGCAAA	180
CTACAAGAAA GTCACCTCTGA AAAAAGTTTC TATGCCTTTG ACATCTCCAA AGATTCAGTC	240
CAAATCGCTG CTAAAAGTGA ACCCAACTGG GCAGTCAATT GGTTCGTTGG CGACTTGGCA	300
CGCCTTCCTA TAAAAGACGC TAGCATGGAT ATCCTGCTTG ATATCTTCTC ACCTGCCAAC	360
TATGGAGAAT TTCGTCGCGT TTTATCCAAA GATGGTATCT TGATAAAGGT TATCCCAACT	420
GAAAATCACC TCAAAGAAAT CCGTCAAAGA GTACAGGACC AGCTGACAAA CAAGGAGTAT	480
TCTAACCAAG ATATCAAGGA GCATTTCAG GAACACTTTA CCATCCTATC TAGTCAAAC	540
CGCTCTCTGA CTAAGACTAT CACAGCAGAA AACTCCAAG CCTAA	585

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACCATCAAAT CTAGTACAAA AAGAGAAAAT ATCCTCCTTT TCATTACCTT ACTTGCCTTA	60
AAGATTCTGT TTAATAGAAC CTTTATCGTA GTATCTACAC AAATTTTAT CAAAAAGATA	120
AGAGCCAATA CACCTGCTGC TGCACCAATA AGCCAACTC CAAGGCCTCC AACCTTAATA	180
TAG	183

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTTACAAAT CCAGTCAAAT CACTCTCCTG ATAGGCGGTC CAAACTTGCA GTGTCGTGGT	60
TCCTTTTATA TAGGCTTATG TGCTTTCTGG GATTCCAAAC CATTCCTGGCA AATCCTTCAA	120
AACCTCAGCG ACAACTGCCT TTTTGTGATT TTACATCTTG ACTTCTTCAA TTACAAACAT	180
CATAAGTTCC TTTCTTGA	198

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TTTATAAAAT CTTATTTTTC TGTCAAGGCT GCAAGTTGTG GAAGAACCTT ACCTTCAAGA	60
AGTTCATTG ATGCTCCACC ACCCGTACTA ATCCATGAGA ACTTGTCTGC ACGGCCAAGG	120
TTAATCGCTG CGGCAGCTGA GTCACCACCA CCGATGATTG ATTTAACTCC TGGTTGTTTC	180
ACGATAGCGT CCATCACACC GATTGTACCA GCTTGGAAAT CTGGGTTTTC AAATACACCC	240
ATAGGTCCGT TCCATACAAC TGTTTTGGCA CCAGTCAAAG CTTCGTCAA TTTGGCGATA	300
GATTTTGGAC CGATGTCAAG ACCAAGGAAG CCTTCAGAAA CTGCTTCACC TTCAGTGTC	360
CGCACTTCAG TGTA	375

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AAAATAAAAT CGGAGGAAAT CCAAATGATT AAAATTCTTG CTGCCTGCGG TGCAGGTGTT	60
AACTCAAGTC ACCAAATTAA AAGTGCTCTA GAAGAAGAAC TTTCAAACCG TGGTTATGAT	120
GTTCACTGTG ATGCAGTCAT GGTGAAAGAT GTAAACGAAG ACCTTATGAA AGGTTACGAT	180
ATCTTTACAC CAATCGCTGC AACAGACCTT GGTTTTGAAC CAGGTATCCC AGTTATCGAA	240
GCTGGACCAA TCTTATTCCG TATCCAGCA ATGAGCGCTC CAGTATTGA CAATATTGAA	300
GCAGCTATTA AAGAACACGG ATTAAGCTAA	330

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AAAATAAAAT CGGAGGAAAT CCAAATGATT AAAATTCTTG CTGCCTGCGG TGCAGGTGTT	60
AACTCAAGTC ACCAAATTAA AAGTGCTCTA GAAGAAGAAC TTTCAAACCG TGGTTATGAT	120
GTTCACTGTG ATGCAGTCAT GGTGAAAGAT GTAAACGAAG ACCTTATGAA AGGTTACGAT	180
ATCTTTACAC CAATCGCTGC AACAGACCTT GGTTTTGAAC CAGGTATCCC AGTTATCGAA	240
GCTGGTCCAA TCTTATTCTG TATCCCAGCA ATGAGCGTTC CAGTATTTGA CAATATTATA	300
CTTCCTGCGA AACAAAATAT GGTATAG	327

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCACAAAAT CCGCTTGGGA AACCAAACGG ATTTTTTACG TGTCAAAGCA TTTGCCAGAA	60
AAAGTCAATA ATATAGGTCA GACCGTAGGT ATAAACCACG AGGGTAAAGG GTTTGGTCAG	120
AATGATGATG GTCATGTAGC GCTTGAAACT CATCTTGGTC AGGGCAGCCA GCATACAGAG	180
AAAGTCAGCT GGGCTAATGG GCCAAATCAT CATAAAAATA AAGAAGCGGT CAAAACGATT	240
GCCCTTATCT AG	252

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTACCGAAAT CACGGAGATT TCCACGAAAA CTGTATCAAC ACCATCGGGA AAGACTTGGT	60
CAACTTGGTA GACCTTCGCT ATTTAGAAAT CGGGGGAAAT TTATTCCGCG CGGTGGCATG	120
TCAATCGACC CCTATTACAA TTACGGTAAG CAAGGAAATA AGTATGAGGN CTTGGCAGAA	180
CAACGCGTTT TCCAACACGA CGTTTATCCA GAGAAAATTG ACAACCGCTA A	231

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

AAAAGGAAAT CGATTATGAA ATTTCTTGAA TTAAATAAAA AACGTCATGC GACTAAGCAT	60
TTTACTGATA AGCCTGTTGA TCCCAAAGAT GTGCGTACGG CTATCGAAAT TGCAACCTTG	120
GCGCCAAGCG CCCACAACAG CCAGCCTTGG AAATTTGTGG TGGTACGTGA GAAAAATGCT	180
GAACTGGCAA AGTTAGCTTA TGGTTCCAAT TTTGAACAGG TATCATCAGC GCCTGTAACC	240
ATTGCCTTGT TTACAGATAC GGACTTAGCC AAACGTGCTC GTAAGATTGC CCGTGTGGT	300
GGTGCTAATA ACTTTTCTGA AGAGCAACTT CAATATTTTA TGAAAAATCT GCCAGCTGAG	360
TTTGCCCGTT ACAGTGAGCA ACAAGTCAGC GACTACCTAG CTCTCAATGC AGGTTTGGTT	420

GCCATGAACT	TGGTTCCTGC	ATTGACAGAC	CAAGGAATTG	GTTCTAACAT	TATTCTTGGT	480
TTTGACAAAT	CAAAAGTTAA	TGAAGTTTTG	GAAATCAAAG	ACCGTTTCCG	CCCAGAACTC	540
TTGATCACAG	TGGGTATATAC	AGACGAAAAA	TTGGAACCAA	GCTACCGCTT	GCCAGTAGAT	600
GAAATCATCG	AGAAAAGATA	G				621

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1620
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AAAGAGGAAT	CTATGTCTAC	GAAATATATT	TTTGTAACCTG	GTGGTGTGGT	ATCGTCTATT	60
GGGAAAGGGA	TTGTGGCAGC	GAGTCTAGGC	CGTCTCTTGA	AAAATCGTGG	TCTCAAAGTA	120
ACCATTCAAA	AGTTTGACCC	TTATATCAAT	ATTGATCCGG	GAACCATGAG	TCCTTACCAG	180
CACGGGGAAG	TTTTTGTGAC	AGATGACGGA	GCTGAGACAG	ATTTGGACTT	GGGTCACTAT	240
GAACGTTTCA	TCGATATCAA	TCTCAACAAA	TATTCCAACG	TGACAACTGG	GAAAATTTAT	300
AGTGAAGTTC	TTCGTAAAGA	ACGCCGTGGA	GAATACCTTG	GGGCAACTGT	TCAAGTCATT	360
CCTCATATCA	CAGATGCTTT	GAAAGAAAAA	ATCAAGCGTG	CCGCTCTAAC	GACCGACTCT	420
GATGTCATTA	TCACAGAGGT	TGGTGGAACA	GTAGGAGATA	TCGAGTCCTT	GCCATTCCCTA	480
GAGGCTCTTC	GTCAGATGAA	GGCAGATGTG	GGTGCGGATA	ATGTCATGTA	TATCCATACA	540
ACCTTGCTTC	CTTACCTCAA	GGCTGCTGGT	GAAATGAAAA	CCAAACCAAC	CCAACACTCT	600
GTCAAAGAAT	TGCGTGCTTT	GGGAATCCAA	CCAAATATGT	TGGTTATTCTG	TACAGAAGAG	660
CCAGCTGGTC	AAGGAATTAA	AAATAAACTG	GCCCAGTTCT	GTGATGTGGC	ACCAGAAGCC	720
GTTATCGAAT	CGTTGGATGT	TGAACACCTT	TACCAAATTC	CACTGAACTT	GCAGGCACAA	780
GGGATGGACC	AAATTGTTTG	TGATCATTTG	AAATTAGACG	CACCAGCAGC	GGATATGACA	840
GAATGGTCAG	CCATGGTGGA	CAAGGTCATG	AACCTCAAGA	AACAAGTTAA	GATTTCCCTT	900
GTTGGTAAGT	ATGTGGAGTT	GCAAGATGCC	TATATCTCAG	TGGTCGAAGC	CTTGAAACAC	960
TCTGGCTATG	TCAATGATGT	AGAAGTTAAA	ATCAATTGGG	TCAATGCCAA	TGATGTGACA	1020
GCAGAGAATG	TAGCAGAACT	CTTGTCTGAT	GCGGACGGGA	TCATCGTACC	AGGTGGTTTT	1080
GGTCAACGTG	GTACAGAAGG	GAAAATCCAA	GCCATCCGCT	ATGCGCGTGA	AAATGATGTT	1140
CCAATGTTGG	GAGTCTGCTT	GGGAATGCAG	TTGACATGTA	TCGAGTTTGC	TCGTCACGTT	1200
TTAGGTCTTG	AAGGTGCCAA	TTCTGCAGAG	CTTGCAACCAG	AAACAAAATA	CCCTATCATT	1260
GATATCATGC	GTGATCAGAT	TGATATTGAG	GATATGGGTG	GAACCCTTCG	TTTGGGACTT	1320
TATCCGTCTA	AGTTGAAACG	TGGCTCTAAG	GCTGCTGCTG	CTTATCACAA	TCAAGAAGTG	1380
GTGCAACGCC	GTCACCGTCA	CCGTTATGAG	TTTAATAATG	CCTTCCGTGA	GCAGTTTGAG	1440
GCAGCAGGTT	TTGTCTTTTC	AGGAGTTTCT	CCAGACAATC	GTTTGGTAGA	AATCGTGGA	1500
ATTCTTGAAA	ATAAATTCTT	TGTAGCTTGT	CAGTATCACC	CTGAACTGTC	AAGCCGTCCA	1560
AACCGACCAG	AAGAACTCTA	CACTGCCTTT	GTTACTGCAG	CGGTTGAGAA	CAGCAATTAG	1620

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AAAACACGAT	CACTGGTCGC	CTCAACGGTA	AAAACATATAC	GACTGTTGCT	GGTACTGGCA	60
TCAATATCTT	TGATGCTGAA	GCTCACTTCC	TTTCAACATA	AAGTCATCGA	AATCCAAGCT	120
GGTGATGAAA	AACAAGAATT	GACTGCTGAA	ACTATCGTCA	TCAACACTGG	TGCTGTTTCA	180
AACGTCTTGC	CAATCCCTGG	ACTTGCTACA	AGCAAAAACG	TCTTTGACTC	AACAGGTATC	240
CAAAGCTTGG	ATAAATTGCC	TGAAAAACTT	GGAGTCCTTG	GTGGCGGAAA	TATCGGTCTT	300
GAATTTGCTG	GCCTTTACAA	TAAACTAGGA	AGCAAGGTTA	CAGTCCTAGA	TGCCTTGGAT	360
ACATTCCCTAC	CTCGTGCAGA	ACCTTCCATC	GCAGCTCTTG	CTAAACAATA	CCTGGAAGAA	420
GACGGTATTG	AATTGCTTCA	AAATATCCAT	ACTACTGAAA	TTAAAAACGA	CGGTGACCAA	480
GTGCTTGTCG	TAAGTGAAGA	CGAAACTTAC	CGTTTCGACG	CCCTTCTCTA	CGCAACTGGA	540
CGCAAACCAA	ATGTAGAACC	ACTTCAACTT	GAAAATACAG	ATATTGAACT	AACTGAACGT	600
GGCGCTATTA	AAGTAGATAA	ACACTGTCAA	ACAAACGTTT	CTGGTGTCTT	TGCAGTTGGA	660
GATGTCAACG	GTGGTCTTCA	ATTTACTTAC	ATTTCACTTG	ATGACTTCCG	TGTTGTTTAC	720
AGCTACCTTG	CTGGAGATGG	CAGCTACACA	CTTGAGGACC	GTCTCAATGT	GCCAAATACT	780
ATGTTTCATCA	CACCTGCACT	TTCACAAGTT	GGTTTGACTG	AAAGCCAAGC	AGCTGATTTG	840
AAACTTCCAT	ACGCAGTGAA	AGAAATCCCT	GTTGCAGCCA	TGCCCTCGTG	TCACGTAAAT	900
GGAGACCTTC	GCGGAGCTTT	CAAAGCTGTT	GTTAATACTG	AAACAAAAGA	AATTCTTGGT	960
GCAAGCATCT	TCTCAGAAAG	TTCTCAAGAA	ATCATCAACA	TCATTACTGT	TGCTATGGAC	1020
AACAAGATTG	CTTACACTTA	CTTCACAAA	CAAATCTTCA	CTCACCCAAC	CTTGGCTGAG	1080
AACTTGAATG	ACTTGTTCG	GATTTAA				1107

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGAGGCAGAT	CTCTAATGCA	AACTCAAGAA	AAACACTCGC	AAGCAGCCGT	TCTTGGCTTG	60
CAGCACTTAC	TAGCCATGTA	CTCAGGATCT	ATCCTGGTTC	CCATCATGAT	TGCGACAGCC	120
CTTGGCTATT	CAGCTGAGCA	GTTGACCTAC	CTGATTTCCTA	CAGATATCTT	CATGTGTGGG	180
GTGGCAACCT	TCCTCCAAC	CCAACCAAC	AAATACTTTG	GGATTGGACT	CCCAGTCGTT	240
CTTGGAGTTG	CCTTCCAATC	GGTCGCTCCC	TTAATTATGA	TTGGGCAAAG	CCATGGTAGT	300
GGCGCTATGT	TTGGTGCCCT	TATCGCATCT	GGGATTTACG	TGGTTCCTGT	TTCAGGCATC	360
TTCTCAAAAG	TAGCCAATCT	TTTCCCATCT	ATCGTAACAG	GATCTGTTAT	TACCACAATT	420
GGTTTAAACCT	TGATCCCTGT	CGCTATTGGA	AATATGGGAA	ATAACGTTCC	AGAGCCAAC	480
GGTCAAAGTC	TCCTGCTTTC	AGCTATTACT	GTTCTGATTA	TCCTCTTGAT	CAACATCTTT	540
ACCAAAGGAT	TTATTAAAGTC	TATCTCTATT	TTGATTGGTC	TGGTTGTTGG	AACTGCCATT	600
GCTGCTAGCA	TGGGCTTGGT	TGACTTCTCT	CCTGTTGCAG	CAGCACCAGT	TGTCCATGTC	660
CCAACCTCCAT	TCTACTTTGG	GATGCCAACC	TTTGAAATCT	CATCTATTGT	CATGATGTGT	720
ATCATCGCAA	CGGTGCTCTAT	GGTTGAGTCA	ACTGGGTTGT	TTATCTGGCC	TTGTCTGATA	780
TCACAAAGGA	TCCAATCGAC	AGCACCGCCT	GCGCAACGGA	TACCGCGCAG	AAGGTTTGGC	840
CTAAATTTTT	GGGGGATTT	TTAA				864

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2334 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTGTTTTGT	CTTCATCGAA	GACTTCGTCA	GTTTCCTATT	TTTACTTTGC	TTTTGACGTC	60
CTTGGTATCT	TGATCTTTGT	AGGCAAGGCG	TATAATTTCA	TCAATCCAAA	GGGGATTAAA	120
ATGGCAAAAC	AAGTGTTTCA	AACGACTTTT	GCGGGTCGTG	AGTTAATTGT	AGAGACTGGT	180
CAGGTTGCTA	AGCAAGCAAA	TGGCTCTGTT	GTTGTACGTT	ACGGTGAGTC	AACTGTCTTG	240
ACTGCTGCCG	TTATGTCTAA	GAAAATGGCA	ACTGGGGATT	TCTTCCCACT	CCAAGTCAAC	300
TACGAAGAAA	AAATGTATGC	GGCTGGGAAG	TTTCCTGGTG	GCTTTATGAA	ACGTGAAGGA	360
CGTCCTTCAA	CAGATGCGAC	CTTGACAGCG	CGTTTGATTG	ACCGTCCGAT	TCGTCCTATG	420
TTTGCGGAAG	GTTTCCGTAA	TGAAGTCCAA	GTCAATCAATA	CAGTGCTTTC	TTATGATGAA	480
AATGCATCTG	CACCAATGGC	TGCTATGTTT	GGTTCATCTT	TGGCACTGTC	TATTTTCAGAT	540
ATTCCATTTG	ACGGACCAAT	TGCTGGGGTA	CAAGTGGGAT	ATGTAGATGG	CCAAATCATC	600

ATCAACCCAA	GTCAAGAACA	AGCAGAGCAA	TCTCTTCTTG	AATTGACAGT	AGCTGGAACC	660
AAGCACGCTG	TCAACATGGT	AGAGTCTGGT	GCCAAAGAAT	TGTCAGAAGA	AATCATGTTG	720
GAAGCGCTCC	TTAAAGGGCA	CGAAGCTGTC	AAAGAATTGA	TTGCCTTCCA	AGAAGAAATC	780
GTTGCTGCTG	TCGGTAAAGA	AAAAGCAGAA	GTGGAATTGC	TTACAGTGGG	TGCTGAATTG	840
CAAGCTGAAA	TCATTGCAGC	CTACAACAGT	GACCTCCAAA	AGGCAGTTCA	AGTAGAAGAG	900
AAATTGGCCC	TGGAAGCTGC	GACTCAAGTA	GTGAAAGACC	AAGTGACTGC	CGTTTACGAA	960
GAAAAATATG	CGGACCACGA	AGAATTTGAC	CGTATTATGC	GTGATGTGGC	TGAAATCTTG	1020
GAACAAATGG	AACACGCAGA	AGTGCGACGT	TTAATTACAG	AAGACAAGGT	GCGTCCTGAT	1080
GGTCGTAAGG	TCGATGAAAT	CCGTCCTTTG	GATGCGGTTG	TCGACTTCCT	TCCTCGTGTA	1140
CATGGTTCAG	GTCTCTTTAC	TCGTGGGCAA	ACTCAAGCTC	TTTCAGTCTT	GACCTTGGCT	1200
CCGATGGGAG	AAACTCAAAT	CATTGATGGT	TTGGATCCAG	AGTACAAGAA	ACGCTTTATG	1260
CACCACTATA	ACTTCCCTCA	ATATTCTGTA	GGGGAAACAG	GTCGTTACGG	TGCGCCAGGT	1320
CGTCGTGAAA	TCGGTCACGG	TGCCCTTGGT	GAGCGTGCTC	TTGCTCAAGT	CTTGCCAAGC	1380
TTGGAAGAAT	TCCCATACGC	TATCCGTCTA	GTAGCAGAAG	TTTTTGAATC	AAACGGTTCT	1440
TCATCTCAAG	CTTCTATCTG	TGCGGGAAC	CTTGCCCTTA	TGGCTGGTGG	TGTGCCAATC	1500
AAGGCGCCAG	TAGCTGGTAT	TGCTATGGGA	CTTATCTCAG	ATGGAAATAA	CTACACAGTA	1560
TTGACAGATA	TCCAAGGTTT	GGAAGATCAC	TTTGGAGATA	TGGACTTCAA	GGTTGCAGGT	1620
ACTCGTGATG	GGATTACAGC	CCTTCAAATG	GATATCAAGA	TTCAAGGGAT	TACTGCAGAA	1680
ATCTTGACGG	AGGCTCTTGC	TCAAGCCAAG	AAAGCGCGTT	TTGAAATCCT	TGATGTCATT	1740
GAAGCAACCA	TTCCAGAAGT	TCGCTAGAA	TTGGCTCCAA	CTGCTCCGAA	AATTGATACG	1800
ATCAAGATTG	ATGTAGACAA	GATTAAGATT	GTCATCGGTA	AGGGTGGAGA	AACCATCGAC	1860
AAGATTATCG	CTGAAACAGG	TGTTAAGATT	GATATAGACG	AAGAAGGAAA	TGTGTCTATC	1920
TACTCTAGTG	ACCAAGATGC	TATTAACCGT	GCCAAAGAAA	TTATTGCTGG	TTTGGTTCGT	1980
GAAGCCAAAG	TGGATGAAGT	TTACCGTGCT	AAAGTCGTTT	GTATCGAGAA	ATTTGGTGCC	2040
TTTGTTAACC	TCCTTTGATAA	GACAGATGCC	CTTGTTTATA	TCTCTGAGAT	GGCTTGGAAT	2100
CGTACCAATC	GTGTAGAGGA	TTTGGTAGAA	ATCGGGGATG	AAGTTGATGT	TAAGGTTATC	2160
AAGATTGATG	AAAAAGGCCG	TATCGATGCC	TCTATGAAGG	CTCTTCTACC	TCGTCCGCCA	2220
AAACCTGAGC	ATGATGAAAA	AGGTGAAAAG	TCTGAGCGCC	CTCACCGCCC	ACGTCATCAC	2280
AAGGATCACA	AACCTAAGAA	AGAATTTACA	GAAACACCAA	AAGATTTCAGA	GTAA	2334

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GACTGTTTGT	CTCAACTCTG	CGACAGCGCT	CTGGAGTTGA	TTTTACGCGT	TTTGGAAGTG	60
GGACCTGGTG	ATGAAGTCAT	CGTTCCAGCC	ATGACCTATA	CGGCTTCATG	TAGTGTTCATT	120
ACGCACGTGG	GAGCAACCCC	TGTCATGGTG	GATATCCAAG	CAGATACGTT	TGAGATGGAC	180
TATGACCTGC	TTGAGCAAGC	TATCACTGAG	AAAACAAAGG	TGATTATCCC	AGTAGAGCTC	240

GCAGGGATTG	TTTGCGATTA	TGACCGTTTG	TTCCAAGTCG	TGGAGAAAAA	ACGTGACTTC	300
TTTACCGCTT	CAAGCAAGTG	GCAAAAGGCC	TTTAACCGTA	TTGTCATTGT	CTCTGATAGT	360
CCCCACGCTT	TGGGATCTAC	TTATAAAGGA	CAACCTTCTG	GTTCTATCGC	TGATTTTACT	420
TCCTTCTCAT	TCCATGCCGT	TAAGAACTTT	ACAACGGCAG	AAGGTGGAAG	TGCGACTTGG	480
AAAGCCAATC	CAGTGATTGA	TGACGAAGAG	ATGTACAAGG	AATTCCAAAT	CCTTTCCTTT	540
CACGGGCAAA	CTAAGGATGC	TCTTGCCAAG	ATGCAACTGG	GGTCATGGGA	ATACGATATC	600
GTTACACCAG	CCTATAAGTG	CAACATGACC	GATATCATGG	CTTCACTTGG	TTTGGTACAA	660
TTGGACCGCT	ATCCAAGTTT	GTTGCAACGC	CGTAAGGACA	TTGTGGACCG	CTATGATAGT	720
GGTTTTGCAG	GTTCTCGCAT	CCATCCTTTG	GCACACAAGA	CTGAAACTGT	CGAATCTTCA	780
CGCCACCTCT	ACATCACCCG	TGTAGAAGGA	GCAAGCCTAG	AAGAACGCAG	CCTCATCATC	840
CAAGAATTGG	CTAAAGCAGG	AATTGCAAGT	AATGTTCACT	ACAAACCGCT	TCCTCTCTTG	900
ACAGCCTATA	AGAATCTTGG	ATTTGATATG	ACGAACTATC	CTAAGGCCTA	TGCCTTCTTT	960
GAGAATGAAA	TTACCTCCC	TCTTCATACT	AAATTAAGCG	ATGAAGAAGT	AGACTATATC	1020
ATTGAGACTT	TCAAAACAGT	TTCTGAAAAA	GTGCTAACTT	TATCAAAAAA	ATGA	1074

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...510
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AATCCCTTGT	CTGTTCAAAT	GGTTCACAAT	ATAGCAGGTA	CGTCATTTTG	GTTGTGTAAA	60
AAAGAGGTGC	TAGAATTAAT	TAATGGTTTT	GAGAAAATAG	ATTCACATCA	GGACGGTGTT	120
GTTTTATTAA	AACTACTTGC	TCAAGGATAC	CAAATTGATA	TAGTGCGAGA	ATTCTTGGTG	180
AATTACTACG	CTCACAGTAA	AGAAAACGGT	ATCACTGGAG	TGACACAAAA	AACAATTAAT	240
GCAGATGAAG	AATATTATAA	TTACTGTAGG	AAATATTTTA	ATTTATTGAG	TTTCAACGAG	300
AGAATATTGG	TTACAAAGAA	ATATTATTCT	TTAAACATAA	AGCGGTTACT	ATTAATAGGA	360
GACAAATGCA	AGGCTTTAAA	AGTAATCAAG	AAGGCAAGAG	AAGAAAAAAT	TTTTAACGAA	420
TTTCTTTTTT	TGAAATATAT	GTTATTATAT	AATTTGGGTT	TTTTCTATTG	TATATATGAC	480
AACTATGTTC	AATTAAAATT	TAGAAAGTGA				510

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TACATATTGT	CGACTCACTT	CGTATTGCAA	GAGCTAAAAA	AGACCAGGAT	TAGGAAGTGC	60
CTTATGAAAT	CACTAGCTAG	ACTACTGAAC	ATTCATGTTT	TTATCAGTAT	TTTCCTTTTC	120
TTTGCCCTTA	TTTCAGGAGC	TGTTTCTCAT	ACAGTTTTAC	TACTCCTACT	CCTCTTTCCT	180
CCTGCGCTCA	ATAAAGGACT	TGAGAAAATA	CAATCAAAAC	GGATACCTGT	CCTCAACGCA	240
GCCCTCTTCT	TTCTCCTCAT	ATCCTTTCCA	CAACTTTTAA	CCAACCCTGT	CCAATGGAAA	300
TTTTCAATAT	TCCTAGTCGT	AACCATCATT	TCAAGTTTGG	CCTACTTCTA	TAAC'TTTTAT	360
CAAGTAGTTA	AAGAAAGTAGA	TCAAAAACAG	TTGATTTAG			399

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGACTCCTGT	CATTGAGCAG	ATGGACAAGA	ATAGGGATGA	GGTCAATGAC	CTCTTGCGCC	60
AGCGAACTAC	CAANGAAAAA	CCTCTTTGCC	CTGTCTGATT	TGGAGACTGG	TATGGTTTAT	120
CTGACGGCAG	CTGCCAAACA	AAATCGGATT	TTGTTAGAGC	ATATTCAAGG	TCATGCCTTG	180
TATCGTAGTT	TTGATGAGAT	TGAGAGAGAA	CAGTTTGATG	ATGCCATGAT	TGAGGCTCAT	240
CAGCTGGTAT	CCATGACAGA	CCTAATCTCT	CAGATTTTAC	AGCAGCTTTC	AGCCTCTTAC	300
AACAATATTC	TAAACAATAA	TCTGAATGAC	AATTTGACAA	CCTTGACTAT	CATTTTCAGTC	360
TTGCTAGCTG	TTTTGGCAGT	CGTGACAGGC	TTTTTCGGAA	TGAATGTTCC	CTTACCTTTA	420
ACAGATGAGC	CCCATGCTTG	GCTCTATATC	AGTTTGGCTA	GTGCAGGTTT	GTGGATTGTT	480
TTATCCTTGT	TACTAAGGAA	AATTGCGAAA	AAAAGTTAA			519

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 819 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...819
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCTTGGCTGT	CTTGTCACAA	ACAACATGCT	ACTTCTGAGG	GGACGAATCA	AAGGCAAAGC	60
AGTTCAGCGA	AAGTTCCATG	GAAAGCTTCA	TACACCAACC	TAAACAACCA	GGTAAGTACA	120
GAAGAGGTCA	AATCTCTCTT	ATCAGCTCAC	TTGGATCCAA	ATAGTGTTGA	TGCATTTTTT	180
AATCTCGTTA	ATGACTATAA	TACCATTGTC	GGCTCAACTG	GCTTATCAGG	AGATTTCACT	240
TCCTTTACTC	ACACCGAATA	CGATGTTGAG	AAAATCAGTC	ATCTCTGGAA	TCAAAAAGAAG	300
GGCGATTTTG	TTGGGACCAA	CTGCCGTATC	AATAGTTATT	GTCTTTTGAA	AAATTCAGTC	360
ACCATTCCAA	AGCTTGAAAA	GAATGACCAG	TTGCTTTTCC	TAGATAATGA	TGCGATTGAT	420
AAAGGAAAGG	TCTTTGATTC	ACAAGATAAG	GAAGAGTTTG	ATATTCTATT	TTCGAGAGTT	480
CCAACTGAGG	CAACTACAGA	TGTCAAGGTT	CACGCTGAAA	AGATGGAAAC	ATTCTTCTCA	540
CAATTTCAAT	TCAATGAAAA	AGCTCGAATG	CTGTCTGTAG	TCTTGCACGA	CAATCTGGAT	600
GGCGAGTATC	TGTTTGTAGG	CCACGTTGGG	GTCTTAGTAC	CTGCTGATGA	CGGTTTCTTA	660
TTTGTTAGAGA	AATTGACTTT	CGAAGAGCCC	TACCAAGCGA	TTAAATTTGC	TAGTAAGGAA	720
GATTGCTACA	AGTATTTGGG	CACCAAGTAT	GCGGATTATA	CAGGCGAGGG	ACTGGCTAAG	780
CCTTTTATCA	TGATAATGA	TAAGTGGGTT	AAACTTTAA			819

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CAGTCTATGT	CAGATAAGAT	TGGCTTATTC	ACAGGCTCAT	TTGATCCGAT	GACAAATGGG	60
CATCTGGATA	TCATTGAACG	GGCGAGCAGA	CTCTTTGATA	AGCTCTATGT	CGGTATTTTT	120
TTTAATCCCC	ACAAACAAGG	ATTTCTTCCT	ATCGAAAATC	GTAAACGGGG	GCTAGAAAAG	180
GCTTTGGGAC	ATCTGGAAAA	TGTTGAAGTC	GTGGCTTCTC	ATGATGAATT	GGTGGTCGAT	240
GTTGCAAAAA	GATTGGGTGC	TACTTGTCTA	GTGCGTGGTT	TGAGGAATGC	GTCGGATTG	300
CAATATGAAG	CCAGTTTTGA	TTACTACAAT	CATCAGCTGT	CTTCTGATAT	AGAGACTATT	360
TATTTACATA	GTCGACCTGA	ACATCTCTAT	ATCAGTTCAT	CAGGCGTTAG	AGAGCTTTTG	420
AAGTTTGGTC	AGGATATTGC	CTGCTATGTT	CCCAGAGTA	TTTGGAGGAA	ATAA	474

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGAATATGT	CTGATAACAA	AACTAGTAAA	ATTCCAACCA	ATCCAGCTAA	TATTGGACTT	60
CTTTTCTTGC	CAATATTTAA	GGCTATTGGG	CCAGCTAAAA	AAGATATACA	AGCTATTGGT	120
CCTGTAATTG	AAGTAGAAAA	AGCAGTTAAA	GATACAGCGC	AAAAAATTAA	AACAAGCCTT	180
GAAAGCTCGG	GATTTGCTCC	AAGTCCGATT	GCTATTTCTT	CACCAAGTTC	AATAATTTCT	240
AGTCTTTTAT	TAAAAAATAA	AACTAATATA	GTAGCAATAA	TACTTACTNA	TTAG	294

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGGAGTATGT	CTTGTTCTAT	CGATTTATTA	AAACATCGGT	ATTTGAAAAA	TATTAAAGAA	60
AATCCTGAAT	TGTTTGTCTG	AATTGAGTTG	GAGTATCCTG	TTGCAAGTTT	AGAAGGGGAT	120
GCTACAGATG	TTGAAGTTAT	GAAGGATCTA	TTTCATTATT	TAGTTTCTAC	TTTGGATCTC	180
ACCGTAGCAA	AGGTAGATGA	TTTTGGCAAT	CTGATCCAGT	TAGTAGATCC	GATAAGTCAG	240
GATGCTATTT	TATTTGAAGT	TTCTTATACA	ACGATTGAGT	TTGCATTTGG	TAAGGCTGAA	300
ACGATTCAAG	AGGTCGAAAA	TCGTTTCAAT	AATTATATGA	ATGTAATTCA	GAGAAAGTTA	360
GCTGAATCAA	ATCATGCTAT	TGTTGGCTGT	GGTATCCATC	CCAACTGGGA	TAAAAATGAG	420
AATTGTCCAG	TGGCTTATCC	ACGCTATCAG	ATGTTGATGG	ATTATTTGAA	TTTGAGTAGA	480
AATATTATTA	AATCAGATTT	ACATCATTTT	CCTGAATATG	GTACTTTTAT	CTGTGGGAGC	540
CAGGTTTCAGC	TGGATATTTT	AAAAACCAAC	TACTTACGGG	TGATTAATGC	TTTTACTCAA	600
ATTGAAGCGG	CTAAGGCTTA	TTTATTTGCA	AACTCTGAAT	TTTCGGGTGC	GGATTGGGAT	660
ACGAAAATTT	CAAGGGATAT	TTTCTGGGAA	GAATCTATGC	ATGGTATCTA	TCCAGAGAAT	720
GTTGGGGTCA	ATGCTAGACT	CCTTAATGAT	GAAACTGATT	TTTTTTGACTA	TCTAAATCAT	780
TCTGCGATTT	TTACTGCGGA	ACGTGATGGG	CAGACCTATT	ATTTTTATCC	TATTCAGGCT	840
GGGGACTATT	TGGCTACGTC	CGAAATCCAA	GCATTTGCTC	TGAATGGGGA	TGAGGTTATT	900
ATTTACCCCC	AAGAGAAGGA	TTTTGAAACT	CATCGTAGTT	ACCAGTACCA	AGATTTAACG	960
ACTCGAGGAA	CAGTTGAGTT	TCGTAGTGTG	TGTACACAGC	CACTTGATAG	GACTTTTGCT	1020
TCTGCAGCTT	TTCACTTGGG	ATTATTGGTT	AATTTAGACA	AGTTAGAAGC	TTACTTAGAA	1080
ACAGCACCTT	TCTTTAAAGT	ATTTGGTTAT	GATTACAAGT	CTTTAAGGAG	ACAATTTTCT	1140
AAGAAAAATC	TTACAGATGA	GGAAGAAACT	ACGATTATTG	AATTTTCCAA	AGACTTACTC	1200
CTACTAGCTG	AGGAGGGACT	AGTGGTGAGA	AATAAGGAAG	AAATGACCTA	TTTACAGCCT	1260
TTGAGAGAAG	AATTGAGCCT	ATAA				1284

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AGCCTAATGT	CTATGTTAAA	AGTTGAAAAT	CTTTCTGTGC	ATTACGGTAT	GATCCAAGCA	60
GTCCGTGATG	TAAGCTTTGA	AGTTAATGAA	GGAGAAGTTG	TTTCCCTTAT	CGGTGCCAAC	120
GGTGCAGGTA	AGACAACAT	TCTTCGCACC	TTGTCAGGTT	TGGTTCGACC	AAGTTCAGGA	180
AAGATTGAAT	TTTTAGGTCA	AGAAATCCAA	AAAATGCCAG	CTCAGAAAAT	CGTGGCAGGT	240
GGTCTTTCAC	AAGTTCAGGA	AGGACGCCAC	GTCTTTCCTG	GCTTGACTGT	TATGGAAAAT	300

CTTGAAATGG	GAGCTTCTT	AAAGAAAAAT	CGTGAAGAAA	ATCAAGCTAA	CTTGAAGAAG	360
GTTTTCTCAC	GCTTTCCTCG	TCTTGAAGAA	CGGAAGAACC	AAGATGCAGC	TACTCTTTCA	420
GGAGGGGAAC	AACAAATGCT	TGCCATGGGA	CGCGCTCTTA	TGTCAACACC	AAAACCTTCTT	480
CTTTTAGATG	AACCATCAAT	GGGACTTGCC	CCAATCTTCA	TCCAAGAGAT	TTTTGATATC	540
ATTCAAGATA	TTCAGAAGCA	AGGAACAACC	GTCCTCTTGA	TTGAACAAAA	TGCCAATAAA	600
GCACTTGCAA	TCTCTGACCG	AGGATATGTA	TTGGAAACAG	GAAAAATCGT	CCTATCAGGG	660
TCAGGAAAAG	AACTCGCTTC	ATCAGAAGAA	GTCAGAAAAG	CATATCTAGG	TGGCTAA	717

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...750
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

AGCATAATGT	CTCAAAAAAA	TAATAAAAAAG	AAAAACAAGC	GAAAAAATCT	GCTGACAAAT	60
ATCCTAGCAG	GATTTCTGAT	ATTACTGTCA	CTGGCTTTGA	TTTTTAATAC	TCAAATTCGA	120
AATATTTTCA	TAGTCTGGAA	TACCAATAAG	TATCAAGTTA	GCCAGGTATC	AAAAGAAAAA	180
TTAGAAGAAA	ATCAGGATAC	AGAAGGCAAT	TTTGACTTTG	ATTCTGTCAA	AGCTATCTCT	240
TCGGAAGCTG	TTCTAACTTC	TCAATGGAAT	GCTCAAAAAAT	TACCAGTTAT	TGGGGGAATT	300
GCAATTCCTG	AATTGGAAAT	GAATTTGCCG	ATTTTAAAG	GACTTGATAA	TGTTAATCTC	360
TTCTACGGAG	CTGGTACAAT	GAAACGCGAG	CAAGTAATGG	GAGAAGGAAA	TTATAGTCTA	420
GCTAGTCACC	ATATCTTTGG	TGTTGATAAT	GCTAATAAAA	TGTTATTTTC	TCCTTTAGAT	480
AATGCTAAAA	ATGGCATGAA	GATTTATCTA	ACCGATAAAA	ATAAAGTTTA	TACTTATGAA	540
ATACGTGAAG	TCAAACGTGT	GACACCGGAT	CGTGTTGATG	AAGTTGATGA	TAGAGATGGG	600
GTCAATGAAA	TCACATTAGT	AACCTGTGAA	GACCTTGCTG	CTACAGAACG	TATTATTGTC	660
AAAGGTGATT	TGAAAGAAAC	AAAAGATTAT	TCACAAACAT	CTGATGAAAT	CCTAACAGCT	720
TTCAATCAAC	CATATAAACA	ATTTTATTAA				750

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AAGAAAATGT	CTAAAAATAT	TGTACAATTG	AATAATTCTT	TTATTCAAAA	TGAATACCAA	60
CGTCGTCGCT	ACCTGATGAA	AGAACGACAA	AAACGGAATC	GTTTTATGGG	AGGGGTATTG	120
ATTTTGATTA	TGCTATTATT	TATCTTGCCA	ACTTTTAATT	TAGCGCAGAG	TTATCAGCAA	180
TTACTCCAAA	GACGTCAGCA	ATTAGCAGAC	TTGCAAACTC	AGTATCAAAC	TTTGAGTGAT	240
GAAAAGGATA	AGGAGACAGC	ATTTGCTACC	AAGTTGAAAAG	ATGAAGATTA	TGCTGCTAAA	300
TATACACGAG	CGAAGTACTA	TTATTCTAAG	TCGAGGGAAA	AAGTTTATAC	GATTCCTGAC	360
TTGCTTCAAA	GGTGA					375

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ACAGGAATGT	CATTTAAGAA	TAACTGGATA	GACAAGGAAG	GCAGAGTATT	TATCTATTTT	60
ACTGTCGAAG	AAATTATGAA	AAGAAGAAAT	ATCTCAAAGC	CAACTGCCAT	AAAAACATTA	120
GATGAGCTTG	ATATAAAAAA	AGGAATAGGA	CTGATCGAAA	GAGTAAGGCT	TGGACTTGGT	180
AAGCCGAACA	TCATTTATGT	TAAAGACTTT	ATGAGTATAT	TTCAGGTAAA	AGAAAATGAC	240
TTACAGAAGT	CAAAAAACTT	AACTTCAGAA	GTAAAAGATT	TTAACCTCAG	AAGTAAAGAA	300
AATGAACTTC	AAGAGGTTAA	GAACCTTGAC	TCTAACTATA	TAGAGAATAA	TAAGAGTAAG	360
TATAGTAAGA	GAGAATATAG	TTTTGGTGAA	AACGGACTTG	GAACATTTCA	AAATGTGTTT	420
TTAGCTGCTG	AAGATATATC	GGATTTACAA	ATCATAATGA	ACTCACAGCT	TGAGAATTAC	480
ATTAGACTTC	CTGCAAAACT	AGAATCCTAG				510

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTAAAGATGT	CTATTATAAC	CTTGCTCCCC	CTCTTGGTGT	CTTCTATGCT	GATTTACTCA	60
GCACCTCTCA	TCTTTACAAG	TATCGGTGGT	GTTTTCTCTG	AACGTGGTGG	TGTGGTAAAC	120
GTTGGCCTTG	AAGGAATTAT	GGTTATGGGT	GCCTTTTCTG	GAGTTGTCTT	TAACCTTGAA	180
TTTGCAGAAC	AATTTGGAGC	AGCAACTCCA	TGGCTATCCT	TGCTTGTAGC	AGGATTGTTG	240
GGTAGGGTNT	TCTTATTCAT	CCAAGGCAGC	GGCGACGGTT	CATTTCCGTG	CAGACCATGT	300
GGTCAGCGGT	ACGGTATTGA	ACTTGATGGC	GCCTGCCTTG	GCTGTTTTCT	TAGTTAA	357

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1044 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1044
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TGGCCTGTGT	CCACTTTTTT	TGTTTTTAAT	GTGAACTATA	CACGAGAAGT	GGTTCGGATT	60
CAAGAAATGG	GAAAGACTGT	AAATTCTTTG	GATTTGTATT	TGAAAGATAT	TAACGAACCT	120
GCAGCGTCTG	TTCTTCGATT	TTTGTAGGAT	GTATCAAAGG	ATTATAAAGT	CTCCATCATC	180
AAAACAGACA	GTGGTGATGA	GGTGGTCAAG	TCTGGTGTTT	TTGATAAAGA	TACCTTCCCC	240
TACCAAGAGT	TTGGGATTTC	TTCTCTTGAT	TTTACCACAG	ATGGTGAAGG	AGTCTATAGT	300
AATAAAGAAA	TTTCCAATAA	ACTTGGTACG	ATTCCGACCT	TTCTAAAAGC	CAAACCTATT	360
CAGCTTATGA	CTTTTCAAAC	CTATATCAAG	GATACATCTC	GTAGTTTAAA	TGGTCGCTAT	420
ACGATAACTT	CTACACAAGA	GATGGACAAG	GATAGGATTG	TACAGAAATG	GAGCGATTTT	480
TTCAAGATAG	ACCAGGCTAC	CTTGCTAGAG	CCGACCTACA	AAAGTGCAGT	GGAAGTCATA	540

AATCGAGATT	TGCTTTTATC	TGCCATTGTT	TTTGTCTTGG	CTATTTTGCT	TCTTGTGTTA	600
GTGACAGTGT	ATCAACCGAT	GATGGAGATG	AAAAGAGTTG	GGGTACAAAA	ATTACTTGGT	660
TTTCAAGATA	GGGCTGTTTT	AGCTGATGTT	GTAAAAGGCA	ACCTTTACCT	CCTCCTAGGT	720
GGGGCTCTTG	TGATCAATCT	AGGCGTGTTT	TTCTTGCTTG	ATTATAAACC	CAAAAGATTT	780
GTTTCCTATA	CTGTGGTTGT	CTCATTTTTT	GCTGTTGCAG	CTTTATCTCT	TTATCAGTTG	840
GTTGACTTAC	CTCTTAATCC	AAAAAATGAC	AATCAGCTCT	CTGCTGAAAG	GTTTTTCATC	900
TTTCAAATTT	GGTCTTATCT	TCAATTATGT	GATGAAAATA	GGGACAAC TA	TTTTACTGAC	960
GGCCTTACTG	ATTGGGGTGG	GCAGAAATTT	AGAACAAGAA	AACAAAGAAC	TTGCTTATCA	1020
GCAACAGTGG	GTAAGTCAAG	GTAA				1044

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAGCCAGTGT	CATTTTGGAG	GAAAATCATG	AAAGCTAGTC	CACATAGACC	AACCAAGGTT	60
CTGATTCATC	TGGGAGCTAT	TCGACAAAAT	ATTTCAGCAA	TGGGGGCTCA	TATCCCTCAA	120
GGAACGCTCA	AGTGGGCTGT	GGTCAAGGCC	AATGCTTATG	GCCATGGAGC	TGTTGCCGTT	180
GCCAAGGCAA	TTCAAGATGA	TGTTGATGGC	TTTTGCGTTT	CCAATATCGA	TGAAGCCATT	240
GAACTCAGAC	AAGCTGGACT	CAGCAAGCCA	ATCCTCATTT	TAGGAGTTTC	TGAAATCGAA	300
GCTGTTGCTC	TAGCTAAAGA	ATATGACTTC	ACCTTGACAG	TGGCTGGACT	GGAGTGGATT	360
CAAGCACTCT	TAGATAAGGA	AGTGGACCTA	ACTGGATTGA	CAGTCCACCT	CAAGATTGAT	420
TCAGGGATGG	GACGGATTGG	TTTLAGAGAG	GCCAGTGAGG	TTGAGCAGGC	TCAAGATTTG	480
CTACAACAAC	ACGCTGTTCT	TGTTGAAGGA	ATCTTTACCC	ACTTTGCTAC	TGCTGATGAG	540
GAATCAGATG	ACTATTTTAA	TGCCCAGTTA	GAACGGTTTA	AAACTATTTT	AGCTAGTATG	600
AAGGAAGTTC	CAGAGCTGGT	TCATGCTAGC	AAATCTGCAA	CGACTCTTTG	GCATGTAGAG	660
ACTATTTTCA	ATGCGGTTCT	TATGGGAGAT	GCCATGTATG	GCCTCAATCC	AAGTGGAGCG	720
GTCTTGGAAT	TGCCTTATGA	TTTGATAACG	GCCTTGACCT	TGGAGTCTGC	TCTGGTTTCAT	780
GTCAAGACAG	TTCCAGCAGG	AGCTTGCAAT	GGCTATGGAG	CAACTTATCA	AGCGGATAGC	840
GAGCAAGTCA	TCGCGACCGT	GCCAATCGGG	TATGCAGATG	GATGGACAAG	AGACATGCAA	900
AATTTCTCTG	TCTTGGTAGA	TGGCCAAGCT	TGCCCAATTG	TCGGCAGGGT	TTGATGGAC	960
CAAATCACTA	TTGATGTC	TAAGCTTTAT	CCGCTAGGAA	CCAAGGTAAC	CTTGATTGGC	1020
TCCAATGGGG	ATAAGGAAAT	CACTGCAACT	CAGGTAGCGA	CCTACCGCGT	AACCATTAAAC	1080
TATGAGGTGG	TTTGCTCCT	CAGCGACCGT	ATTCCGAGAG	AATATTATTA	G	1131

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ATTAAAGTGT	CGATAATGAT	TAAAGTTATA	GCCAAGACGA	ATGACAATGG	AGCCAGCGCC	60
GTTCCCATAA	CAATACCAAT	TGGAGCAGGT	GTTGTCCAAG	GTAAAATAAT	ACTGAAACTA	120
TTCATTTGTA	GAACATCTAC	AAAAAATTTT	ATAATCCAAA	CATTGATAAT	AGGAGCAGTA	180
ACAAACGGAA	TAAAGAAGAT	AGGATTTAAA	ACAATTGGAG	CACCAAATAG	GATTGGTTCA	240
TTTACGCCAA	AGAAAGTAGG	AACTACAGAC	GCACGTCCGA	CAATTCCTAT	TCTTTTTGAT	300
TTACATAACC	ACATAAACAT	AAATGGAAC	ACTAGTGTTG	CACCAGTACC	ACCCATTGTT	360
ACAACAAAAG	TTTGA					375

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TGGAAGGTGT	CTCAAGCGAG	GCAGCTTCAT	ATGCAGGCTT	GCAAAAACCTT	GATAAGTTGG	60
TTGTTCTTTA	TGATTCAAAT	GATATCAACT	TGGATGGTGA	GACAAAGGAT	TCCTTTACAG	120
AAAGTGTTTC	TGACCGTTAC	AATGCCTACG	GTTGGCATA	TGCCTTGGTT	GAAAAATGGAA	180
CAGACTTGGA	AGCCATCCAT	GCTGCTATCG	AAACAGCAAA	AGCTTCAGGC	AAGCCATCTT	240
TGA						243

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTTCCTTCGT	CTGGAAAATG	GCGGTGCCTT	CCACGATGGA	GATTTGATTG	TGGACGAGTT	60
GATGCGCATT	ATACAGGTGA	AAAAATGAGT	TTCACAGTAG	CAGTAAAAGA	AGAAATCCTG	120
GGCCAACACC	ATCTGAGCTG	GCAATGAATTA	TCTGCCATTA	TCAAAAATGTC	TGGTAGCATC	180
GGTCTCTCGA	CTTCGGGCTT	GACTTTTGTCA	GTTGTGACAG	AAAATGCCAA	ACTGGCCCGT	240
CACCTCTATG	AGTCCTTTCT	CCATTTCTAT	GAAATCAAAT	CTGAAATTCTG	TCACCACCAA	300
CGGAGCAATC	TTCGCAAGAA	TCGCGTCTAT	ACCGTTTTTA	CAGATGAAAA	GGTGCAGGAT	360
TTGTTAAGTG	ATTTGCACTT	GGCAGACTCT	TTCTTTGGCC	TGGAAACAGG	TATTGATGAG	420
GCGATTTTAT	CGGATGAGGA	AGCAGGTCGT	GCCTATCTCT	GTGGCGCTTT	CTTGGCAAAT	480
GGGAGCATTG	GTGACCCTGA	GTCAGGCAAG	TACCAGTTGG	AAATCAGTTC	TGTTTATCTG	540
GACCACGCGC	AAGGAATTGC	CTCCCTTCTC	CAACAGTTTT	TACTGGATGC	CAAGGTGCTT	600
GAGCGCAAGA	AGGGGGCTGT	GACCTATCTC	CAGCGAGCAG	AAGACATTAT	GGACTTCTTG	660
ATAGTAATCG	GAGCCATGCA	GGCACGTGAT	GATTTTGAGC	GGGTTAAGAT	TTTGCGAGAA	720
ACCCGTAACG	ACCTCAATCG	GGCTAATAAT	GCCGAGACAG	CTAATATCGC	TCGGACAGTT	780
TCTGCCAGCA	TGAAGACCAT	TAACAATATC	AGTAAAATCA	AAGATATCAT	GGGCTTAGAA	840
AATTTGCCAG	TAGATTTGCA	GGAAGTGGCG	CAACTGAGGA	TTCAGCACCC	AGACTACTCT	900
ATCCAGCAGT	TAGCAGATAG	TCTCAGCACC	CCTCTGACCA	AAAGTGGTGT	CAATCACAGA	960
CTCAGAAAAA	TCAATAAGAT	AGCGGATGAA	TTATAA			996

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CTGACTTCGT	CAGTCTTATC	TACAACCTCA	AAGCAGTGCT	TTGAGCAGCC	TGCGGCTAGT	60
TTTCTAGTTT	GCTCTTTGAT	TTTCATTGAG	TATAAGATCA	TTACATTGTT	TATAAGTTTA	120
AAAATAAAAA	AAGGAGTTTT	TATCATGAAA	AACTGGAAAA	AATATGCTTT	TGCATCTGCT	180
AGTGTAGTCG	CTCTGGCTGC	AGGTCTTGCT	GCTTGTGGAA	ATTTGACAGG	TAACAGCAAA	240
AAAGCTGCTG	ATTGAGGTGA	CAAACCTGTT	ATCAAAATGT	ACCAAATCGG	TGACAAACCA	300
GACAACTTGG	ATGAATTGTT	AGCAAATGCC	AACAAAATCA	TTGAAGAAAA	AGTTGGTGCC	360
AAATTGGATA	TCCAATACCT	TGGCTGGGGT	GACTATGGTA	AGAAAATGTC	AGTTATCACA	420
TCATCTGGTG	AAAACCTATG	TATTGCCTTT	GCAGATAACT	ATATTGTAAA	TGCTCAAAAA	480
GGTGCTTACG	CTGACTTGAC	AGAAATTGTAC	AAAAAAGAAG	GTAAAGACCT	TTACAAAGCA	540
CTTGACCCAG	CTTACATCAA	GGGTAATACT	GTAAATGGTA	AGATTTACGC	TGTTCCAGTT	600
GCAGCCAACG	TTGCATCATC	TCAAACTTTT	GCCTTCAACG	GAACCTCTCCT	TGCTAAATAT	660
GGTATCGATA	TTTCAGGTGT	TACTTCTTAC	GAAACTCTTG	AGCCAGTCTT	GAAACAAATT	720
AAAGAAAAAG	CTCCAGACGT	AGTACCATTT	GCTATTGGTA	AAGTTTTTCAT	CCCATCTGAT	780
AACTTTGACT	ACCCAGTAGC	AAACGGTCTT	CCATTTCGTTA	TCGACCTTGA	AGGCGATACT	840
ACTAAAGTTG	TAAACCGTTA	CGAAGTGCCCT	CGTTTCAAAG	AACACTTGAA	GACTCTTCAC	900
AAATTCTATG	AAGCTGGCTA	CATTCCAAAA	GACGTCGCAA	CAAGCGATAC	TTCTTTTGAC	960
CTTCAACAAG	ATACTTGGTT	CGTTCGTGAA	GAAACAGTAG	GACCAGCTGA	CTACGGTAAC	1020
AGTTTGCTTT	CACGTGTTGC	CAACAAAGAT	ATCCAAATCA	AACCAATTAC	TAACCTTCATC	1080
AAGAAAAACC	AAACAACACA	AGTTGCTAAC	TTTGTATCTT	CAAACAACCTC	TAAGAACAAA	1140
GAAAAATCAA	TGGAATCTT	GAACCTCTTG	AATACGAATC	CAGAACTCTT	GAACGGTCTT	1200
GTTTACGGTC	CAGAAGGCAA	GAACTGGGAA	AAAAATTGAAG	GTAAAGAAAA	CCGTGTTTCGC	1260
GTTCTTGATG	GCTACAAAGG	AAACACTCAC	ATGGGTGGAT	GGAACACTGG	TAACAACTGG	1320
ATCCTTTTACA	TCAACGAAAA	CGTTACAGAC	CAACAAATCG	AAAATTCTAA	GAAAGAATTG	1380
GCAGAAGCTA	AAGAATCTCC	AGCGCTTGGA	TTTATCTTCA	ATACTGACAA	TGTGAAATCT	1440
GAAATCTCAG	CTATTGCTAA	CACAATGCAA	CAATTTGATA	CAGCTATCAA	CACTGGTACT	1500
GTAGACCCAG	ATAAAGCTAT	TCCAGAAATG	ATGGAAAAAT	TGAAATCTGA	AGGTGCCTAC	1560
GAAAAAGTAT	TGAACGAAAT	GCAAAAACAA	TACGATGAAT	TCTTGAAAAA	CAAAAAATAA	1620

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CCCTCCTCGT	CTTCATTTTT	TACTTATTCT	TGTGAACAAG	CTGCTAGACT	CAAGGCTAGC	60
AAAGCTGCTC	AAGACAAGGT	ATCTTTTTTT	CATTTCTACT	CCTTTATTTC	TAATAGTTTA	120
TCTACTTCTG	ACGATAAACA	TTCGACTAAT	CTTTTAATCT	CTTCCCGGTT	TTACTTGGA	180
AGTTTCTGCT	GTCAATTTCT	CAAAGGGACC	CACCAAATG	GCCACGTCC	CTTGAGACCG	240
TGA						243

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAGGGCTCGT	CAGTGAAACT	GGAAAACATT	GACAAATCCA	TTCAAAAACA	GGATATTTTG	60
CAAGGCATTT	CGCTTGAAGT	CAGTCCTCAA	AACTGACAG	CCTTTATTGG	TCCAAATGGT	120
GCTGGAAAAT	CGACTCTTCC	TCTCCATCAT	GAGCAGACTA	ACCAAGAAAG	ATCAGGGAGT	180
TCTCAGTATC	AAAGGACGTG	A				201

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

AGAATGCCGT	CTTTGATAAA	GAGTACACGT	TTAGCTCTGC	TAGCTGCTGC	TGTTGAGTGG	60
GTTACCATGA	GAATGGTTTG	GCCGCGCTCA	TTGATTTTCAT	CAAAGACATC	AAGTAAGGCT	120
GCAGATGACT	TGGAGTCAAG	AGCTCCTGTC	GGTTCGTCCG	CAAGGAGAAAT	TTCAGGTTCA	180
GTGATGATGG	CGCGTGCTAC	TGCTACACGC	TGTTTCTGGC	CACCAGAAAT	CTCGTAA	237

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATACTAACGT	CCAGAAGAAA	ACTTTCTCTT	TCTCTTGAAG	AGTGTCAACT	AATGTTAGAG	60
GAGGGAACAA	AGGATCAACT	AGCTGAACTG	ACCTACCCCT	TTGGTCGTGG	AGTCAATCTC	120
TCCTTTGGCA	TAAAGGATGT	TCCAAAACCTC	TATCAAAAAG	TGATGGAGGC	AAACTATCCT	180
ATTTATCGTC	TCTTGACCAA	AAGAAAAGTTT	CGTGTCAGTG	ATCCCTATAT	CTATCCTCAT	240
AAATTGTCAG	TTTGGATCC	AGATGGCTAT	TTTTTAAGAT	TTAGCGAGTA	G	291

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AAAGAAACGT	CAAAATGCTCA	TGAAACAACG	AATACAGGTA	TCAAAACTAT	GACAAAACAA	60
ATCCCTAAAT	TTACTAAAGA	TACTGCTCAA	CTTTACACCT	GTAAATGGTT	GTTGTATAAT	120
AAAGTTACAA	AGATGTACGA	CCACACTGTT	GTAAATCATA	GTGTTTCGCGA	ATATATTACT	180
GATAGCATTT	CTACAAATAC	AAGTAAAGAG	AGCGGATGA			219

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AGCGTTGCGT	CCGAAAGTCT	ATCCAGACAC	GGCTCTTTAA	AAACAAAAGG	AGAAATGATG	60
CATACTTATT	TGCAAAAGAA	AATTGAAAAT	ATCAAAACAA	CCCTAGGTGA	AATGTCAGGT	120
GGTTACCGTC	GTATGGTTGC	GGCTATGGCT	GATTTAGGAT	TTTCAGGAAC	TATGAAGGCT	180
ATCTGGGATG	ACCTCTTTGC	CCATCGTAGT	TTTGCCCAGT	GGATTTATTT	GCTGGTTTTTA	240
GGAAGTTTTT	CTCTCTGGCT	GGAGTTGGTT	TACGAACATC	GTATTGTTGA	CTGGATTGGG	300
ATGATTTGTA	GCTTGACAGG	GATTATCTGT	GTAATCTTTG	TATCGGAAGG	TCGAGCAAGT	360
AATTATCTTT	TTGGCTTGAT	TAACTCTGTT	ATTTACCTTA	TTTTGGCCCT	ACAGAAAGGC	420
TTTTATGGTG	AGGTGCTGAC	GACACTTTAC	TTACAGTCA	TGCAGCCAAT	TGGACTTCTA	480
GTTTGGAATTT	ATCAGGCACA	GTTTAAGAAAG	GAAAAGCAGG	AGTTTGTCGC	GCGTAAACTG	540
GACGGCAAGG	GCTGGACAAA	GTATCTTTCC	ATTAGTGTGC	TTTGGTGGTT	GGCCTTTGGC	600
TTCAATTTATC	AGTCTATTGG	TGCCAATCGT	CCCTATCGTG	ATTCAATCAC	AGATGCAACC	660
AATGGGGTAG	GGCAAATCCT	CATGACAGCT	GTTTACCGTG	AACAGTGGAT	ATTCTGGGCG	720
GCTACCAATG	TTTTTTCAAT	CTATCTCTGG	TGGGGAAAAA	GCCTGCAAAT	TCAAGGGAAA	780
TATCTAATTT	ATCTCATTA	CAGTCTAATT	TGGTTGGTAT	CAATGGAACA	AGGCCACTAA	840

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CGCTCTGCGT	CTTCTGTAAA	AGGAGCTTCC	AAGTCAATGG	TATCTCCCAA	AACGTTGAAG	60
ACACGTCCCA	AAGTTTCTTT	ACCTACTGGT	ACAGAGATTG	GACGACCTGT	GTCCAATACT	120
TCCATTCCAC	GAGTCAACCC	ATCTGTTGAT	TCCATGGCGA	TAGTACGAAC	CATACCATCT	180
CCTAACTCCA	AGGCTACTTC	AAGGACGATT	TTTGTTTTTC	TTTCGTCATT	TTTGTAG	237

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

AATTTAGCGT	CAGAAACAAA	TCACGAAATC	GATTCAAATT	TTGCAGGTCG	TTTAAATATC	60
CTGCGCGCAG	GTGTTCTTGG	TGCTAACGAT	GGAATTATTT	CCATTGCTGG	TGTGGTTATC	120
GGGGTTGCCA	GTGCCACGAC	CAATATCTGG	ATTATCTTTT	TATCAGGATT	TGCGGCTATC	180
TTAGCTGGTG	CCTTTTCAAT	GGCTGGTGGA	GAATATGTAT	CCGTTTCAAC	TCCAAAAGAT	240
ACCGAGGAAG	CTGCCGTTTC	GCGAGAAAAA	CTCTTGTTAG	ACCAAGATAG	GGAAGTAGCC	300
AAAAAATCCC	TCTATGCTGC	TTATATCCAA	AATGGAGAAT	GCAAACTTC	TGCCCACTC	360
TTGACCAATA	AGATCTTTCT	TAAAAATCCA	CTCAAGGCTC	TGGTAGAGGA	AAAATATGGG	420
ATTGAGTATG	AAGAATTTAC	CAATCCTTGG	CACGCTGCCA	TTTCTAGCTT	CGTTGCCTTT	480
TTCTTAGAA	GTTTGCCTCC	AATGCTGTCA	GTGACCATAT	TCCCAAGTGA	ATATCGCATC	540
CCTGCTACTG	TCCTTATTGT	CGGTGTGGCC	CTTCTTCTCA	CTGGTTACAC	TAGTGCCAGA	600
CTTGGAAGG	ATCCGACTAG	AACAGCTATG	ATTCCGAACC	TTGCTATTGG	TCTCTTGACC	660
AGGGGAGTTA	CCTTCTGCT	CGAACAACTT	TTCAGCATTT	AG		702

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

AAAATGGCGT CTTGTTACGC CAAGTCATCA ATGTTATTGA TGAAGTTGAT TTCAATAGCC	60
CTGAAGATCG TCATTCGTTT AATGATATTT ACGAAAAAAT TCTTAAAGAT ATTCAAAATG	120
CTGGGAACTC AGGAGAATTT TATACGCCAC GTGCAGCGAC TGATTTTATT GCCGAAGTTC	180
TTGACCCAAA ACTTGAGAGAA TCAATGGCAG ACCTTGCTTG CGGAACAGGA GGCTTCTTGA	240

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATGAATACTT TAGGAGATAA ATTGATGGAA TTGAGTGCTA TTTACCATAG GACTGAGTCG	60
GAGTATGCCT ATCTTTATAA GGATAAGAAA CTCCATATTC GAATTCGAAC TAAGAAAGGG	120
GACATTGAAA GCATCAACTT GCACTATGGG GACCCTTTTA TCTTTATGGA GGAGTTTTAT	180
CAGGATACAA AAGAAATGGT CAAGATAACT TCTGGTACCT TATTTGACCA TTGGCAGGTT	240
GAAGTGTCTAG TTGACTTTGC ACGTATCCAG TATCTTTTTG AGCTCAGAGA TACAGAAGGT	300
TAA	303

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CTTCGTCAGT	CTTATCCGGC	AACCTCAAAG	CAGTGCTTTG	AGCAGCCTGC	GGCTAGTTTC	60
CTACAGATTT	TAGTTGGAAC	TCGATTCAAT	TCATGTGACA	ACGTGAAAAT	CGTTAGAGCA	120
TTTTATATAG	AATATACATG	GGAATGGAGC	TTACTCCCAT	TCCCATATTT	AATAGAAAAA	180
GAGGAACTCA	ATGCTACATT	ATACAAAAGA	AGACTTGCTC	GAATTGGGTG	CAGAAATCAC	240
TACGCGTGA						249

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CAAAGTCAGT	CACATATATA	CGGTAAGGCG	ACGTTGGCGC	GGTTTGAAGA	GATTTTTTGAA	60
GAGTATAAAA	ATCCTCAAGA	TACTTCTTTC	TATCCTTTAG	TTTATAAGGA	GAATACCTAT	120
GAAAAAACTG	CTATTTCTAT	CTTGTCTCTC	CTAATGTTAG	GAGTTTGCTG	CCTGTTTCCTA	180
TTCAGCCAGC	AAAGCTATAA	AAAACCTCGT	CAATACTATG	CTAACGACCA	GAACCTGCCC	240
AGTAGGATAA	CTTATAGTGA	ATATAGCGAC	AAATGA			276

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...927
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

AGATGCCAGT	CACAGATCGT	CTGGTTTGTG	GAGGATACCT	ATATGATTCA	AGCAAGAAAC	60
AAGTTAAGCC	AAGAAGAGCT	ATCTGAGGCG	AAAAAAGTAA	TTAACTGTTG	CCAAAACAT	120
GACGGTACCT	ATCGCGATCC	CTATCTCTCT	AACATGCTTA	ATTTTGATCC	AAACATGCC	180
GCCTTTTTC	TTTATTATGA	AAAAGGCGAA	CTTGTTGGTT	TATTAACTGT	CTATGCAGAT	240
GACCAAGATG	TAGAAGTGAC	GATACTGGTT	CATCCAGGTC	ATCGCCGTCA	GGGGATTGCG	300
CGTGCAATTGT	TTACTAGTTT	TGAGAGAGAA	ACAGCTTCTT	TCCCCATTCT	GTCAGTCACT	360
TTTCAGACAG	AACGTATTTT	TTTAGAGAAT	CATCCTGACT	TTGCCAGTAA	CTGGGGACTA	420
ATCGAGGATG	AAGAGACAGA	AACCTGGTTA	GGTAAGGATA	GAAGACCATA	TCAGTTAGCA	480
AAACTTTCTA	ATCTTGAAGT	TTTGTTAGCA	GATAGTTCGT	ATCAGGAGCA	AATTAGCCAG	540
TTAAAATTTT	AGGCATTTTC	AGGGGAACAT	GAATCGAGAG	AAGTTGTGGA	TAGATATGTC	600
GCTGAAGCTC	TGAAGGATCC	AGAAAGTCGC	TTATATATTT	TGTTAAAAGA	CGGTCAGGTT	660
ATTGGGACTT	GCACGGTTGA	TTTATCGAGC	GATACGAATT	ACTTCTACGG	TTTAGCAATA	720
TCAGAACCTG	AACGTGGGAA	AGGCTATGGA	AGCTACTTAG	CAAAATCCCT	TGTCAACCAA	780
CTAATTGAGC	AAAATGATAA	GGAATTTTCAG	ATTGCAGTGG	AAGATAGCAA	TGTAGGTGCC	840
AAACGTTTGT	ATGAAAAAAT	TGGCTTTGTC	AAACAGACAC	AGGTGGTTTA	TCTGAATGAG	900
AAAGGAGCAA	GGGATTCCGA	AGTGTAG				927

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 686 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TTTGTACTTT	ATTCCAGTTG	CCATCGGTAT	GCTTCTGGGA	ATCGGCTTAT	TTTCCTACCC	60
GATTGAATGA	CCTGCTTGAA	AATTATCAGG	TTTTTGTATT	ATGGAGCTTT	GCGGGAGCTA	120
TTATCGGTAC	AGTTCCTAGC	CTCCTCAAAG	AATCAACTCG	AGAATCTGAC	CGAGACAAGA	180
TTGATTTAGC	TTGGTTATGG	ACAACCTTTA	TCATTTCTGG	ATTAGGACTC	TATGCCTTAA	240
ATTTTGTCTG	TGGAACCTTA	AGCGCCAGCT	TTCTTAACTT	CGTCCTAGCA	GGCGCACTAT	300
TGGCCCTTGG	CGTCTTGTTT	CCTGGCCTCA	GTCCATCAAA	TTTACTTTTG	ATTTTGGGAC	360
TCTATGCTCC	TATGTTGACT	GGTTTTAAAA	CTTTTGATCT	CTTGGGAACC	TTCTTTCCGA	420
TTGGAATTGG	TGCAGGTGCA	ACTCTCATCG	TTTTTTCAAA	ATTGATGGAT	TATGCCTTAA	480
ACAACCTACCA	CTCACGCGTC	TATCATTTCA	TCATCGGTAT	CGTCCTATCA	AGTACCCTTT	540
TGATCTTAAT	TCCAAATGCA	GGAAACGCTG	AAAGTATCCA	ATACACAGGA	CTTTCACCTG	600
TCGGTTATGT	CATCATCGCC	TTCTTCTTTG	CGCTGGGAAT	CTGGCTTGGT	ATTTGGATGA	660
GTCAATTGGA	GGATAAATAT	AAATAA				686

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TGCCGAAAGT	CATTTGGGAC	AGGATGCTTA	TTAGGAGCTG	TAGTAGCAAG	CTTTATCGGA	60
CTAGAAAAAG	GTCAAGAATT	GAAATCATTA	GAAACAGCAA	TGTTAGTTTA	CAATATCGCT	120
GGAGAAATGG	CAGAAAAACG	TCCAAATGGA	CATCTTCTTG	GGACATTTAA	AGTTGAATTT	180
ATAAATGCCT	TATACGAGAT	TACAGATGAA	GATGTAAAGG	AATTCAAAG	AGTGAAGTAA	240

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCGCTCTGGT	CGAAAAGAAG	GGATAGGATT	CGAACGAGGA	ACTTGCCAGA	GAAGTGGCTG	60
ATATCATTTA	CTACACCGTG	CGCAATCGTA	GCTATTAATC	ATATTGACCT	TACCAAGACT	120
GTCTTTGAGA	AAGACAAAAC	CGCAGCCGTT	AATTACCAAC	ATAAACATAA	TTTGAAGGA	180
TTCTTGAAGG	GAAAGTAG					198

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GGAGGCTGGT	CTATGAAGTG	CTTGTTATGT	GGGCAGACTA	TGAAGACTGT	TTTAACTTTT	60
AGTAGTCTCT	TACTTCTGAG	GAATAATGAC	TCTTGTCTTT	G TTCAGACTG	TGATTCTACT	120
TTTGAAAGAA	TTGGGGAAGA	GAAGTGTCCA	AATTGTATGA	AAACAGAGTT	GTCAACAAAG	180
TGTCAAGATT	GTCAACTTTG	GTGTAAAGAA	GGAGTTGAAG	TCAGTCATAG	AGCGATTTTT	240
ACTTACAATC	AAGCTATGAA	GGATTTTTTC	AGTCGGTATA	AGTTTGATGG	AGACTTCCTG	300
TTAAGAAAAA	TTTTCGCTTC	ATTTTAAAGT	GAGGAGTTGA	AAAAGTACAA	AGAGTATCAA	360
TTTGTTGTAA	TTCCCTAAG	TCCTGATAGA	TATGCTAACA	GAGGATTTAA	TCAGGTTGAG	420
GGCTTGGTAG	AGGCAGCAGG	CTTTGAGTAT	CTGGATTTAT	TAGAGAAAAG	AGAAGAGAGA	480
GCCAGTTCTT	CTAAAAATCG	TTCAGAGCGC	TTGGGGACAG	AACTTCCTTT	CTTTATTAAA	540
AGTGGAGTCA	CTATTCCTAA	AAAAATCTTA	CTTATAGATG	ATATCTATAC	TACAGGAGCA	600
ACTATAAATC	GTGTTAAGAA	ACTGTTGGAA	GAAGCTGGTG	CTAAGGATGT	AAAAACATTT	660
TCCCTTGTA	GATGA					675

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1017 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TATTCATGGT	CATGGTCGTC	AAGCTGGCAA	ACTCTTGCGA	GAAGCCCGTC	AGAACTAGCC	60
CAGTTACTAA	GGACAAAACC	TCAACATATC	TTTTTCACTT	CTGGTGGGAC	TGAAGGCAAT	120
AATACTACCA	TCATTGGCTA	CTGTCTTCGT	CACCAAGAAC	AAGGAAAACA	TATCATCACA	180
ACTGCCATCG	AGCACCATGC	TGTCCCTGAA	ACAATTGATT	ACTTGGTTCA	ACACTTTGGG	240
TTTGAAGCAA	CCATTATCCA	GCCAGAAAAT	CAAGAAATCA	CAGCCCAGCA	AATTCAAAAG	300
GCTTTACGTG	ACGATACGAT	TTTGGTTTCT	ACTATGTTTG	CCAATAATGA	GACAGGAAAC	360
CTACTTCCCA	TCGCTGAAAT	TGGCCAAATA	CTCAAGCAAC	ACCCTGCTGC	CTATCATGTT	420
GATGCAGTTC	AGGCTATTGG	TAAAATCCCA	ATTTCATTCAG	AAGAATTGGG	CATTGATTTT	480
CTCACTGCTT	CTGCCCACAA	ATTCCATGGT	CCTAAGGGAA	TCGGTTTTCT	CTACGCATCT	540
AGCATGGACT	TTGATTCCCTA	TCTACATGGC	GGAGACCAGG	AACAGAAAAA	ACGTGCAGGA	600
ACTGAAAATC	TGCCTGCCAT	CGTAGGCATG	GTTGCAGCCC	TAAAAGAAGA	CCTAGAAAAA	660
CAAGAAGAAC	ATTTTCAACA	TGTACAAAAT	CTAGAAACTG	CCTTTCTGGC	AGAGCTGGAG	720
GGCATTTCAGT	ATTACTTGAA	TAGAGGAAAA	CATCATCTCC	CTTATGTTCT	CAATATTGGA	780
TTTCCTGGTC	AGAAAAATGA	CCTCTTACTC	CTTCGGCTAG	ATTTAGCTGG	AATTTCATC	840
TCTACTGGCT	CAGCCTGTAC	TGCAGGCGTT	GTCCAATCCA	GCCATGTTCT	TGAAGCCATG	900
TATGGCGCAA	ATTCAGAACG	CTTGAAGGAA	TCCCTTCGCA	TCAGTTTGTG	GCCACAAAAT	960
ACCGTTGAAG	ACCTACAAAC	CCTCGCAAAA	ACCTTAAAAG	AAATTATCGG	AGGTTAG	1017

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATACGATGGT	CATTGATTTG	TACCATGATT	TACTTTCAAA	ATGTTAGTAA	GTTGTATGGT	60
GATAAAGACG	CCTTGAGTAA	TCTCAATTTG	CAGATTGAAA	ATGGAGAGAT	TATGGGCTTG	120
ATTGGTCATA	ATGGGGCTGG	AAAATCGACC	ACTATAAAAT	CCCTAGTCAG	TATCATTTC	180
CCCAGCAGTG	GTCGTATTTT	GGTAGACGGT	CAGGAGTTAT	CGGAAAATCG	CTTGGCTATT	240
AAACGAAAGA	TTGGCTACGT	AGCAGACTCG	CCTGACTTAT	TTTTACGCTT	AACGGCCAAT	300
GAATTTTGGG	AATTGATCGC	CTCATCCTAT	GATCTGAGTA	GATCTGACTT	GGAGGCTAGT	360
CTAGCTAGGC	TATTGAACGT	TTTTGATTTT	GCTGAAAATC	GCTATCAGGT	TATTGAAACT	420
CTTTCTCACG	GAATGCGTCA	GAAAGTCTTT	GTCATCGGAG	CACTCTTGTC	TGATCCCGAT	480
ATTTGGGTCT	TGGATGAACC	CTTGACTGGT	TTGGATCCCC	AGGCTGCCTT	TGATTTGAAA	540
CAGATGATGA	ATGAACATGC	ACTAAAAGGG	AAGACAGTCT	TGTTTTCAAC	TCATGTCCTA	600
GAGGTGGCAG	AGCAAGTCTG	TGATCGGATT	GCCATTTTGA	CAAAGGGGCA	TCTGATTTAT	660
TGTGGTANTG	TAAAGGACTT	GAGAAAAGAT	TACCCAGACC	AGTCTTTGGA	AAGTATCTAC	720
CTTAGTCTTG	CTGGTAGAAA	AGAGGAGGTT	GCGGATGCGT	CTCAAGGTCA	TTAA	774

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GGCTGCAGGT	CTGGTGACAG	AAACTCCTGT	TATCATCACC	AACCAAGATG	CTTATACAGC	60
GACTATTACT	GGAACCTTATC	CGACAACGAT	CCAAGCTGGA	GCATCTCTCA	TGGTCGCTAC	120
ACGAATCTAA	TACTCTTCGA	AAATCTCTTC	AAACCACGTC	AGCTCTATCT	GCAACCTCAA	180
AATAGTGTTT	TGAGCAACCT	GTGGCTAGCT	TCCTAG			216

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TCAACCACTT	TGGGCAATAG	TGAGAACTGC	CCCGTGCTTT	TTTATTTTGA	GAAAATATGG	60
AGTTTGTTCGT	TGAAATTACT	TGATTGTATT	TTGGACTATC	AAGAAAGATT	CAATGGAAAA	120
ACATGTCAAG	TATCAACGAA	TTATAAGTAT	TTAGAGATTT	TCAAAGTGAA	TTTTTGTTTG	180
ACTGATTTAC	ATCATTTTATT	TGACTTATAC	AAAATCACAC	GAGATTATGC	TAGTCAAACA	240
AAACCTGCTA	TTCAAGCTGG	TGTTTTTATT	TTAGAAGATT	TTAGAAATAT	CCTATGTACA	300
ATGATGTAA						309

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1512 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTACTTTTTC	CTTTTCCTCA	TTATAAAAGA	GTAAATAGCT	ATAATCTCCC	TTTTCATGCA	60
CTTCCACATC	ATAAAGCTGG	TCAATCACTT	CCAACCTGCTC	ATCAAACCTGA	ATCGTATTTT	120
GCATCCGAAT	CTTCACATCA	AGTCCTCTTT	CTTGTCCTTT	GTCTTACTAT	NTTACCAAAA	180
AGAGCAGGAT	TTTGCTATAA	TGGTCATATG	AACGAAAAAG	TATTCCGTGA	CCCAGTTCAC	240
AACTACATCC	ATGTCAATAA	TCAAATCATC	TATGACTTGA	TTAATACAAA	AGAATTTTCAG	300
CGTTTGCGCC	GGATCAAACA	ACTGGGAACT	TCCAGTTATA	CCTTCCACGG	TGGAGAACAC	360
AGTCGCTTCT	CTCACTGTCT	AGGAGTCTAT	GAAATTGCAC	GACGCATCAC	AGAGATTTTC	420
GAAGAAAAAT	ATCCTGAGGA	ATGGAATCCT	GCCGAGTCTC	TCTTGACCAT	GACCGCTGCT	480
CTCCTACATG	ACCTTGGGCA	TGGCGCCTAC	TCCCATACTT	TTGAACATCT	CTTTGATACA	540
GACCATGAAG	CCATTACTCA	GGAGATTATT	CAAAATCCTG	AGACAGAGAT	TCACCAAGTC	600
TTGCTACAAG	TAGCGCCCGA	TTTTCCAGAA	AAAGTTGCCA	GTGTCATAGA	CCATACCTAT	660
CCTAATAAGC	AGGTCGTGCA	GCTCATTCTT	AGTCAGATTG	ACGCAGATCG	CATGGACTAT	720
CTCTTGCGCG	ACTCCTATTT	TACAGGAGCA	TCCTATGGGG	AATTTGACCT	GACTCGCATC	780
CTCCGAGTCA	TTCGTCCTGT	CGAAAAATGGT	ATCGCCTTTC	AGCGCAATGG	CATGCACGCC	840
ATCGAAGACT	ACGTCCCTCAG	TCGCTACCAG	ATGTACATGC	AGGTTTATTT	CCACCCAGCA	900
ACACGCGCCA	TGGAAGTTCT	CCTACAGAA	CTTCTCAAGC	GCGCCAAGGA	ACTCTACCCT	960

GAGGACAAGA	ATTTCTTTGC	ACGAACTTCC	CCACATCTCC	TGCCTTTCTT	CGAAAAAAT	1020
GTGACCTTGA	CTGACTATCT	GGCTCTGGAT	GATGGCGTGA	TGAATACCTA	CTTCCAGCTT	1080
TGGATGACTA	GTCCTGACAA	AATTCTTGCA	GATTTATCTC	AACGCTTTGT	CAACCGCAAG	1140
GTCTTTAAAT	CCATTACCTT	TTCACAAGAG	GACCAAGATC	AACTTACTAG	CATGAGAAAA	1200
TTGGTTGAGG	ACATCGGCTT	TGATCCCGAC	TACTATACTG	CCATTCATAA	GAACCTTGAC	1260
CTCCCTTATG	ATATCTATCG	TCCCGAATCT	CAAAATCCAC	GGACACAGAT	TGAGATTTTA	1320
CAAAAAATG	GAGAACTGGC	CGAACTCTCT	AGCCTGTCTC	CTATCGTCCA	ATCCCTTGCT	1380
GGCAGTCGCC	ACGAGAGATA	TCGCTTTTAT	TTTCCAAAAG	AAATGTTGGA	CCAAAACAGC	1440
ATCTTTGCAA	GCATTACCCA	GCAATTTTTA	CACCTGATTG	AGAACGATCA	TTTTACCCCA	1500
AATAAAAACT	AG					1512

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...510
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CACGCTTTTC	CTGATGGGGT	GACGATTGAT	GCTCAATTTT	CAACATTGAA	TGGGCGTCCC	60
CTAACAGAAG	CTACAGTCGG	AGATGATTTA	TATGCTACCG	AGACTGAGTC	TCCAACCCAA	120
ACCATTAAAAG	TCGGAAAAACA	GCAGATGAAT	GGCTCGACCC	TGCTCAATTA	TGCTCGTTTC	180
CGTGATGATG	ATGAGGCGGA	TTACGGCCGT	ACAAAAAGAC	AGCAACAAGT	TTTAACAGCA	240
ATTTTAGAGC	AAATTAAAGA	TCCCACTAAA	CTTTTCACTG	GTTCTGAAGC	TCTTGAAAG	300
GTTTTGCTA	TGACCTCAAC	CAACGTACCT	TATACTTTCC	TCCTAACAAA	CGGTTTATCT	360
GTTTGGATG	GAGCAAAAAA	TGGTATTGAA	AAATTGACGA	TTCCAGAACT	GGGTGACTGG	420
GTAGACGCTT	ATGATGTTTA	TGGAGGCTTG	GGCTTGCTGG	TTGATCAAAA	CAAATATCAA	480
ACCAAGCTCG	CTCAAATGGG	CTTGAGATAA				510

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

GGAGCTTTTC CAAGTAGAGA GGCAATTTCT CTATTTGATT TTCCTTCTTT TTTCCCATCT      60
TCTAATCTTA ACATTTGGCT ATCTACCCAA CCTATCTTGG CACAGATTTA TGCCTTCCCC      120
TTAGCTACTG CAACTATGGC TGCTATTTTA AGTTTCTTAT TTTTTTTCCT ATCTTTTTTAC      180
AAGAAAAATA AACAAATACG GTTTTACTCT GGCATTTTGC TCTTACTATC GCTCATATTA      240
CTATTATTCG GAACAGATAA AACCTTTTCT TCTGCATCAA ATAAGACTAA AACCTTAAAA      300
TTAGTAACTT GGAACGTCGC TAATCAAATA GAAGCACAAC ATATTGAGCG AATTTTTTAGC      360
CATTTTGACG CCGATATGGC TATATTCCCT GAACTAGCTA CCAATATCAG AGGTGAGCAA      420
GAAACCAGA GAATCAAACCT ATTGTTTCAT CAAGTTGGAC TTTCTATGGC CAACTATGAT      480
ATTTTCACTT CTCCACCTAC CAATAGTGGA ATAGCTCCTG TGACTGTGAT TGTCAAGAAA      540
AGTTATGGTT TCTATACAGA AGCTAAAACT TTTCATACAA CACGGTTCGG GACAATTGTA      600
TTACATTCGA GAAAAACAAA TATACCAGAT ATCATTGCCT TGCATACTGC TCCTCCTCTG      660
CCAGGTTTAA TGGAAATCTG GAAGCAAGAC TTAAACATCA TTCATAATCA ATTGGCTTCA      720
AAATATCCAA AGGCTATTAT TGCAGGTGAT TTTAATGCAA CTATGCGTCA TGGAGCACTT      780
GCAAAAAATA GCTCTCATAG GGACGCATTA AATGCACTGC CACCTTTTGA AAGAGGAACT      840
TGGAATAGCC AAAGTCCAAA ACTTTTTAAT GCAACAATAG ATCATATTTT ATTGCCTAAA      900
AACCCTACT ATGTTAAAGA TTTAGACATT GTAAGTTTTC AAAACTCTGA TCATAGATGT      960
ATTTTACAG AAATCACATT TTAA                                     984
  
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

TTTGACTTTC CTGATAGAGT TGTTACATC TTATTTCAAT CTACTATATT TTATAGAACA      60
GACTACTCTG AAAGTAGTTT CAGACCTCTT ATGATTTTCGT ATCAGCTTGA ATGTCATCAA      120
AAAAAGATAG CAGGCTTGAA AACCTGCTAT CTCCTTCTAT TTTTACAAAA TCAAATGTTT      180
AGAATTCTTC TCTTATTGTT CTCTCTTTTT CCCTAG                                     216
  
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(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1308
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ATGCAATTTTC	CAGAAGGATT	TGTTGAAAAA	TATAAAGAGA	TACTAGGAGA	TGAGGCAAGA	60
GATTTTCTTG	CCTCTTTTGA	GGAAGAAGCG	GTTTCGGCCT	TTCGGGTCAA	TCCCTTANAA	120
GAAGAACAAC	TTTCCTTTTC	TGATGCCATT	ACTCAAACCC	CTTGGGGCCA	CTATGGGAAA	180
GTTTCAGGGA	NATCGCCTGA	NCATGCTACA	GGTTTAGTTT	ATNCGCAAGA	AACTGCTGCT	240
CAAATGGTGG	CTCAAGTAGC	CCAACCCAGT	CCTGGTATGA	AGGTCTTGAA	ATTGGCTGCT	300
GCACCGGGGG	GCAAATCAAC	TCAACTGGCA	GCCTATCTAG	CAGGGGAGGG	GCTACTTGTT	360
TCCAATGAAA	TTTCAAGCAA	ACGGGCTAAG	ATTTTGGTTG	AAAACATGGA	GCGTTTGGGA	420
GCGACAAATG	TCGTGGTGAC	CAATGAATCT	GCCGACCGCT	TGGTCAAGGT	CTTTAAAGGC	480
TATTTTGACT	TAATCGTTCT	TGATGCCCTT	TGCTCTGGTG	AAGGAATGTT	TCGTAAGCAA	540
CCTGATGCTA	TGGACTATTG	GAGCTTAGAT	TATCCGAGTC	AATGTGCTAG	CTTGCAAAGA	600
GAAATTCTCT	GGGAGGATGC	AGTGACCATG	TTAGCTGAAG	GTGGTCATCT	GGTTTATTCTG	660
ACCTGTACCT	GGGCACCCGA	GGAAAACGAA	GAGATTGTCA	ATTGGTTGCT	GGAAGAGTAT	720
GATTTTGACT	TGTTGCCAGT	AGAGCATATC	AATGGAATGG	TAGCTGGTAT	TGACCTGCCA	780
GAAACGGCTC	GGATGTATCC	TCATCAGTTT	AAGGGAGAGG	GTCAGTTTGT	TGCCCATCTA	840
CAGTTTAAGG	GTAACAATCC	AGCTCCTAAA	TTTAAGGCAA	GTAAGAGTAA	CCTCAGCCGT	900
GAACAAGTTG	CCTTGTGGCA	GGAATTTGCC	CAAAACCATT	TGAAGGTCAA	TCTACCGGGT	960
ATCTTGACAG	CTTTTGGAGA	CCAGCTTTAT	CTCTTGCCAG	AACTTTTGCC	AGATTTAGGG	1020
AAGCTCAAGA	TTGCTCGCAA	TGGACTGCAT	CTGGGCACCT	TTAAGAAGAA	ACGCTTTGAG	1080
CCCAGTTTCG	CTCTTGTTT	AGCCTTGAAA	CCGAGTCAGG	TCGAACAGTC	GGTTGAAATT	1140
GGCCAAGAAG	CGTTTGTCAA	GTATGCGGCT	GGAGAAATCG	TTCAGCTGGC	AGAAAGTCTG	1200
CCAAATGGTT	GGTACCAAGT	TTTGGTTAAA	GGCAATGGCT	TGGGCTTTGC	AAAGGTTACT	1260
GGAAATGTTT	TGAAAAATTA	TTTTCCAAAA	GGCCTCAGAT	TCAAATGA		1308

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CTATCGTTTC	CAATAGTTAT	CCCCCGCTAC	CAGGCAGGTT	ACCTACGCGT	TACTCACCCG	60
TTCGCAACTC	ATCCAGAGAA	GCAAGCTCCT	CCTTCAGCGT	TCTACTTGCA	TGTATTAGGC	120
ACGCCGCCAG	CGTTCGTCCT	GAGCCAGGAT	CAAACCTCTCA	TTAAAAGTTT	GAGTTCTCAC	180
TCATTTCTGT	CACTGACAGA	TTTATTGTTT	TTTTCATTTGT	TCAGTACTAC	AACTTATGTT	240
GTAGCGCCCT	GCACATTGGT	TCGTCTTGTT	CAGTTTTCAA	AGGTCCTTGT	CACCTTGCTTC	300
TCTCAAGCGA	CAACTATATT	AGTATATCAC	AGCCACTTTC	ACTTGTCAAC	ACTTTTTTTGA	360

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GCGCATTTGT	TTCGTACCTC	GTTAATATTT	TTTAGAAAAG	ATATCAAGGT	TTCTGGTGGG	60
AAAACATCGT	TAAAGTCAGG	TATGTTTG TG	CTTATAAAAC	TTACTAAATC	CCGTGCGATT	120
TCATTTTGGA	GTGAATTAGG	CAGGTTTTCA	ATAATCGTGC	GTAAATCTCC	AAACTCTAGA	180
TAA						183

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 768 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AAGGAGCTTC	CTAGTATGGG	AACATTTTCA	GTCAGACACC	TAGACTTATT	TTACGGGGAT	60
TTTCAAGCCT	TAAAAAATAT	TTCGATTCAA	TTACCAGAAA	GACAGATTAC	TGCCTTGATA	120
GGCCCATCTG	GTTGTGGTAA	ATCAACTTTT	CTAAAAACCC	TTAATCGGAT	GAACGATTTG	180
GTTCTTCTT	GCCATATTGA	AGGCCAAGTC	CTCTTAGATG	AGCAAGATAT	TTATAGTAGC	240
AAATTCAACC	TTAATCAGCT	ACGTAAGCGT	GTAGGGATGG	TTTTTCAACA	GCCTAATCCC	300
TTTGCCATGT	CTATCTATGA	TAACGTGGCT	TATGGCCCAA	GGACACATGG	TATTCGAGAC	360
AAAAACAAT	TAGATGCCTT	AGTGGAGAAA	TCTTTAAAAG	GGGCAGCCAT	TTGGGAAGAA	420
GTCAAAGATG	ATCTTAAAAA	GAGTGCCATG	TCCTTATCTG	GCGGTCAGCA	GCAACGCCTT	480
TGCATTGCGC	GAGCTTTAGC	AGTAGAACCT	GATATTCTGT	TAATGGATGA	GCCGACTTCA	540
GCCTTAGACC	CTATCTCCAC	TTTAAAAATT	GAAGACCTCA	TTCAGCAACT	AAAAAAGGAT	600
TATACGATTA	TCATTGTAC	CCATAACATG	CAACAAGCTT	CACGTATTTT	AGATAAAACT	660
GCTTTTTTCT	TAACAGGAGA	AATTTGCGAA	TTTGGAGATA	CCGTTGACGT	GTTTACCAAT	720
CCAAAAGATC	AGCGCACAGA	AGACTATATT	TCAGGACGGT	TCGGATAA		768

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TTTAACATTC	CTAAAAATAAT	TCCTGATAGA	CCAAAATCTG	CATCTGAGAA	AGTTGATCCT	60
TGGAAACCGA	GTCCTCCCAA	AACTGGCATT	AAAAAGACTG	GAAGAAAACT	GATTAAAAATA	120
CCTTGTAATA	ATGCTCCAAT	AGTGGCTCCA	CGAACACCAC	CAGATGCATT	CCCAATGACA	180
CCTGCAGTCG	CTCCACAGAA	GAAATGA				207

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

AAGCCGATTC	CCTCACCGTT	AATTCCCATG	CGCTTGATTT	TTAATGGTAT	TTTTTGTTTC	60
ACTTTCAGAT	TCATACCCCT	ATCTTATCAC	ATTTTGAGTT	ATAATAGAGC	TATGAAAATC	120
ACAAAACCTG	AAAAGAAAAA	AAGACTCTAT	CTGATGGAGC	TTGATAATGG	CGACAAATGC	180
TATATCACCG	AAGATACAAAT	TGTTTCGTTTT	ATGTTATCGA	GAGATAAGGT	GATAAGCGAA	240
GAGGAATTGA	AAGAGATTCA	AGACTTTGCT	CAATTTTCTT	ATGGTAAGAA	TCTGGCCCTC	300
TACCACTTAT	CCTTTAAAGC	ACGCACTGAA	AAAGAAGTCA	GAGAATATCT	GAAAAAATAC	360
GATATTGATA	AAAACATCGT	TTCTCAAGTT	ATTGCTAATC	TTAAAGAAGA	TAAGTGGATT	420
AATGATGGTC	AGTACGCTTA	TGCTATCATC	AATACCAATC	AACTTTCAGG	AGACAAGGGT	480
CCTTATGTGC	TGACTCAGAA	ACTAGCTCAA	AAAGGGATTT	CAAAATCTAC	TATAGAAGAG	540
AACTTGAAAG	AATTTGATTT	TTCTGAAGTT	GCTCAACGTG	TAGCTAATAA	ACTATTGAAA	600
AAATATGAGG	GAAAACCTCC	AGCTCGTGCC	CTGCAAGATA	AGATTATCCA	GAACCTGACT	660
AACAAGGGCT	TCTCTTATTC	TGATGCTAAA	ATTGCCTTTG	ACGACTTAGA	TAGCCAAGTT	720
GACCAAGAAA	CGACTCAAGA	ACTCATCTTC	AAGGAACTTG	ATAAGCAATA	TACTAAGTAT	780
GCTCGAAAGT	ATGAAGGATA	CGAACTGAAG	CAGCGTTTAA	CTCAAGTTTT	AGCACGAAAG	840
GGCTACGATT	TTTCGGATAT	AGCAAGCGCT	CTTAGAGAAT	ATCTTTAA		888

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GCAATAGTTC	CTAGAAAGGC	TAGGAAAAGG	AGGAAAGGAT	GGCTTGCTAA	ATCTACGGCT	60
AAACGTTTGA	GCGTCTGGTT	TACAGTTTGT	CGTTTCATTC	TAGTCCTCCT	TTCCATGTTG	120
GGATGCATTG	ATTCACAAT	AGACTTGGCT	GGATTTCATC	AAGTCATCGT	GCTTGCCAAC	180
AGCTAG						186

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CCCGGCTCTC	CTATTTTCAA	AAAATATAGG	AGAATTAAAA	TGGCAGAAAT	TACAGCTAAA	60
CTTGTA AAAAG	AGTTGCGTGA	AAAATCTGGT	GCCGGTGTTA	TGGACGCTAA	AAAAGCGCTT	120
G TAGAAACAG	ACGGTGACAT	CGAAAAAGCG	ATTGAATTGC	TTCGTGAAAA	AGGTATGGCT	180
AAGGCAGCTA	AGAAAAGCTGA	CCGTGTTGCT	GCAGAAGGTT	TGACTGGTGT	TTATGTTAAC	240
GGTAATGTTG	CAGCAGTTAT	TGAAGTAAAC	GCTGAAACTG	ACTTCGTTGC	AAAAAACGCT	300
CAATTCGTTG	AATTGGTAAA	TACTACAGCT	AAAGTCATTG	CTGAAGGAAA	ACCTGCTAAC	360
AATGAAGAAG	CTCTTGCTTT	GATAATGCCT	TCAGGTGAAA	CTCTTGAAAGC	TGCATACGTA	420
TCTGCAACAG	CAACTATCGG	AGAGAAAATC	TCATTCCGTC	GCTTTGCATT	GATTGAAAAA	480
ACAGACGCAC	AACACTTTGG	AGCATACCAA	CATAACGGTG	GACGTATCGG	TGTTATTTCA	540
GTTGTTGAAG	GTGGAGACGA	AGCACTTGCT	AAACAATTGT	CAATGCACAT	CGCAGCGATG	600
AAACCAACAG	TTCTTTCTTA	CAAAGAATTG	GATGAGCAAT	TCGTTAAAGA	TGAGTTGGCA	660
CAATTGAATC	ACGTTATCGA	CCAAGACAAC	GAAAGCCGTG	CAATGGTTAA	TAAACCAGCT	720
CTTCCACACT	TGAAGTATGG	ATCAAAAAGCT	CAATTAAC TG	ATGATGTTAT	TGCTCAAGCT	780
GAAGCTGACA	TCAAAGCTGA	ATTGGCTGCA	GAAGGCAAAC	CAGAAAAAAT	CTGGGACAAA	840
ATTATTCCAG	G TAAAAATGGA	TCGCTTCATG	CTTGATAACA	CTAAAAGTTGA	CCAAGCTTAC	900
ACACTTCTTG	CACAAGTTTA	CATCATGGAT	GACAGCAAGA	CAGTTGAAGC	ATACCTTGAA	960
TCAGTTAACG	CTTCGGTAGT	TGAGTTTGCT	CGCTTTGAAG	TTGGTGAAGG	TATCGAGAAA	1020
GCTGCAAACG	ACTTCGAAGC	TGAAGTTGCA	GCTACAATGG	CAGCAGCCTT	GAATAACTAA	1080

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGGATGTTGT TTAGGCCGAC TCCTCCGGTT ACCATTACGG AAACCTTGTTG GATCGGTGCC	60
TTGACTGCAG AGATATATGC TGGACTGAGA GTACTACCTG GGAAGAGTTT GATGATTTCA	120
CTACCGGCTT CAAGTGCAGT CGTGATCTCT GTGAGGGTAA TACAGCCTGG AATGTACGGT	180
GTGCTGTAG	189

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 600 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TCCTGTACTC CTCCCCACCT CCCCCGTCCC CACTCTGGCG CGAGGGGCGC GACCCGCCGC	60
ACCCCCCAGC GCAGCCGGCC GCAGCCTCCC CAGATCCGCG GCAACCAAAC GGNGCAGCNG	120
GCCACCACAC ACGCACCCCC CCCC GCCCCG GCCNCGCC ACCCGCCACA ACCCAGAGCG	180
CGCCACGCAG CCCAGCACAG ACAGCAAGGC GACGAGCCAC CCCC GCCCCG CACGGGACCC	240
CCGGGCCCCC GCCCCGCGAC CCCCNGCCCC CCACAGGGAG AGAAAACCAA GCCACCCCGA	300
CCCACCAACG CACCACCGNG GTCCAGCCTC ACCAANGANA TTCCAACNAA GTCAATAAAG	360
TTCAGAAGGA AGGGAATTNN GGANNGGTCA GGAAGAGCCA CTTTGTGACAA TTTTAACCAA	420
TGTAGTAAAC CTCACCCACT CCCAAGTATC AGGAATATCA TAAGGAACAT CAATTTCTTG	480
AGTACTTCCA TCAGCAAAC TCCCATATG TTTCTTATGT GCTTCAAGTA TATAAAAAGG	540
CGTAAAAATA CGCCTATAGA TAATGGGGTT GAAATAGGTT TATTGTTGAT GAGATTGTAG	600

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GTATTCAC	CTTGGCTG	TT AAGAAG	CAAT TTCA	ATAGTG	AGCGAAG	CAA GAGCA	CTCCT	60
AGAGCAGC	AG GCAAAT	CCCAT GACC	ACCAGA	CCCACA	AGGA CTGG	CAAGAT	ACTAA	120
ATTGAGGA	AAGATGCC	CG TGGT	AAAAGC	GGAAAG	TCAA AGTAC	ATCAG	CACAA	180
ATGGCTGA	TAAATGCA	AT GGT	CGAAAG	T CGACG	TGTGT	TTGTC	CATAAC	240
AATTTTCT	AT AA					AGGTTC	CTCCTC	252

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACATTCACTC	CAAACAAA	AGC TGCT	GAAATC	ATCTTG	AAAAG	TTTTGA	ACTC	AGCTGT	AGCT	60
AACGCTGAAA	ACAAC	TTTGG	TTTGGATA	AAA GCTA	ACTTGG	TAGTAT	CTGA	AGCAT	TCGCA	120
AACGAAGGAC	CAACTAT	GAA ACGT	TTCCGT	CCACGT	GCGA	AAGGTT	CAGC	TTCACCA	ATC	180

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GTAATAACTC	CTTGCCATCC	ACCCACCAAA	AATCCTGATA	AAATAGCTGG	TGTACTCCAA	60
GGCAATGTTA	CCCCTGAGAA	TGGCTGCATG	AAACCTGTTG	CAATAGCTCC	ATATACTATC	120
ACAGCTGCAA	GTACAGGAAC	AAGAATGAAA	GGTACAAACA	TAACTGGATT	CATGACAATC	180
GGAAATCCAA	ATACAACTGG	CTCATTTACG	TTAAATATTG	CTGGAAAAGC	TGCAACTTTT	240
CCTAAGGCTT	GGTATTGTTT	TGATTTTGCT	GCAAAAAGCA	TGGCAACTAC	AAGACCAAAC	300
GTAATCCCTG	AACCTGATAG	AATTAAAAAT	GAATCTAAAA	ATTGTTGA		348

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TTTCTAGCTC	CAGCTGGAAT	TTCAGCCAAT	GAAGTAAAGC	AAGATGTAAC	ATCTGAAGTG	60
GTAATAGGTG	TGCTAGATTC	TAAGGAGGAA	TTGAAAGAGT	CAGAAAATGA	TGCTCCAAAA	120

CTAGAAACTC	CTCTTAGAGA	GGAGCCAAGA	CTAGCTCCTC	AAACGCTTCC	GGAAGCAAGT	180
GAAGTTCTTG	AAAACAAAAG	GGAAGAGTCA	AAAGTAGAGA	TAACAGAGCC	AGCTCAAGCG	240
GATGATATCC	GCAAGGTTGT	TGGGGAATTA	GCCAAGGATA	TAAGTATTAC	TAAGTTGTAT	300
ATGACAGGTC	ATTCTCTTGG	AGGCTACCTA	GCTCAGATTG	CAGCGGTTGA	AGATTACCAA	360
AAATATCCTG	ATTTTATATA	CCATGTATTG	AGGAAAGTGA	CAACTTTCAG	TGCTCCTAAA	420
GTCATTACTT	CCAGAACTGT	TTGGGATGCT	AAGAATGGTT	TCTGA		465

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...537
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAACGAGCTC	CACCAGCAGC	CTTGACTCCC	ATATCAGATC	CAACTGTTTC	ACGCATTAAT	60
CTAACATCTG	CTATCGTAGC	ACCACCAGTT	GAAAAGCCAG	TAGATGTTTT	AACAAAGTCA	120
GCCCCAGCTT	TTTGGGCCAA	TTGGCAAACA	ACAAATTTTT	CTTGGTCTGT	CAGAAGGCAA	180
GCTTCAATAA	TGACTTTCAC	TAACTTATCA	CCACTTGCTT	CCACTACTGC	GCGAATATCT	240
GACTCAACCA	AGGCTAAATT	ACCTGATTTG	AGAGCTCCAA	CATTGATCAC	CATATCAATC	300
TCATCTGCAC	CATTTTGGAT	AGCTTCTTTT	GTCTCAAATG	CTTTCACGGC	TGAAGTTGTT	360
GCTCCCAAAG	GGAAACCTAC	TACTGTGCAA	ACCTTAACAT	CTGTGCCTTC	AAGTCCTTTT	420
TTAGCATGTT	CAACCCAGGT	CGGATTAAAC	CAAAACTGCG	CAAAGTCATA	TTCTCTAGCC	480
TCAGACAACA	AACTATCAAT	TTGTTTTTTC	TGTGCATCTT	GTTTGCCTAG	CGTATGA	537

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TTGTTTTATC CTATTTCTAT TTCATTTTCAC TATATAATTG CTATTGTTTT CTTTTTCATG	60
ATTTTAATCT TACTGTACAG ATTTGATACA GTAAACTCCT TTCTAGCTTT ATACTTTATC	120
ATTTCTAACT TAATTATAGT CTTATTTTTA ATAAAGTTCA ATTATTTATA TGTAATTC	180
CTCATCAGTA AAAAATAA	198

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

TTGATTTATC CTGTTCTTAT TTCATTTTAC TATAGTTCTA TGAATTATGA AGGAAGTAAA	60
CAACTAACTG ATGCACGATT TAAATGTCTT GTTGGTGTTC AACGCACGAC TTTTGAAGAG	120
ATGTTAGCTG TATTAAAAAC AGCTTATCAA CTTAAACACG CAAAAGGTGG ACGAAAACCT	180
AAATTAAGCC TAGAAGACCT TCTTATGGCC ACTCTTCACT ATGTGCGAGA ATATCGAACT	240
TATGAAGAAA TTGCGGCTGA TTTTGGTATC CACGAAAGCA ACTTACTCCG TCGGAGCCAA	300
TGGGTGAAG TAACTCTTGT TCAAAGTGGT GTTACGATTT CAAGAACTCC TCTCAGCTCT	360
GAGGACACGG TAATGATTAT TGATGCGACG GAAGTATAA	399

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AAAGGCTATC	CCATGCATAT	TCACTATAAC	ACAAATCAAA	CAACTTTACC	ACTAGAAATC	60
AGTTCCTTCT	TGCCACAAGA	TCATCTCGTT	TTTACTATTG	AAAAAGTGGT	GAATACCTTG	120
GAGGATTGTC	ACTTCCACGC	CTTCTATCAT	GCCTTTGATC	GCCCGTCTTA	TCACCCCTAAA	180
ATGCTTGTAT	CTACTCTTCT	ATTTGCCTAT	TCACAAGGGA	TTTCTCTG	TCGAAAAATT	240
GAAAAATGGA	AGAGTTAG					258

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

AAAGGCTATC	CCATGCATAT	TCACTATAAC	ACAAATCAAA	CAACTTTACC	ACTAGAAATC	60
AATTCTTTCT	TGCCGCAAGA	CCATCTCGTC	TTTACTATTG	AAAAAGTGGT	GAATACCGAT	120
GAAAAGGAGG	TAAACCATCT	GATTAAATAT	GCCATGTTTG	ATAAGGAACA	AAAGAGAGGC	180
TATAAACAGT	CAGCTAGAAA	CTTAGCGAAT	TGGCACTATA	ATGACAAGGA	GGATAGCTAT	240
ACACATCCTG	ATGGCTGGTA	TTATCGTTTT	CACCATACCA	AATATCAGAA	AACACAGACA	300
GACTTTCAAC	AAGAAATCAA	GGTTTACTAC	GCCGACGAAC	CTGAATCAGC	CCCTCAAAAG	360
GGACTGTATA	TGAACGAACG	CTATCAAAAAC	TTGAAAGCTA	AAGAATGTCA	GGCGCTTTTA	420
TCTCCCCAAG	GTAGACAGAT	TTTCGCTCAA	CGCAAGATTG	ATGTGGAACC	TGTCCTTGGG	480
CAGATAAAGG	CTTCTTTGGG	TTACAAGAGA	TGTAATCTGA	GGGGCAAGTG	A	531

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

TTGTTGACTT	TGTCAGTTTT	ATCTACAACC	TCAAAACAGT	ATTTTGAAC	GTCTGCGCCT	60
AGCTTTCTAG	TTTGCTCTTT	GATTTTATT	GAGTATACCA	CTATTTTACT	CCCTCTGGCA	120
AGGGACTTTG	TCTATGTGGA	GGGATTGGGC	TCCTATGTGG	TGGAGCTTTT	CTGTTCTTTC	180
TGA						183

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TTATGTCTGT	TTTCTGTATG	TCTAGCATTT	CCCCGTCGCT	TGTTTGTTTT	TGCTGATGAT	60
AGCTTATCGG	CAAACTCTAA	AGTTGTATCT	GGTGAGGCTC	AGTTTGAGAA	TGGCTCATCA	120
GTGCGGTTTC	GAGATACGCA	AGTAAATATT	TTAAGCGATG	AAGTTCTTGA	GGTTGTCAAT	180
CCAGATGGAA	GTGTAGACAC	TATTGAACGA	CGTGCTGACG	GCGTCTATAT	CAATGGGGCA	240
TTTTATATGG	CTTATCAAAA	GAATGAAATC	GACCTAAATA	TATCTTTTAG	ATCATACGAT	300
CCTAATGTTT	GGAATTACGT	CAACACAATA	CATGGGAATA	AACAAGCTAA	CACATTCGCT	360
AACTTCATGA	CTGGTGCTGG	AATCAGTTAT	ATGATTGGTA	GGATAGGTGC	TTTATTGGGG	420
GGGCCATGGG	GTGCAATAAT	TGGTGGAGCA	TATTTTGGTA	TACAAGCTTA	TCAGTCTTAC	480
TTGGATTAC	AAAGCCCAT	TCCATACTAC	ATAACAAGTA	CTTATATCCA	TGTTGCTCAA	540
AGAAAATGGA	AGTTTATCAC	TGAATACTAT	AGAACTCAA	ACTATACTGG	GTATGTAAAA	600
ACCGTAACAA	CCTATGTGAA	TTTCTAA				627

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...396
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GCACGCCATC CTCTAGTCCT GTACTCCTCC CCACCTCCCC CGTCCCCACT CTGGCGCGAG	60
GGGCGCGACC CGCCGCACCC CCCAGCGCAG CCGGCCGCGAG CCTCCCCAGA TCCGCGGCAA	120
CCAAACGGNG CAGCNGGCCA CCACACACGC ACCCCCCCCC GCCCCGGCCC NCGCCACCC	180
GCCACAACCC AGAGCGCGCC ACGCAGCCCA GCACAGACAG CAAGGCGACG AGCCACCCCC	240
GCCCCGCACG GGACCCCCGG GCCCCCGCCC CGCGACCCCC NGCCCCCAC AGGGAGAGAA	300
AACCAAGCCA CCCCAGACCA CCAACGCACC ACCGNGGTCC AGCCTCACCA ANGANATTCC	360
AACNAAGTCA ATAAAGTTCA GAAGGAAGGG AATTNN	396

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CCAATCAATC CATACTTGCA ACATCGTTGC ACATCTTATT TAGGAGGTTT AGTAATGAAC	60
AAGAAACAAT GGCTAGGTCT TGGCCTAGTT GCAGTGGCAG CAGTTGGACT TGCTGCATGT	120
GGTAACCGCT CTTCTCGTAA CGCAGCTTCA TCTTCTGATG TGAAGACAAA AGCAGCAATC	180
GTCAGTGATA CTGGTGGTGT TGATGACAAA TCATTCAACC AATCAGCTTG GGAAGGTTTG	240
CAGGCTTGGG GTAAAGAACA CAATCTTTCA AAAGATAACG GTTTCACCTA CTTCGAATCA	300

ACAAGTGAAG	CTGACTACGC	TAACAACCTTG	CAACAAGCGG	CTGGAAGTTA	CAACCTAATC	360
TTTGGTGTG	GTTTTGCCCT	TCATAATGCA	GTTGAAGAAG	CAGCTAAAGA	ACACACTGAC	420
TTGAACTATG	TCTTGATTGA	TGATGTGATT	AAAGACCAAA	AGAATGTTGC	GAGCGTAACT	480
TTGCTGATA	ATGAGTCAGG	TTACCTTGCA	GGTGTGGCTG	CAGCAAAAAC	AACTAAGACA	540
AAACAAGTTG	GTTTTGTAGG	TGGTATCGAA	TCTGAAGTTA	TCTCTCGTTT	TGAAGCAGGA	600
TTCAAGGCTG	GTGTTGCGTC	AGTAGACCCA	TCTATCAAAG	TCCAAGTTGA	CTACGCTGGT	660
TCATTTGGTG	ATGCAGCTAA	AGGTAAAACA	ATTGCAGCCG	CACAATACGC	AGCCGGTGCA	720
GATATTGTTT	ACCAAGTAGC	TGGTGGTACA	GGTGCAGGTG	TCTTTGCAGA	GGCAAAATCT	780
CTCAACGAAA	GCCGTCCTGA	AAATGAAAAA	GTTTGGGTGA	TCGGTGTGTA	TCGTGACCAA	840
GAAGCAGAAAG	GTAAATACAC	TTCTAAAAGAT	GGCAAGAAT	CAAACTTTGT	TCTTGTATCT	900
ACTTTGAAAC	AAGTTGGTAC	AACTGTAAAA	GATATTTCTA	ACAAGGCAGA	AAAAGGAGAA	960
TTCCCTGGCG	GTCAAGTGAT	CGTTTACTCA	TTGAAGGATA	AAGGGGTGTA	CTTGGCAGTA	1020
ACAAACCTTT	CAGAAGAAGG	TAAAAAAGCT	GTCGAAGATG	CAAAAGCTAA	AATCCTTGAT	1080
GGAAGCGTAA	AAGTTCCTGA	AAAATAA				1107

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CAAATGAATC	CAATCCAAAG	ATCTTGGGCT	TATGTCAGCA	GAAAGCGACT	GAGAAGTTTT	60
ATTTTATTTT	TGATTTTATT	GGTCTTATTG	GCCGGAATTT	CAGCCTGTTT	GACTCTGATG	120
AAGTCCAACA	AAACAGTAGA	AAGCAATCTT	TATAAATCAC	TCAATACATC	TTTTTCTATT	180
AAGAAGATAG	AGAATGGTCA	GACATTCAAG	TTGTCAGACC	TAGCATCTGT	AAGCAAGATT	240
AAGGGGCTGG	AAAATGTCTC	TCCTGAACTT	GAGACGGTCG	CAAACTAAA	AGACAAGGAA	300
GCAGTGACTG	GCGAGCAGAG	CGTGGAGCGT	GATGATTTAT	CAGCTGCAGA	CAATAACTTG	360
GTTAGCTTAA	CGGCTCTTGA	GGATTTCATCC	AAGGATGTAA	CCTTTACCAG	TTCGGCTTTT	420
AATCTAAAAAG	AAGGGCGACA	CCTTCAAAAA	GGGGATTCCA	AGAAAATCCT	TATCCACGAA	480
GAATTGGCTA	AGAAGAACGG	TCTTTCACTT	CATGACAAGA	TTGGCTTGGA	TGCTGGTCAG	540
TCTGAATCTG	GAAAAGGACA	AACAGTAGAG	TTTGAGATTA	TTGGCATCTT	TTCTGGTAAA	600
AAACAAGAGA	AATTCACAGG	CTTGTCTTCT	GACTTCAGTG	AAAATCAAGT	CTTTACAGAC	660
TATGAAAGTA	GCCAAACCTT	TTTGGGCAAT	AGTGAAGCTC	AAGTCAGTGC	AGCACGCTTC	720
TATGTAGAAA	ATCCTAAGGA	AATGGACGGA	CTCATGAAGC	AGGTAGAAAA	CTTGCCCTTG	780
GAAAATCAAG	GCTACCAAGT	CGAAAAGGAA	AACAAGGCTT	TTGAACAAAT	CAAAGACTCA	840
GTTGCAACTT	TCCAACCTT	CCTGACCATC	TTCTTTTATG	GGATGTTGAT	AGCAGGAGCT	900
GGAGCCTTAA	TTCTGGTTTT	GTCTCTCTGG	TTGAGAGAAC	GGGTCTATGA	AGTGGGGATT	960
TTACTTGCAC	TTGGAAAAGG	CAAGAGCTCG	ATCTTCCCTAC	AATTCTGTTT	AGAGGTAGTT	1020
TTGGTATCTC	TTGGAGCTTT	GCTTCCAGCA	TTTGTTGCAG	GAAATGGAAT	CACAACCTTAC	1080
CTACTCCAAA	CTCTACTAGC	AAGTGGAGAT	CAGGCAAGCT	TACAAGATAC	ACTAGCCAAA	1140

GCAAGCAGTT TATCAACTAG CATCTTATCT TTTGCAGAAT CCTATGTTTT TCTAGTTCTG	1200
CTTAGTTGCT TATCTGTAGC CCTTTGTTTC CTATTCTTAT TTAGAAAATC ACCGAAAGAA	1260
ATTTTATCAT CTATTAGTTA A	1281

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1176
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CTAAAGGATC CTATTCAATT ACTAGAACTA TCACATACTC AAGGTCAGCT CACAGATGAG	60
CAACTATTTT GGTTACAATG TCTACTAAAT TTAAGTCAAA CAAATAATTT AGTCAAAATT	120
AAAAAAATAG AGGAACATAA ATATGATTAC AAAACAGAAT GTAATAGTGT TCTACAATTT	180
TTACTAGATA AAACGTAAA TTCTGAAGGA AGGATCACTT CTTCAACAGA ATTTGGAAAT	240
TTCGTAAGTA ATTTATCATT CCAACACGGA ATAGCTGGAC TACTGTTTCC TCTAAATAAA	300
TTGTACCCCC CAGAACTGGA TTCTAAAATA CTCTCTATCA TCAAGAAGGC AGTGACAATT	360
AGAACGACAC ATACATATGA ATATCAATAC TCACTGCTAT TTGGTGATGC AGGCTATCTA	420
TGGTTACTCC TACATTTATT TTCTATCAGT AAAAATCAAT ACTATCTACA ATTAGCAAAC	480
GTCACCGCTA AAAAATTAAT AGAGAATTAT GATACTCTAG AGGAAATAGA CTTTGCATTG	540
GGAAAATCTG GTGTCCATT ATCATTAATA AAATACTATC AATTTACCAA TGACAATACT	600
CTTAAATTT TCATCCACAA TAGTATAGGG GAAATTTATC ATTATTTCCCT ACAAAGAGAT	660
ACAGCCAAAAG AAAGCATTTT AGACTATAGC TTTGCTCATG GATATTGTGG AATTGCATAT	720
GCTTTATTTG CCTATTCTAA AGTCTTAGAA CCTTCTATGT TCTATAATGA TCTCCATACA	780
TTCCATACTG AATTAAAAAA ATTATTAGAA AAAGTTACTT CTAATACTGA AAATTTAGGA	840
AATTTACAAC TTTCTTGGTG CAAAGGAATT TCCGGAATAA TCTTATATCT TTGTATGTAC	900
GATTGTGACG GAAACAAAGA TATTATTAGT AAATATCAAG AATTTGTTTT TAACCATCAT	960
CTAAAAATGA TGACAGGATA TTGCCACGGA ATAAC TAGCT TACTACAAAC CACTGTCTAC	1020
AATCAAAACA AATTACTGAT GAAAAAAATC CAACAGGTAA TTTTAGCATG TTCTGAACGA	1080
GATGATCACG GTTTACTGAT GTTTCAAGGA GATAGTGGTA AAGCAGATTT GTTTGACTTC	1140
GGAATAGGAA GCATGGGGTA TATTGGTGTC TATTAA	1176

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AAGATAAGTC	CATTGCGGAT	GCACTTGCCA	ACTTTGCTGA	AGAACAAGGA	AAAATCGCAG	60
AGGAGTCGTC	AAATGAGCTC	ATCTAAAACA	ATCGGAATTA	TCGGTGGCGG	TCAACTGGGT	120
CAGATGATGG	CCATTTCTGC	TATCTACATG	GGCCACAAGG	TTATCGCGCT	GGATCCTGCG	180
GCGGATTGCC	CGGCCTCTCG	CGTGGCGGAA	ATCATTGTGG	CACCTTATAA	CGATGTGGAC	240
GCCCTCCGTC	AGTTGGCAGA	CCGTTGCGAT	GTCCTCACTT	ATGAGTTTGA	AAAATGTCGAC	300
GCTGACGGTT	TGGATGCCGT	TATCAAGGAT	GACAACTCCC	TCAAGAAAACA	GATTCTGCCG	360
CATTTGCAA	AATCGTATTT	TAGAAAAGGA	CTTTTGTCA	AACAAGGCTC	AAGTCACTGT	420
GGCACCTAC	AAGGTCGTGA	CTTCTAG				447

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GTACGGAGTC	CACGTATCGT	ATTTGCCAAC	AAAATGGACA	AAATCGGTGC	TGACTTCCTT	60
TACTCTGTAA	GCACACTTCA	CGATCGTCTT	CAAGCAAATG	CACACCCAAT	CCAATTGCCA	120
ATCGGTTCTG	AAGATGACTT	CCGTGGTATC	ATTGACTTGA	TCAAGATGAA	AGCTGAAATC	180
TATACTAACG	ACCTTGGTAC	GGATATCCTT	GAAGAAGACA	TCCCAGCTGA	ATACCTTGAC	240
CAAGCTCAAG	AATACCGTGA	AAAATTGATT	GAAGCAGTTG	CTGAAACTGA	CGAGAATTGA	300

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CAAGTTGGTC	CGGAAGTTCA	ACTCGTTTTTC	TTAGACCCTC	CCTATACCAA	GGAACAAATC	60
GTAGCAGATA	TTGAAAAAAT	GGCTGAGAGA	GAGCTTTTTT	CTGAAGATGT	TATGGTTGTG	120
TGCGAGACGG	ATAAGGCCGT	TGAAC TTCCA	GAAGAAATTG	CCTGTCTGGG	TATCTGGAAG	180
GAAAAGATTT	ATGGAATTAG	TAAGGTGACA	GTCTATGTCA	GATAA		225

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ATTAAGACTT	TTGTATCAGC	AAATTTATTG	GAAATTTTTT	CAAATACGAT	TTGGGTTTCT	60
TCCATTATAC	TTGTTTTTGT	AACGGAGTTA	TTAAATAAAA	CGGAAAGTTA	CTGGGGATAT	120
TCTAATACAG	CATACTCTAT	TGGTATTATA	ATTAGTGGCT	TAATTGCTTT	TAGGCTATCT	180
GAAAAGTTCC	TTGCTGCTAA	ATGGGAAAGT	ATTCTTTTTT	CTCTGTAGC	TATGGCAATA	240
GTGACACTGA	CTATTCTATA	TTTTCCAAAC	GCACAGATGT	TTTTATTATT	TTTCTTTT	300
GTTGGTATGT	TATCGCAACT	AAAAGAAGTT	CCTGAAAGTG	TATTTCTTCA	GGAAACAGTA	360
GAGGAAAATC	ATTTAGTTAA	TGTCTATTCC	GTCTTGAAG	TGATTTCTAC	ATTAGCATTT	420
TCAGTATTTG	TTTTGCTAAT	GAGCTATATT	ACTGAGAGTT	TTGGTATTAG	CATCAGTTTT	480
TGGCTATCAG	CCATTTGTCT	GATGATAGAA	GCTATTTTAA	TTTATATCAG	ACGAGATTAT	540
TTTAAATGA						549

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 903 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GTCTATATGT	TACTTGAAAT	TTCGATAAAA	AACTTTGCCA	TTATTGAGGC	TATTTCCCTC	60
AATTTTGAAA	AGGGGATGAC	TGTCCTGACT	GGTGAAACGG	GTGCAGGGAA	GTTCGATTATC	120
ATTGATGCCA	TGAATATGAT	GTTGGGAGCT	CGTGCGACGA	CAGATGTTAT	TCGTTCATGGT	180
GCACCAAAGG	CAGAGATTGA	GGGGCTTTTC	TCAGTTGAGA	ATAGTCGTCT	TTTACAGGAA	240
ATTTTTGATG	AGCAAGGTTT	AGAGTTAGGT	GATGAAATTA	TCATCCGTCG	GGAAATCTTG	300
CAAAATGGTC	GTAGTATCAG	CCGTGTAAAT	GGTCAGATGG	TTAATCTGTC	TGTTTTGCGA	360
GCTATTGGGC	AACATCTTGT	AGATATTCAT	GGTCAGCATG	ACCATGAGGA	GTTAATGCGT	420
CCCCAACTGC	ATATCCAGAT	GTTGGATGAA	TTTGGTGATG	CCGCTTTTTG	GGACTTGAAA	480
GAAACCTATC	AAACGAGTTT	TGATGCCTAT	CGGAAAATGC	GCAAGCAGGT	TCTGGAAGTC	540
AAGAAAAACC	AACAGGAACA	CAAGGCACGT	ATCGAAATGT	TGGAATTTCA	AATGGCAGAG	600
ATTGAGGCAG	CAAACTTGCA	GGCTGGAGAA	GACTTGGATC	TCAATCAAGA	GCGAGATAAA	660
CTCCTCAACC	ACAAAAATAT	TGCGGATACA	CTGACCAATG	CCTACAGTAT	GTTGGACAAT	720
GAAGATTTTT	CAAGTCTGGC	CAATGTTTCG	TCAGCCATGA	ATGACATGGA	AAGTGTTCGAA	780
GAGTATGACC	CTGAATACCG	TGAAATTTCA	AGCTCTCTGT	CTGAGACCTA	CTATGTTTTA	840
GAAGACATTA	GCAAACGTTT	GGAAGCTATC	ATTGAGGACC	TTGATTTTGA	TGGCAATCGC	900
TGA						903

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1995 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

ATTAGTATGT	TTTCGATTAAC	CAATAAGTTA	GCGGTATCGA	ACTTGATTAA	AAACCGCAAA	60
CTCTACTATC	CTTTTGCGCT	GGCTGTTCTC	TTGGCAGTCA	CTCTCACCTA	TCTCTTTTAC	120
TCTCTAACCT	TCAATCCTAA	GATTGCGGAA	ATCCGTGGAG	GAACAACCAT	TCAGGCTACA	180
CTTGGAATTTG	GTATGTTTGT	CGTCACCCCT	GCGTCAGCCA	TTATCGTTCT	CTATGCCAAT	240
AGTTTTGTCA	TGAAGAAAACG	TTCCAAGGAA	CTAGGAATTT	ATGGCATGTT	GGGCTTGGAG	300
AAGCGTCATC	TTATCAGTAT	GACCTTTAAG	GAGTTAGTGG	TATTTGGGAT	TCTAACTGTT	360
GGAGCGGGTA	TCGGTATTGG	AGCCTTGTTT	GACAAGTTAA	TTTTCGCTTT	CCTGCTCAAA	420
CTAATGAAAT	TGAAGGTTGA	GCTGGTTGCT	ACCTTCCAGA	CGAAAGTTGT	CATTACAGTG	480
CTTGTTGTCT	TCGGTTTGAT	TTTCCTAGGC	CTCATGTTCC	TGAATGCCCT	TCGAATCGCC	540
CGTATGAATG	CCCTCCAGCT	CTCTCGTGAG	AAAGCTAGTG	GAGAGAAAAA	AGGTCGCTTC	600
CTTCCTCTCC	AAACCATTCT	TGGTTCCATA	AGTTTAGGAA	TTGGCTATTA	TCTTGCCCTT	660
ACGGTAAAAG	ATCCTCTTAC	AGCCTTAACA	ACCTTCTTCA	TAGCTGTTTT	ACTGGTTATC	720
TTTGGAAGTT	ATCTCTTGTT	TAATGCAGGG	ATTACCGTTT	TCCTCCAAAT	CTTAAAGAAA	780
AATAAGAAAT	ACTATTACCA	ACCAAATAAC	CTCATATCTG	TTTCTAACTT	GATTTTCCGT	840
ATGAAGAAAA	ATGCAGTTGG	ACTAGCAACT	ATCGCTATTT	TGTCAACAAT	GGTTTTGGTA	900
ACCATGTCAG	CAGCGACAAG	CATTTTCAAT	TCCGCAGAAT	CCTTTAAAAA	AGTTCTAAAT	960
CCTCATGATT	TTGGGGTTTC	AGGACAAAAT	GTTGAAAAAG	AAGATTTGGA	CAAACCTTG	1020
AGCCAGTTTG	CAAGTGACAA	TGGTTATAAG	ATTAAAGAAA	AAGAAGTGTT	TCGTTACACT	1080
TACTTTGGTG	TTGCGAACCA	AGAAGGAAAT	AAGTTAACCT	TTTTTGAAAA	AGGACAAAAT	1140
CGTGTCCAAC	CCACAACAGT	TTTCATGGTA	TTTGACCAAA	AAGATTATGA	AAATATGACT	1200
GGTCAAAAAC	TGTCTCTATC	AGGAAATGAG	GTCGGTCTCT	TTGCCAAAAA	TGACGGACTG	1260
AAAGGACAGA	AAACTCTAAT	TCTGAATGAT	CATCAATTTT	CTGTAAAAGA	AGAATTTAAT	1320
AAAGATTTTA	TTGTCAACCA	TGTCCCAAAT	CAGTTTAATA	TTTTGACTGC	TGATTACAAT	1380
TACCTTGTTG	TACCTGATTT	ACAAGCCTTT	TTGAACCAAT	TCCCAGATTC	GGATATCTAT	1440
AATCAGTTTT	ACGGTGATAT	GAATGTAAAT	GTCAGTGAAG	AAGAACAAC	CAAGGTCGCT	1500
GAGGAGTATG	AAAACTACCT	CAATCAATTT	AATGCTCAAT	TAGACACAGA	AGGTAGCTAT	1560
GTTTATGGTA	GCAATCTAGC	AGATGCTAGT	TCTCAGATGA	GTGCCCTCTT	TGGTGGTGTC	1620
TTCTTTATCG	GTATTTTCTT	ATCCATTATC	TTTATGGTCG	GAACTGTTCT	GGTCATCTAC	1680
TACAAACAAA	TTTCTGAAGG	CTACGAAGAC	CGTGAACGCT	TTATTATCTT	GCAGAAAGTC	1740
GGTTTGGACC	AAAAGCAAAAT	CAAGCAAACC	ATCCACAAAC	AGGTTTTAAC	TGTTTTCTTC	1800
CTTCCTTTGC	TCTTTGCCCT	CATACATCTC	GCCTTTGCCCT	ACCATATGCT	TAGCCTGATT	1860
TTAAAAGTGA	TTGGTGTAAT	GGATACGACT	ATGATGTTGA	TTGTGACCTT	GTCTATCTGC	1920
GCTATCTTCC	TCATCGCCTA	TGTGCTGATT	TTCATGATTA	CTTCAAGAAG	TTATCGCAAG	1980
ATTGTGCAAA	TGTAA					1995

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ACATTCATGT TTTTATCAGT ATTTTCCTTT TCTTTGCCCT TATTTTCAGGA GCTGTTTCTC	60
ATACAGTTTT ACTACTCCTA CTCCTCTTTC TTCCTGCGCT CAATAAAGGA CTTGAGAAAA	120
TACAATCAAA ACGGATACCT GTCCTCAACG CAGCCCTCTT CTTTCTCCTC ATATCCTTTC	180
CACAACTTTT AA	192

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

ATATCCATGT TTCTCTTGT CCTTATTTTA ACCATTCAGG AAATTTTCGAG AACCCCTCTAC	60
AATTTCCAGT CAAATAAATT GCATTCGTTT TCTCAAGCAG GTATACTAGT ATGGATAAAT	120
AAAAAATTTA GAAAATTTAA GAATAGAAAA GAGAACAAAT CTTATGGCAA AAGATATTCG	180
TGCTTACTT TACTACCTT ATACTCCAAT TGA	213

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

TCGTTAATGT	TGGAACAGGC	ATTCAAAGAG	AAGCACTACG	AGAATACGAT	TCTCCATAGT	60
GACCAAGGCT	GGCAATACCA	ACACGATTCT	TATCATCGCT	TCCTAGAGAG	TAAGGGAATT	120
CAAGCATCTA	TGTCACGCAA	AGGAAACAGC	CAAGACAACG	GTAGGATGGA	ATCTTCTTTT	180
GGCATTTTTAA	AATCCGAAAT	GTTTTATGGC	TATGAGCAAA	CATTTAAATC	ACTTAATCAA	240
TTGGAACAAG	CCATTATAGA	CTATATTGAT	TATTACAACA	ATAAGAGAAT	TAAGATAAAA	300
CTAAAAGGAC	TTAGCTCTGT	GCAATACAGA	ACTAAATCCT	TCGGATAA		348

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CCTTGTTTCC	CAAAAATACG	GAGAAGCGAA	GGCTCAGGAA	CTTTTTATAG	ACAATCCTCG	60
AAAAATTGTA	ATGGATCAAC	TAATTTAGGA	GAAATGATGA	AAGAACAAAA	CACGATAGAA	120
ATCGATGTAT	TTCAAGTACT	TAAAACCTTG	TGGAAACACA	AGTTAATAAT	TTTATTAGTG	180
GCGCTTGTA	CAGGGGCGGG	AGCTTTTGCA	TATAGCACTT	TTATTGTTAA	ACCAGAATAT	240
ACGAGCACCA	CGCGTATTTA	CGTCGTCAAC	CGTAATCAAG	AAGGTAAGTC	GGGACTGACG	300
AATCAGGACT	TGCAGGCAGG	AACTTATCTG	GTAAAAGACT	ACCGCGAAAT	TATCCTTTTCG	360
CAAGATGTAT	TGGAAAAGGT	AGCGACAAAT	TTGAAAATTGG	ATATGCCAGC	AAAAGCGTTA	420
ACTAGCAAAG	TTCAAGTGAC	TGTACCAACC	GACACTCGTA	TCGTCTCAAT	CTCTGTCAAG	480
GATAAAGAAC	CAGAGGAAGC	CAGTCGCATT	GCTAATTCTC	TACGAGAAGT	TGCTGCAGGA	540
AAGATCGTCG	CTGTAACGCG	AGTATCTGAT	GTAACGACGC	TTGAAGAAGC	GCGGCCAGCT	600
ACGACTCCCT	CTTCTCCCAA	TGTTTCGACGT	AACACCTTAG	TTGGTTTTCT	TGGAGGAGCC	660
GTCGTAACAG	TAATTACTGT	TCTTTTGATT	GAGTTGCTCG	ATACCCGTGT	GAAACGTCCT	720
GAAGAAGTTG	AAGAGGTGCT	GCAAGTGCCA	CTTCTAGGAG	TCGTTCCAGA	TTTGGATAAA	780
ATGAAATAG						789

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AAAATCTTCC	CAGGCCTTGA	TANATATGAC	TTTGATGCTG	CTAAATTGAA	CAAGAAAATC	60
GGTTTCTGGG	GATCTAAATT	CTTCATCGGT	TTCATCCTTG	GTATCGTTAT	TGGTATTATG	120
GGAATCCAC	ATCCAATTGC	AGGTGTTGCA	GATGCAGATA	AATGGCGTCT	TGTTATCAAA	180
GGATGGTTGT	CTCTTGGTTT	GACTGCCCGT	GTATCTTTGG	AACTCTTCTC	ACTTATCGGT	240
TCATGGTTCA	TCGCAGCCGT	AGAACCACTA	TCACAAGGTA	TTACAAACGT	TGCTACTAAA	300
CGTCTTCAAG	GACGTAAATT	CAATATCGGT	CTTGACTGGC	CATTCATCGC	TGGTCGTGCT	360
GAAATCTGGG	CTTGTGCCAA	CGTACTTGCA	CCAATCATGT	TGATTGAAGC	AGTGCTTCTT	420
TCAAAAGTTG	GAAATGGTAT	CTTGCCACTT	GCAGGTATCA	TCGCTAGGGG	TGTTACTCCA	480
GCTCTCTTGG	TTGTAACTCG	TGGTAAATTG	CTCCGTATGA	TTATCTTCGG	AACACTCTTG	540
TTGCCACTCT	TCCTTCTTTC	AGGTACACTT	ATTGCACCAT	TTGCAACAGA	ACTTGCTAAA	600
GGTGTAGGTG	CCTTCCCAGA	AGGTGTGAGC	CAAACCTCAAT	TGATTACTCA	CTCTACTCTT	660
GAAGGACCAA	TCGAAAAAAT	TCTTGGTTGG	ACAATTGGTA	AACTACAAC	TGGTGATATC	720
AAAGCAATCC	TTGGTGCAGT	AGCCTTCCTT	GTATTCTATA	TCGGTATCTT	TGCTTGGTAC	780
AGAAAAACAAA	TGATCAAACG	TAACGAAGAG	TACGCAGCAA	AAGCAAAATA	A	831

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ACTTCGCTCC	CCATCACAGC	TCAATGTTAT	AGAATTAAGC	ATTTGACTCA	ATTCACACCT	60
CACTGCTTAG	ACAGACTCTT	CCAATCGTCT	GCTTTAGTTA	GCCTACTGCG	TCCCTCCATC	120

ACTACATACT CTAGTACAGG AATATCAACC TGTTGTCCAT CGGATACACC TTTCGGTCTC	180
TCCTTAGGTC CCGACTAA	198

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...636
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

AGTAAGATGT TTCATAAAGA ATTACTAAAA CTATATTTTA TTTGTGGAAC GACTACTTGC	60
CAAGGAAAAA ATCTATATAC AGTCGTTGAG GAAGCCTTAA AAGGTGGTAT AACCTTATTT	120
CAATTTTCGAG AAAAAGGTGA GAGTGCTTTA GAAGGCTTAG AAAAAGTTGA GCTAGCTATC	180
CAAATTAAAG AACTTTGTAA AAAATACAAT GTTCCATTTA TCGTTAATGA CGATATAGAT	240
TTAGCAATGG AAATTGACGC CGATGGCGTA CATGTTGGTC AAGATGATAT TGGTGTGAT	300
GAAATTAGAA AATTGATGCC AGATAAAATA ATTGGTCTTT CTATAAGAAA CGAAGAAGAA	360
TTTCAACAAT CAAAAGTTGA ATATGTAGAT TATGTAGGTG TTGGGCCTGT ATTTGATACC	420
CAGTCAAAAG ATGATGCTGG TGGTGCTATA GGTATGAAG GTCTTGAATT GATGAGAAAA	480
CTATTGCCAC AAATGCCTTT AGTTGCAATT GGTGGGATAC AGACGAAACA TATTAAAGAC	540
ATTATAAAGA CCAATGTTGA CGGCGTTTCA ATCATTTCCG CAATATCGTA TGCAAAAAAT	600
ATAGAAAAAA CTGTTCCGGA AATGAGTGAA CAATAG	636

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

AGGCGGATGT	TTCTGGAACG	GTGGTGTTTG	CAAATGAGTC	AGACATATCA	GATTAAACAA	60
AACGATATTG	TCGTTGACTT	ACCTAAGACA	GTAGGAGCTG	GATACGGACA	GTTCTGGCGC	120
TCAAGAAGTC	TTTATCGTGT	AGTCAAAGGG	TCCCGTGGTT	CGAAGAAGTC	CAAGACAACC	180
GCTTTGAATT	ATGTTATCCG	TC'TTTTGAAG	TATCCCTGGG	CCAAC'TTGCT	TGTTATTTCGT	240
AGATACTCGA	ATACCAACAA	GCAATCAACT	TATACGGATT	TTAAATGGGC	GTGTAATGTG	300
TTGGGTGTGA	CTCATT'TGTT	TAAAT'TTAAC	GAGTCTTTGC	CTGAAATAAC	CATAAAAGCG	360
ACTGGTCAAA	AAATCCTATT	CCGTGG'TTTG	GATGATGAAC	TCAAAAT'TAC	ATCTATTACA	420
GTCGATATCG	GTAGTCTGTG	TTGGGCATGG	TTCGAGGAAG	CATATCAAAT	TGAGACTGAA	480
GACAAAGTTCA	GCACGGTTGT	TGAGTCTATC	CGTGGTAGCT	TAGATGTACC	TGATTTCTTT	540
AAACAAATCA	CAGTCACATT	TAACCCGTGG	AATGAGAGGC	ATTGGCTCAA	GCGTGTATTC	600
TTCGATGAAG	AGACGAGACG	GGCTGACACA	TTCGCTACTA	CAACCACTTA	TAAATGCAAT	660
GAGTGGCTTG	ATGAAGTCGA	TATCAAACGC	TATGAGGATT	TGTATCATAC	GAACCCCGA	720
CGTGCTAGAA	TCGTTTGTGA	TGGCGAATGG	GGAGTTGCTG	AAGGTTTAAT	CTACGAAAAC	780
GTGACTGTCA	AGGATTTCAA	TAAAGATGAA	TTACTACAAG	ATTCAAGCTAA	TAAATTATGT	840
ATCGGTCTTG	ACTTTGGTTT	TACTCATGAT	CCAAC'TGCTT	TGTGTTGTTT	GTTGATAAAT	900
GACACGACGA	AAGAGATTTA	TGTCT'TTGAT	GAGGCGTATA	AAGTCGGATT	GATAACCAAA	960
GAAGTTGCGA	AGATGATAAA	AGACAAAGGT	TATCATCGCT	CACAAATCAT	TGCTGATAGC	1020
GCAGAGTCAC	GGCTGATTGA	AGAGCTCAGG	TCAGAACATG	GCATATCTAG	AATAAAAGAG	1080
AGTCGGAAAAG	GTAAGGATAG	TATTATGGCA	GGCGTATCCA	AATTGCAAGG	ATACGCTATT	1140
TATGTGCATC	CAGATTGTAA	AAACATCATG	GATGAATTTT	ATAGTTACTG	CTACCAGCGA	1200
GATAAAGAAG	GCAACTGGTT	GAATAAACCA	GAGGATAAAA	ACAACCACTT	GATGGACGCT	1260
TTGCGTTACA	GCCTTCAATG	TATCGAAGGT	GGAAAAGCAA	CCGTCCGCAG	ACGTTCTGAT	1320
TATGGTCTAT	AG					1332

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

AAGCAAATCC	CGATATTCCG	AGGAGGTGGT	TGCATGAAGA	AAGTGAAATT	AGGGCAAGTG	60
GCTACTTTTA	TCAATGGCTA	TGCTTTTAAA	CCTCAAGATT	GGTCATCTGA	AGGGAAAGAG	120
ATTATCAGAA	TACAGAATCT	GACTAAACT	TCAAAAGGGA	TAAATTATTA	TTCGGGTACG	180
ATTGATAAAA	AATACATTGT	TGAAGCTGGT	GATATTCTTA	TTTCGTGGTC	GGGTACATTA	240
GGGGTTTTTC	AGTGGTGTGG	AAGATCCGCA	GTGTTAAATC	AGCACATTTT	TAAAGTGGTT	300

TTTGATAAGA TAGATATAGA TAAATCGTAT TTTAAATATG TTGTTGAAAA AGGTTTACAA	360
GATGCTGTAA AACATACTCA TGGTCAACAA TGA	393

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGGAGAATCC CTATTGTGTC AAATAAACCA ATAGCAGATA TGATTGAAAC CATTGAGCAT	60
TTTGCTCAGA CACAGCCTAG CTATCCTGTC TATAATGTTT TGGGGCAGGA ACACACTTAT	120
GGCGATTTAA AGGCTGATTC GGATAGTTTG GCTGCAGTCA TTGACCAACT AGGCTTGCCT	180
GAGAAGTCTC CTGTGGTTGT TTTTGGTGGC CAAGAATATG AAATGTTGGC AACCTTTGTA	240
GCGCTGACTA AGTCAGGTCA TGCCTACATT CCAATTGATA GCCATTCGGC CTTGGAGCGA	300
GTTTCAGCTA TTTTAGAAGT AGCAGAGCCA AGCTTGATTA TTGCCATTTT AGCCTTTCCC	360
TTGGAGCAGG TTTCTACACC AATGATAAAT CTAGCTCAGG TTCAAGAAGC CTTTGCCCAA	420
GGGAACAACCT ATGAAATCAC GCATCCAGTC AAGGGAGATG ATAATTACTA CATTATCTTT	480
ACTTCTGGTA CGACTGGTAA GCCTAAGGGA GTGCAGATTT CACATGATAA TCTCCTCAGC	540
TTTACAAACT GGATGATTAC GGATAAGGAA TTTGCGACAC CGAGTCGTCC GCAAATGCTG	600
GCACAGCCAC CTTATTCTTT TGACTTGTCT GTCATGTATT GGGCACCAGC CTTGGCACTT	660
GGTGGTACGC TTTTCACTCT TCCTTCAGTC ATCACTCAGG ACTTTAAGCA ACTCTTTGCG	720
GCTATCTTTT CATTGCCAAT CGCTATCTGG ACATCAACAC CATCCTTTGC AGATATGGCC	780
ATGTTGTCTG AATACTTCAA CAGTGAGAAA ATGCCTGGAA TCACGCATTT TACTTTGAT	840
GGTGAAGAAT TGACGGTCAA AACAGTCAA AAAGTGCAGC AGCGTTTCCC AAATGCCCGT	900
ATCATCAATG CTTACGGCCC AACAGAAGCG ACAGTAGCTC TGTCAGCAGT TGCCGTGACA	960
GACGAGATGT TAGCGACTCT CAAACGCCTA CCAATCGGCT ATACCAAGGC TGATTCTCCA	1020
ACCTTTATCA TTGACGAGGA AGGAAATAAA CTGCCAAATG GTGAGCAGGG AGAAATCATT	1080
GTTTCTGGGC CAGCTGTTTC AAAAGGTTAT ATGAACAATC CTGAAAAAAC AGCAGAAGCC	1140
TTCTTTGAGT TTGAAAATCT GCCAGCCTAT CACACAGGCG ATGTGGGAAC CATGACAGAT	1200
GAGGGCTTGC TTCTCTACGG CGGACGCATG GACTTCCAGA TTAAGTTTAA CGGTTACCGC	1260
ATTGAGTTAG AAGATGTCTC TCAAAACCTC AACAAGTCTC GCTTTATCGA ATCTGCTGTC	1320
GCAGTACCGC GCTATAACAA GGACCACAAG GTACAAAATC TATTGGCTTA TGTCATCTTA	1380
AAAGACGGTG TTCGTGAGCA GTTTGAGCGA GATATCGATA TTACCAAGGC CATCAAGGAA	1440
GACCTGACAG ACATCATGAT GTCCTACATG ATGCCATCTA AATTCCTTTA CCGAGACAGT	1500
TTGCCACTAA CTCCAAATGG AAAGATTGAC ATCAAAGGAT TGATTAACGA GGTGAATAAG	1560
AGATGA	1566

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3093 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3093
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CACTATGTGT	TCCAGAAATAT	CTTACAAAAAT	TATTTGTTAT	TGAGGAAGTT	GTATGTAAAT	60
AATGAGGAAA	TAAAAATGGA	AAATAAAAAA	ATAGCAAAAC	AGATTTTAAT	AGCTACGGCT	120
GTTTAAACAA	GTTTTTTAGG	AAGTAATTTG	GTTTATGCAG	ATGTAGTTCA	AAGTAATTCT	180
AATAACAGAG	CTAGTACTGA	AACTGCTAGA	GTAACAGGGA	ATAACTTAGA	AAAACTTATT	240
ACTAAAGATA	AAGAAAATTGA	TAAAGAGATG	ACATATCTTT	CAGATATGGA	TTGGTCTTCT	300
GCAACTCATG	GTGATATAGA	TAAAACAAAA	ACAGTACAAA	AAGATGCTCC	ATTTACAACA	360
GGAAATAAAAG	GAGAGCATAC	TAAGATTTCA	TTGCTCACTT	CTGATGATAA	AGTTAAATAT	420
TTTGATAAAG	GAATAGGAAC	AGTCGCAGAT	TCTCCATCAG	TAATCAGCTA	TGATATCAGC	480
GGTCAAGGGT	TTGAAAAATT	TGAAACTTAT	ATAGGAATTG	ATCAAAGTGC	TAATAGTTCT	540
AGATCAGACC	ATGCAGTAGT	GGATAGAATA	GAAATAGAAA	TTGATGGAAA	GGTTGTCTAT	600
TCTAGTAGTG	TAAC TAATCC	AGAAGGATTC	AGATATAATA	CCCAGGCACA	ATTTATTAGT	660
GTGACAATTC	CACAAAACGC	TAAAAAAATA	TCCTTAAAAT	CATTTCGCAGG	AGAACATACA	720
TGGGGTGATG	AGGTGTGATT	TGCTGATGCT	AAACTTATTA	AAACTGTTAG	TACTCAAAC	780
ATAACTCCAG	ATCTTCTTAA	TAAAGGAATT	AATGGAGGAG	TATATCTTTC	TGATTTAGAA	840
TGGGTTGATG	CTACTCATGG	TGATGACGAT	AAATCAAAAA	CAGTTCAGAA	AGATAAACCG	900
TTTACACCTG	GTAATAACGG	GTCTAATAAT	AAAAATAAAAT	TACTAATTGA	CGGTAAGGAA	960
GTCGAATTTA	ATAAGGGATT	GGGAACTGTA	GCAAGTAACC	CGTCTAGTAT	AAAAATATGAT	1020
GTTTCGGGTG	CTAATGTTAC	AAGATTTATT	TCCTATGTCG	GAATTGATAG	GAGTGCAAAT	1080
CATTTAAATT	CAGATTACGC	AGATATTCAA	AAATTTGAAG	TTGTTGCGGA	TGGTAAAGTC	1140
ATTTACTCAT	CAGATTCAAA	ATATCCAAAA	GGAATTAAGT	ATGATATATC	GGCATTTCTG	1200
GTTGATGTTG	AAATTCCCAA	AGATACACAG	ACAATAGAAC	TTAAATCATA	TTCAGGGAAA	1260
TATACATGGG	CTGACGAATT	GGTTT TAGGT	GGAGCCTTGT	TTATGGCAAA	TGGTAAATTT	1320
AAGAATCCTA	ATGATTGGTC	AGAAGTTGAT	AAACGTCGTG	AAATTAATAA	TGAACATCCG	1380
TTACTTATGA	TGCCTTTATA	TGCTAACGGA	GAAGAGTTTA	ACCAAGGGAA	ATATACTTTT	1440
TGGGGAGGAG	ATACATTAAC	AGGTAAGTGG	GAGAATATAC	CAGATGACTT	AAAACCATAT	1500
ACTGTTATAC	AGTTACATCC	AGATGATCTT	CCTAAAAGAG	ATGGAGCTGC	TAGAGATTTT	1560
TATGAACATA	TGCTAGAAGA	AGCAGCGAAA	TATGTAAATC	CTAAGACTGG	AAAAAATGAA	1620
CCTATTCCAG	TTATTCTAAC	GGTTTACACT	GCTGGTAATA	TGCCTTATTA	TACTTCGGCA	1680
CATTGGTTAA	GTACCAGCTG	GATTGATAAA	ATGTATCAAA	AATATCCAAA	TTTGCATGGT	1740
ATTTTCAGTA	CTGAGAATTA	TTGGATT TGG	GCAAATGATA	TTGAAAATAA	GGCGGCAGAT	1800
TACTTAAAAG	TATCAGCTAA	AAATGGAGGA	TATTTTATAT	GGGCTGAACA	AAATAATGGT	1860
TCTGCAATAG	AAAAAGCATT	TGGAAAAAAC	GGTAAGATAG	CATTT CAGAA	ATCTGTTGAT	1920
AAGTACTGGA	AGAACCTTAT	TTTCATGTTT	AAAAATACAC	CTGCTGCTGA	GGGAAATGAT	1980
TCAACTACAG	AAAGTTATAT	GAAGGGGACTT	TGGCTTTCAA	ATCATACTTA	TCAATGGGGT	2040
GGTTTGATGG	ATACTTGGA	GTGGTATGAG	ACAGGTAAAT	GGAAACTGTT	TGCAAGTGGT	2100
AATATCGGAA	AAAGTCAAGG	AGATAGACAA	TGGTTGACTG	AACCAGAGTC	TATGCTAGGA	2160

GAAGAAGCTT	TAGGGGTTTA	CCTTAATGGA	GGTGTAGTTT	ATAATTTTGA	ACACCCAGCT	2220
TATACCTATG	GTGTAAATAA	TAAAGAAAGC	TTACTCTTTA	GCGAAGTAAT	AAAAGAATTT	2280
TTTAGATATG	TAATAGCGCA	TCCAGCACCA	TCCAAAGAAA	AGGTACTTGA	GGATACAAAA	2340
GTATTCATAC	ATGGAGACTA	TTCAAATAAA	GGAAATGGTA	AGTTCCTTGT	AAACGTAAAT	2400
ACTGATAGAG	AACAAACTCC	ATTATACATG	ACTGGTCGTT	ATAATGTTAT	TCCAGCTATT	2460
CCAGGTGTTT	TAAAAACAGA	TAAATTGAAA	GAGTCTGTTT	CTGGTAGCCG	TATTCAGATT	2520
AAGGAAATCA	CTTCTCCAGA	ATTTAGCTCT	ACTCAGGCTA	GAAAAGAATA	CTTAAATAAG	2580
CTGTATCCTA	TGAATTATGA	AGGAGATATC	TTTGCTCAGA	AATTAGATAA	TAGATGGTTT	2640
GTCTATAATT	ATAAGGTAAA	TGAGAATGTT	AAACAGACTG	GGAAATTAAA	ATTTAATTCT	2700
TTAGAAATGG	ATGTTGAATT	TGAACCTCAT	ACCTATGGTA	TTTTTGAGAG	AATAAGTAAT	2760
GGATTGAAAG	TGAATTTAAA	TAATTTTAGA	ACAAATAAAG	ATTCACATATG	GTCTAATGCT	2820
CAAGATGCAA	ATCAGGCAAA	GAAACTACCA	CAATTGACCA	AGAAAGGTGC	GATTAAGTGG	2880
ATTGAAGAAC	ATTATATCAA	AGATACTCAG	TTTGGAGAGA	AAAGGGTTAC	AAAGATAGTA	2940
TTAAGAGGTA	TAGATAAACT	TCCTACTATT	CATTTCATTAT	CAGGAACAAA	TAATTCCTAT	3000
GATCAGCCAT	CTCTCAATTT	TGATCAGAAA	AATCATATGG	TTACTATTAC	CATTAACAGT	3060
AACGGAAATC	TTGAATTCGA	ACTTCATTTT	TAG			3093

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CCCCCCCCC	CCCCNCCNC	CCNCCCCC	CCCCCNCCC	CCCCCCCCC	CCNNCCNCC	60
CCCCCCCCC	CCCCCCCCC	CCCCNCCC	CCCCCCCCC	CCCCCCCCN	CNCCCNCC	120
CCNNNNNCC	CNCCCCNNN	NNNNNCNNN	NNNNNNNTT	TTTTGNNNN	NNNNNNNNN	180
NNNNNNNNN	NNNNNNNNN	NAACTTAGGA	TTGCTAGGCA	GAAAGACATT	GGCCAACATA	240
TGGTCAATAC	GGCCACCCAA	GGCACCAGAA	ATAGTAACCT	GA		282

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...209
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CCCCCCCCC	CCCCNCCCN	CCCCNCCCC	CCCCCCCNC	CCCCCCCCC	CCCNNCCNC	60
CCCCCCCCC	CCCCCCCCC	CCCCCNCCC	CCCCCCCCC	CCCCCCCCC	NCNCCCCNC	120
CCCCNNNNNC	CCNCNNNNN	NNNNNNC	NNNNNNNT	TTTTTTG	NNNNNNNNN	180
NNNNNNNNNN	NNNNNNNNN	NNAACTTAG				209

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 624 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

ATTGTCTACC	CCTTTTTTTG	TGTTTCGGAG	GTAACATGA	AAAGAATAAT	TCCAGTTTAT	60
ATATTCCAAC	AAGTAAATGT	CCTATTGGTA	TCTCTATACT	TATTGAAATT	TCTTTGTATC	120
GGTGAGTTAA	CTATACTACA	GATTCCTCTAT	GGTTCGTCAC	TCATTTCCTT	TTTATGGATG	180
TATGGCCAAC	GCAAACAAGC	TCATAAGGTA	AATATGAAAT	CTAGGATGAA	ATGGCTTGGT	240
ATTGGATTCT	TTAGCCTACT	GATTATAAGT	CTATGTTTTA	GCCTAATCCA	TGCGCAAGAA	300
AGCACGAATC	AAGCAAACCT	AATTGGACTT	CAACATCAAG	TTCCCTTGGT	TTTATTTTTA	360
TTGTTTTTAA	TCAATGCGAG	TATGGTTGAA	GAATTTCTGT	ATAGAGAAAT	TTTATGGAAC	420
TTGGTTAGAA	AATTAGATAT	TCGAGTTGCT	TTGACAAGTG	TTTTATTTGC	CTTAGCACAT	480
CATCCAGGAA	CCATTATAGC	TTGGTGTGTT	TATGTATCGC	TGGGGATGTT	TTTAGGGCTT	540
GTACGCTACA	AATTGGACTT	ATGGGGCAGT	ATGGGGCTAC	ATTTGGTGTG	GAGCCTACTA	600
GTTTATAGTT	TGCTGCTTTT	TTAA				624

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1110 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

ATCCAATACC	CGTGGTGGAA	GATGTCAAAT	GTGATTTGTA	GTGATTCAAG	TTACTCTTTT	60
CACAATAAAA	ATTTTCATGAT	TTTCATAAGG	AGGAAATCAC	TAATGGTAGT	TAAAGTTGGT	120
ATTAACGGTT	TCGGACGTAT	CGGTCGTCTT	GCTTTCCGTC	GTATCCAAAA	CGTAAAAGGT	180
GTTGAAGTTA	CACGCATCAA	CGACCTTACA	GATCCAGTTA	TGCTTGCACA	CTTGTTGAAA	240
TACGACACAA	CTCAAGGTCG	TTTCGACGGT	ACTGTTGAAG	TTAAAGAAGG	TGGATTGCGA	300
GTTAACGGTA	AATTCGTTAA	AGTTTCTGCT	GAACGTGATC	CAGAGCAAAT	CGACTGGGCT	360
ACTGACGGTG	TAAAAATCGT	TCTTGAAGCT	ACTGGTTTCT	TTGCTAAGAA	AGAAGCAGCT	420
GAAAAACACC	TTAAAGGTGG	AGCTAAAAAA	GTTGTTATCA	CTGCTCCTGG	TGGAAAACGAC	480
GTTAAAAACAG	TTGTATTCAA	CACTAACCAC	GACGTTCTTG	ACGGTACTGA	AACAGTTATC	540
TCAGGTGCTT	CATGTACTAC	AAACTGCTTG	GCTCCAATGG	CTAAAGCTCT	TCAAGATAAC	600
TTTGGTGTTG	TTGAAGGATT	GATGACTACT	ATCCACGCTT	ACACTGGTGA	CCAAATGATC	660
CTTGACGGAC	CACACCGTGG	TGGTGACCTT	CGCCGTGCTC	GCGCTGGTGC	TGCAAACATC	720
GTTCTTAAct	CAACTGGTGC	TGCTAAAGCT	ATCGGTCTTG	TAATCCCAGA	ATTGAACGGT	780
AAACTTGACG	GATCTGCACA	ACGCGTTCCA	ACTCCAAC TG	GATCAGTTAC	TGAATTGATA	840
GCAGTTCTTG	AAAAGAACGT	TACTGTTGAT	GAAGTGAACG	CAGCTATGAA	AGCAGCTTCA	900
AACGAATCAT	ACGGTTACAC	AGAAGATCCA	ATCGTATCTT	CAGATATCGT	AGGTATGTCT	960
TACGGTTCAT	TGTTTGACGC	AACTCAAACT	AAAGTTCTTG	ACGTTGACGG	TAAACAATTG	1020
GTTAAAGTTG	TATCATGGTA	CGACAACGAA	ATGTCATACA	CTGCACAACT	TGTTCTGACT	1080
CTTGAATACT	TCGCAAAAAA	TGCTAAATAA				1110

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 963 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ACCGCCACC	CGCCGCGGCT	ATCCGCCATC	GGTGTTCGCC	GCGCTGCCAC	GCTTGATGGA	60
GCGTGCCGGG	CAATCCGAGC	GGGGCTCGAT	CACCGCGCTC	TACACCGTGC	TGGTGGAAGG	120
CGACGACATG	AGCGAGCCGG	TGGCCGACGA	GACCCGCTCG	ATTCTCGACG	GGCACATCGT	180
GCTGTGCGCG	AAGCTGGCCG	CCGCCAACCA	CTATCCGGCC	ATCGACGTGC	TGCACTCGGT	240
GAGCCGGGTC	ATGAACCAGA	TCGTGACGA	CGATCAGCGC	CATGCGGCCG	GACGCTTGCG	300
CGAATGGCTG	GCGAAGTACG	AGGAAGTCGA	GTTGCTGCTG	AAGATCGGCG	AATACCAGAA	360
AGGCCAGGAC	AGCGAAGCCG	ACCAGGCCAT	CGAGAAGATC	GCGGCGATCC	GCCAGTGGCT	420
GCGCCAGGGT	ACCCACGAAA	CCAGCGATTA	CGCACAGGCC	TGCGCGCAGT	TGCGGAGCCT	480
CTGCGCATGA	GCCTGGCGCT	GCTGTTGCGC	GTCCGACGCC	TGCGCCTGGA	CCGGGCCGAG	540
CGCGCCCAGG	GCCGCCAATT	GCTACGGGTT	CGCGCCGCGG	CGCAGGAACA	CACCGAGCGC	600
CAGGCGGCGC	AACGGGACTA	CCGCGACTGG	CGACTGGCCG	AAGAGCAACG	GCTGTTTCTC	660
GCCTGCCAGG	CGCCCATGCT	CGACCGCCGG	CGCCTGGAAG	CCTGGCAGCA	GCAGGTAGGA	720
CTGCTGCGGG	AAAAGGAAGC	CGGCCTGGAA	CAGGACTGCG	CCGAGACCGC	GCAGCGCCTC	780
GAAGGGGAGC	GCGAGCGCCT	GCGGCAGTGC	CGGCGAGAAC	TGCTGGAACG	CCAGCGGCAA	840
CTGGAGAAGT	TCGCCGAACT	GGAGCGCCAC	GTCGACGCCG	AGCGCCAGGG	GCTGCGCGAA	900
CGCAGCGAGG	AAGGCGAACT	GGAAGAATTC	ACCCGCCACG	AGACCTGGCC	ATGCTCAAGC	960
TGA						963

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GCTTTTAACC	CTATCAATAA	TGTGGCTTTT	CAACCACGCT	TCGGCATTCA	ACCCTGCCTG	60
TCCGTAGGCA	TTTTTTACTC	GGGTTTATAT	TTGCTAGAAA	ACATCATCTC	ATTTTCTAAG	120
CTTTATTACT	ATATCATGTT	TTTAAGAACT	TGTAAAGTAT	TTTTTGATAA	AAAACAAAAA	180
TATAATAGAT	TGAAACTAGA	ATAG				204

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

CCAAACAACC	CTTTTGTGTT	TTGCTTAGAA	GCGGATAATC	AAGAACAAC	CTTTGATCAG	60
GTCAGCAAGCT	TGTTGGAAGA	ACGAGAAATT	GTCACCTCCTA	CTTATCGTGA	AGCCTTGATC	120
ACGCGTGAAA	AGTCATTTCC	AACTGGTTTA	GATATGGAAT	TTCTAGGAAA	GGACTTGCCA	180
AATGTAGCGA	TTCTCACAC	AGATATTGTT	CACAATCTGG	CTGAAAAAGT	TGTGGTCGTT	240
CGATTAGAGA	AACCGGTGAC	TTTCCATAAT	ATGATTGCGC	CAGGTAAGGA	AGTAGAAGTA	300
TCCTTGCTCT	TCTTTATCAT	CAATAATTCA	AGTTCAAGTC	AAACAAATAT	TCTGGCTCAG	360
TTGATGGACT	TTTTCACAGG	AAATGGTCAT	CTTGAAGACC	TATCAAAAAT	TTCTGAACCA	420
GAAAACTTT	ATGCTTACAT	TGCTGAAGCA	ACCGCTTAA			459

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

ACTCCAAACC	CTCCTCTACT	TCATGCGAAA	AGAGGATTAG	AAAGCGAAAA	TCATTTTATG	60
AAAAAACCAG	TTATTGGGAT	TACAGGAAAC	GAAAAAACTC	ATCCAGATGA	TGACATCATG	120
ATGAGCTACG	CAGCAAAAGG	CTTTGTTGAA	GGCGTTAAAG	ATGCTGGAGG	GATTCCCATC	180
ATCCTACCGA	TTGGTGATCA	AGAAATGGCC	TGCCACTATA	TCAGTTTGAT	TGACAAGCTC	240
ATCTTAACAG	GTGGGCAAAA	TGTCGATCCA	AAATTTTATG	GCGAACCCTA	AACCATTGAT	300
AGCGATGACT	ATCACCTTCA	AAGAGATATC	TTCGAACTGG	CCCTCATCAA	GGAAGCTATT	360

AAACAGAAAA	AGCCCATTTT	CTCTGTCTGC	CGTGGTACCC	AACTCTTTAA	CGTTGCCATG	420
GGTGGAACCT	TGTACCAAGA	TATCGAAGAC	CATTGGCAGG	ATTCTTCTGT	TGAGTACACA	480
ACTCAACGCT	TGGTGACAGA	ACCAGATACC	GTTCTCCAAG	AAATCTATGG	AGAAATCTCT	540
CATATCAACT	CCTTCCACCA	CCAGAGCATC	AAGGACTTAG	CACCAAATTT	AAAAGTTGTG	600
GCTCATGATC	CTAAAGATGG	TATCATTGAG	GCTGTCATGA	GTACGGATGA	TGTCGCCTTT	660
CTCGGTGTCC	AATGGCATCC	AGAACTTCTT	TTTGAAAATC	GTCCCAAAGA	TAAGAAACTC	720
TTTGACTATG	TCGTTAATGA	ACTTTAG				747

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...996
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GTCATGAGCC	CCATTTGTGA	ACCCCATTTT	TCAGATACGA	GTTATGGTTT	CAGACCAAAT	60
AGGTCATGTG	AAAAAGCCAT	CATGAAGCTC	TTAGAATACT	TAAATGACGG	CTATGAGTGG	120
ATAGTGGATA	TAGACCTAGA	GAAATTTTTT	GATACAGTTC	CTCAAGATAG	ATTGATGTCC	180
TTAGTACATA	ACATTATCGA	AGACGGAGAT	ACGGAATCCT	TGATTTCGTAA	GTATCTTCAT	240
TCAGGTGTTA	TCATTAATGG	TCAACGTTAT	AAAACACTAG	TTGGTACACC	ACAGGGAGGA	300
AATTTATCTC	CTCTCTTATC	CAATATCATG	CTTAATGAAT	TGGACAAGGA	ATTAGAAAAG	360
AGGGGACTTC	GATTTGTGCG	CTACGCAGAT	GATTGTGTGA	TTACGGTCGT	AAGCGAGGCA	420
GCCGCTAAGC	GTATGATGTA	TTCAGTCAGT	CGTTTTATTG	AAAAACGGCT	AGGTTTGAAA	480
GTAAACATGA	CCAAGACTAA	GATTACCAGA	CCAAGAGAGT	TGAAATATCT	AGGTTTGGG	540
TTCTGGAAAT	CATCAGATGG	TTGGAAAAGT	CGTCCACATC	AAGATAGTGT	TCGGAGATTT	600
AAGCTTAAAT	TGAAGAACT	AACACAGAGG	AAATGGAGTA	TAGACCTAAC	AAGACGTATT	660
GAGCAACTGA	ATTTGTCTAT	TCGAGGATGG	ATAAACTATT	TCTCATTGGG	AAATATGAAA	720
AGTATAGTCG	CCAGCATAGA	TGAGCGCTTG	CGTACTCGCC	TACGAGTGAT	TATCTGGAAG	780
CAATGGAAGA	AGAAATCGAG	ACGATTATGG	GGATTGCTTA	AGTTAGGGGT	TCCTAAATGG	840
ATAGCAGATA	AGGTATCTGG	CTGGGGCGAC	CATTATCAAT	TAGTAGCTCA	GAAGTCGGTA	900
CTTAAACGTG	CTATATCAAA	ACCAGTCCTG	GAAAAACGTG	GACTGGTTTC	GTGTTTGGAT	960
TATTACCTTG	AACGACATGC	GTTAAAAGTT	AGTTGA			996

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...666
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TGGTTCTTAC	CAAGGCTACG	CTACGATATT	GAAGTAGGGA	ACCAACTAGC	TCAAGACCTT	60
GGTGTCAAGG	TTAAATACAT	TTCAGTCGAT	GCTGCCAACC	GTGCGGAATA	CTTGATTTC	120
AACAAGGTAG	ATATTACTCT	TGCTAACTTT	ACAGTAACTG	ACGAACGTAA	GAAACAAGTT	180
GATTTTGCCC	TTCCATATAT	GAAAGTTTCT	CTGGGTGTCG	TATCACCTAA	GACTGGTCTC	240
ATTACAGACG	TCAAACAACT	TGAAGGTAAA	ACCTTAATTG	TCACAAAAGG	AACGACTGCT	300
GAGACTTATT	TTGAAAAGAA	TCATCCAGAA	ATCAAACCTC	AAAAATACGA	CCAATACAGT	360
GACTCTTACC	AAGCTCTTCT	TGACGGACGT	GGAGATGCCT	TTTCAACTGA	CAATACGGAA	420
GTTCTAGCTT	GGGCGCTTGA	AAATAAAGGA	TTTGAAGTAG	GAATTACTTC	CCTCGGTGAT	480
CCCGATACCA	TTGCGGCAGC	AGTTCAAAAA	GGCAACCAAG	AATTGCTAGA	CTTCATCAAT	540
AAAGATATTG	AAAAATTAGG	CAAGGAAAAC	TTCTTCCACA	AGGCCTATGA	AAAAACACTT	600
CACCCAACCT	ACGGTGACGC	TGCTAAAGCA	GATGACCTGG	TTGTTGAAGG	TGGAAAAGTT	660
GATTAG						666

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1179
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

AAGGAGTTAC	CTATGAATTA	CCTTGTTATT	TCTCCCTACT	ATCCACAAAA	CTTTCAACAG	60
TTTACCATCG	AACTAGCTAA	TAAAGGCATC	ACAGCCTTGG	GAATTGGTCA	AGAGTCTTAC	120
GAGCAATTGG	ATGAGCCCTT	GCGCAATAGC	TTGACCGAGT	ATTTTCGTGT	TGATAATCTT	180
GAGAACATAG	ATGAAGTCAA	ACGTGCAGTT	GCTTTTCTCT	TTTATAAACA	TGGTCCAATT	240
GACCGCATCG	AGTCTCACAA	TGAATACTGG	CTTGAGCTAG	ACGCAACACT	CAGAGAACAA	300

TTCAATGTTT	TTGGTGCCAA	ACCAGAGGAT	CTCAAAAAGA	CGAAATATAA	GTCTGAAATG	360
AAGAACTTT	TCAAAAAAGC	AGGTGTTCC	GTGGTACCTG	GAGCTGTTAT	CAAGACGGAA	420
GCAGATGTTG	ATCAAGCAGT	GAAAGAAATC	GGTCTTCCAA	TGATTGCCAA	ACCTGATAAT	480
GGAGTGAGAG	CAGCCGCAAC	CTTTAAACTT	GAGACAGAAG	ACGATATCAA	TCACCTCAAG	540
CAAGAATGGG	ACCATTCAAC	CCTTTATTTT	TTTGAAAAAT	TTGTCACTTC	CAGCGAAATC	600
TGTACCTTTG	ACGGGCTCGT	GGACAAGGAT	GGAAAGATTG	TCTTCTCAAC	AACCTTTGAC	660
TACGCCTATA	CACCGCTTGA	CCTCATGATT	TATAAGATGG	ACAATTCTTA	TTATGTGCTC	720
AAGGATATGG	ATCCTAAACT	GCGCAAGTAT	GGGGAAGCAA	TTGTCAAAGA	ATTTGGTATG	780
AAAGAACGGT	TTTTCCATAT	TGAGTTCTTC	CGTGAGGGGG	ACGATTATAT	TACCATCGAG	840
TACAATAACC	GCCCTGCAGG	TGGTTTTACC	ATTGATGTTT	ATAACTTTGC	TCATTCCCTG	900
GACCTTTATC	GTGGCTATGC	AGCTATTGTC	GCAGGAGAGG	AGTTCCCGGC	GTCAGACTTT	960
GAAACTCAGT	ATTGTTTGGC	TACTTCTCGC	CGTGCAAATG	CTCACTATGT	TTATTTCAGAA	1020
GAGGATTTGC	TTGCCAAATA	TAGCCAGCAG	TTCAAGGTTA	AAAAAGTCAT	GCCAGCTGCC	1080
TTCGCGGAAC	TTCAAGGAGA	TTACCTGTAT	ATGCTGACCA	CTCCGAGTCG	ACAAGAAATG	1140
GAGCAGATGA	TTGCAGATTT	CGGACAACGT	CAAGAATAA			1179

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCCCCGCTAC	CAACCGTCAC	GCCTCGCGAG	CCACACTTCG	CACACCATAG	CGGACTACCA	60
CTCTACGCCG	CTCTAACACG	CGGAGCCTGC	TCCAAC TTCT	CTTCCCCCAC	CCCCCATACA	120
CCCACGCTCC	CCCTCCAGCA	GATCCCATCG	CAACTTCTCC	CTTTGTTCCC	AAACCCCGTG	180
GCCTCACCAC	GGCACACATC	CGTGCAAGCC	ATATCTCCCT	GCCGACACGG	CCCTCCTCAC	240
ACCAACTGCC	CCCCACTCAC	CCCACTCCAC	CCGTCCCCCG	ACCGCCCCCG	CCTCAACCCC	300
GGCCACCCCA	CTTCCCTCCA	CCCCCGTTTC	CCCCGCATGC	CGCCCCCCTC	CACGCGGCCA	360
ATCCCCCACC	GCGCGCGAGC	AACTCCCCCC	CCCCACCCCC	ACCACCGCCC	GCCGCACGCC	420
AACCCCCCCA	CGCCCCCCCC	CGCAGGAATC	CGCCGCCCCA	CCCCGGGCCC	ACACCGCACC	480
GGCCTCACC	CCCCACCCCG	CCCCCGCACA	CCCCCCCCAC	TCCGCCACCA	GCCCACACCG	540
GCCCCCCTAC	CACACCCCCA	ACGAACGAGC	CGCCCCGCCC	CACGCCAGCC	CCAAAACCCC	600
CCCGCCACCC	ACCCCGCCCC	GCCGCCNACC	TACCGCCCAT	GCTCGCGACC	CCCCGCACCG	660
AGCNAGCCAC	NNCNNGNCCN	NNNNNNNNNT	TTTCNNNNNN	NNNNNNNNNN	NNNNNNNNNN	720
NNNNNNNNNN	NNACTACACA	AACTGGCAAG	CAGTTGGCGA	CCTTGACTTT	GCTAACGACC	780
GTACTGCCTA	CATGA					795

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TCCATCTCGT	TTGACGAGAC	AGCCATTTTT	GGAGAATTGA	TCCGCTATCT	GGACCAGTAT	60
GAGGATGTGA	TTCTACGGGA	AATTAAGGCT	CAATTTCCAG	ATGTTGCAGT	TGATAAACTC	120
ATGGAAGAGT	ATATAAAGGC	AGGCTTGATT	CTACGTGAAA	ATAAGCGCTA	TTACCTCAAT	180
TTTCCTACGC	TTGAATCACT	TGATAGTCTT	GAAGTGGATC	AAGAGATTTT	TGTCAGAGAA	240
GCTAGTCCGG	TCTATCAAGC	CTTGTGGGAG	CAGAGTTTTG	AGACGGAATT	GCGCAATCAA	300
ATCAATGCAG	CTATTTTAGT	TGAAAGACGG	ACTTTGCGCG	CATTAAAATG	A	351

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTCTTAATAC	CAGCCATTGT	TAAGCCAGAA	GTTTTTAGCT	CTGCCAAGCC	ACATAGTGTG	60
TTTACTACTA	TGTGTCCATG	TCACCATGAA	TCGCCGAACG	ATTTAACGAG	AAAGTATGAC	120
TTTTACGTTT	ATCCCAACTC	AATTATGACA	TTTTTTTCAA	AAGTCAATAT	ATCTCACTTT	180
TTCAACGACA	AGAAAGAGGC	TGCCAATCGA	CCAACCTCTT	GTTTTTAA		228

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTCTTAATAC	CAGCCATTGT	TAAACCAGAA	GTTTTTAGCT	CTGCCAAGCC	ACATAGTGTG	60
TTTACTACTA	TGTGTCCATG	TCACCATGAA	TCGCCGAACG	ATTTAACGAG	AAAGTATGAC	120
TTTTACGTTT	ATCCCAACTC	AATTATGACA	TTTTTTTCAA	AAGTCAATAT	ATCTCACTTT	180
TTCAACGACA	AGAAAGAGGC	TACCAATCGA	CCAACCTCTT	ATTCTGAACC	CATCACTCCA	240
TCACTTTTTA	GCTTCATTCT	CTTTCCTTAGC	GACTGCAATC	TGGTATTCTGA	CTTGGTCATT	300
CCCCTTACCG	GTACAACCAT	GAGCAATTGT	AGTCGCTCCT	ATCTGATGCG	CTATTTCAAC	360
CAATTTTTTA	GAAATCAGAG	GGCGGCTCAA	GGCAGATACC	AAGGGATACT	TTTGTTTCATA	420
ATAGGCATGT	GA					432

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AAACCAATAC	CTAATATTAT	CAGTCTTGCT	GCTGAAAAAC	CATCTTTTTT	AGCTAGTAAA	60
AATAATATTA	AAGATGATGT	TAGTCCACAA	GTTATTGAAA	TAATTCCAGT	AGTTAAACTA	120
TTTGTTTTTA	ATACCAATAT	GCAAAAGACC	GCTGCAATAG	ATGAAGAACT	TGTGACACCG	180

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CAGAAAATAC	CGACTATACA	GTCTGTCATCA	AATAAGGAGA	AGAACATGTC	AAATATTTTAC	60
GATAGTGCAA	ACGAACTCAG	TCGCGGTCTA	CGCGGATTAC	CAGAATACAA	GGCTGTTAAA	120
GCAGCTAAAAG	ATGCGATTGC	AGCAGATGCT	GAGGCAAGCA	AAATCTTTAC	AGAATATCTT	180
GCCTTTCAAG	AGGAAATTCA	AAAAC TAGCA	CAGACAGGTC	AAATGCCAGA	TGCGTCCTTC	240
CAAGCTAAGA	TGGAAGGCTT	TGGTAAACAG	ATTCAAGGAA	ATAGCCTCTT	GTCAGAATTC	300
TTTACCAAGC	AACAACAATT	GGCCATTTAC	CTTTCTGACA	TTGAAAAAAT	TGTTTTTGAA	360
CCAGTTTCAG	AATTGCTGAA	ATAA				384

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

ACATCGATAC	CAGCTCAGAA	CTTGAGGGCC	GTATCACTGC	TCGCCAACTT	GTCGAAGAAA	60
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ATCGCCCAGA	GTACAATATC	GAATATATCG	AACTCTTGTC	TGACAAATTG	CTCGATTACG	120
AAAAAGAAAC	TGGCGCCTTC	GAAATTACGG	AGTTCTAATA	TGGCCTACAC	TCTTAAACCT	180
GAAGAAGTTG	GTGTTTTTGC	CATCGGTGGT	CTAGGAGAAA	TCGGGAAAAA	CACTTACGGA	240
ATTGAATACC	AAGACGAGAT	TATCATCGTC	GATGCTGGGA	TTAAATTCCC	AGAAGATGAC	300
TTGCTTGGTA	TCGACTATGT	CATTCCTGAC	TACTCTTACA	TCGTAGACAA	TATCGACCGC	360
GTCAAGGCTG	TTTAAATCAC	ACACGGACAC	GAGGACCACA	TTGGTGGGAT	TCCGTTCCCTA	420
CTCAAGCAAG	CAAAATGTCCC	TATTTATGCT	GGACCGCTTG	CCTTGGCTTT	GATCCGTGGG	480
AAACTCGAAG	AACACGGCCT	CTTGCGCAAC	GCCAAACTTT	ACGAAATCAA	CCACAACACC	540
GAGTTGACCT	TTAAAAATCT	CAAGGCAACT	TTCTTTAGAA	CGACTCACTC	TATTCCAGAG	600
CCTTTGGGGA	TTGTCATTCA	TACTCCTCAA	GGGAAAAATCG	TCTGTACGGG	TGACTTTTAAG	660
TTGCACTTTA	CTCCAGTTGG	AGAACCTGCG	GACTTGCAATC	GTATGGCTGC	GCTTGGTGAA	720
GAAGGCGTGC	TCTGTCTCCT	GTCTGACTCG	ACAAATGCGG	AAGTACCAAC	CTTTACCAAC	780
TCTGAAAAAG	TCGTGGTCA	GTCCATTATG	AAGATTATCC	AAGGTATTGA	AGGACGTATC	840
ATCTTTGCAT	CCTTTGCCTC	AAATATCTTC	CGTCTCCAGC	AGGCAACAGA	AGCTGCTGTT	900
AAGACTGGAC	GCAAGATTGC	GGTCTTTGGT	CGTTCTATGG	AAAAGGCCAT	TGTCAACGGA	960
ATCGATCTTG	GCTACATCAA	AGCTCCTAAG	GGAACCTTTA	TCGAGCCAAA	TGAAATCAAA	1020
GATTATCCTG	CAGGAGAAGT	TCTTATCCTC	TGTACAGGTA	GTCAGGGTGA	GCCTATGGCA	1080
GCCCTCTCTC	GTATCGCCAA	CGGAACCCAC	CGTCAAGTAC	AATTACAACC	AGGTGATACC	1140
GTTATCTTCT	CTTCTAGTCC	CATCCCTGGA	AACACTACTA	GCGTCAACAA	GCTGATTAAC	1200
ATCATTTCTG	AAGCTGGTGT	CGAAGTTATC	CACGGTAAAG	TGAACAAATAT	CCATACATCT	1260
GGACACGGTG	GTCAGCAAGA	GCAAAAACTC	ATGCTCTGCT	TGATTAAGCC	AAAATACTTC	1320
ATGCCTGTCC	ACGGTGAATA	CCGCATGCAA	AAAGTCCACG	CTGGACTAGC	AGTGGATACT	1380
GGTGTGAGA	AGGACAATAT	CTTTATCATG	AGCAATGGCG	ATGTGCTTGC	CCTTACTGCT	1440
GACTCAGCTC	GTATCGCAGG	TCATTTCAAC	GCCCAAGATA	TCTATGTCGA	TGGAAATCGT	1500
ATCGGTGAAA	TTGGCGCAGC	TGTCCTCAAA	GATCGTCGCG	ATCTATCTGA	AGACGGTGTC	1560
GTTCTGGCAG	TCGCAACTGT	TGACTTCAAA	TCGCAGATGA	TTCTGTCTGG	CCCAGATATC	1620
CTCAGCCGAG	GCTTTGTCTA	CATGAGAGAG	TCTGGAGACT	TGATTGCGCA	AAGCCAGCGT	1680
ATCCTCTTCA	ATGCCATTTC	TATCGCACTG	AAAAATAAGG	ATGCTAGCGT	GCAATCTGTC	1740
AATGGTGCCA	TTGTCAACGC	TATTCGCCCC	TTCTCTATG	AAAATACCGA	ACGTGAACCG	1800
ATCATCATCC	CGATGATCCT	CACACCAGAT	GAAGAATAA			1839

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

AGCATTGTAC	CAGGGATGAT	GGTGATACCA	TTACCAGTAC	CAGCAAGTCC	AAGGATAGAA	60
GCCAAATCCAC	CACCGATTGC	ACCAGCAATC	AATGAAAGGA	AGAATGGTTT	ACGGAAGCGC	120
AAGTTCACCC	CGAAGATAGC	AGGCTCTGTA	ATACCTAGGA	AGGCAGAAAG	AGCAGCCGGG	180

AAAGCAAGTG TTTTCAGTTT TGGATTTTTT GTTTTAACAC CAACCGCAAC AGTAGCAGCA	240
CCTTGA	246

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GGAGACTCGT	TTAGAAGGAG	TAAACCGTCG	ATGACAGAAA	CCATTAAATT	GATGAAGGCT	60
CATACTTCAG	TGCGCAGATT	TAAGGAGCAA	GTCCTTCCTC	AGGAAGATTT	GA CTGAAATC	120
CTGACAGCAG	CCCAGATGGC	ATCATCTTGG	AAGAATTTCC	AATCCTACTC	TGTGATTGTG	180
GTACGAAGCC	AAGAGAAGAA	AGATGCCTTG	TATGAATTGG	TACCTCAAGA	AGCCATTCGC	240
CAGTCTGCTG	TTTTCCCTTCT	CTTTGTCGGA	GATTTGAACC	GAGCAGAAAA	GGGAGCCCGA	300
CTTCATACCG	ACACCTTCCA	ACCCCAAGGT	GTGGAAGGTC	TCTTGATTAG	TTTCGGTCGAT	360
GCAGCTCTTG	CTGGACAAAA	TGCCCTTGTTG	GCAGCTGAAA	GCTTGGGCTA	TGGTGGTGTG	420
ATTATCGGTT	TGGTTCGATA	CAAGTCTGAA	GAAGTGGCAG	AGCTCTTTAA	CCTACCTGAC	480
TACACCTATT	CTGTCTTTTG	GATGGCACTG	GGTGTGCCAA	ATCAAACCTCA	TGATGTGAAA	540
CCGAGACTGC	CACTAGATAA	TGTAGTCTTT	GAGGAAGAAT	ACCAAGAACA	GTCAACTGAG	600
GCAATCCAAG	CTTATGACCG	TGTGCAGGCT	GACTATGCTG	GAGCGCGTGC	GACCACAAGC	660
TGGAGTCAGC	GTCTAGCAGA	ACAGTTTGGC	CAAGCAGAAC	CAAGCTCAAC	TAGAAAAAAT	720
CTTAAACAGA	AGAAGTTATT	GTAG				744

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

AGCTCAGTAC	CTCTTCCAAT	TGGACCTGTT	CCCTTCACTC	TGCAAAACTT	TGCAATCGGC	60
TTGATTGCTA	CTGTCTTTAG	ACCGAGAGAG	GCTGTACTTT	CTGCTGGACT	CTATCTTCTT	120
CTAGGTGCTA	TCGGTCTTCC	TGTCTTTGCA	GGAGGTGGAG	CTGGTTTTCA	GGCTTTAGTT	180
GGCCCTACTG	CAGGCTATCT	TTGGTTTTAT	CTCGTTTACT	CTGGACTTAC	TTCTCTCTTA	240
ACCAACAGCA	AGAGTGGTGT	TGTTAAGATT	TTTCTTGCAA	ACCTCTTGGG	TGATGCCCTT	300
GTCTTTGTCG	GCGGGATTCT	CAGCTTGCAT	TTCTAGCTG	GAATGGCATT	TGAAAAAGCT	360
CTTGTTGTGG	GGGTCTTCC	CTTTATCATT	CCAGACCTTG	GCAAACCTTCT	GGCTATTAGT	420
TTTATTAGCC	GTCCCTACT	TCAACGCCTT	AAAAATCAGA	CTTACTTTAC	TAACTAA	477

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GATTATCCAC	CTCAGGAACC	CTTCATCACG	GCTACTATGA	AAGAAGTTGA	TGAATTGGCA	60
GAAGTGGACA	TCGAGGTGAT	TTCTCTGGAT	TGTACCAAGC	GTGAACGCTA	CGATGGTTTG	120
GAAATTCAAG	AGTTCATTCT	TCAGGTTAAG	GAGAAATATC	CTAATCAGCT	TTTGATGGCT	180
GATACTAGTA	TCTTCGAAGA	AGGGCTAGCA	GCTGTAGAAG	CAGGAATTGA	CTTTGTCGGA	240
ACAACCTTAT	CAGGCTACAC	ATCCTACAGT	CCAAAAGTAG	ACGGTCCAGA	TTTTGAATTG	300
ATTAAGAAAC	TCTGTGATGC	CGGTGTAGAT	GTCATTGCAG	AAGGAAAAAT	TCATACACCA	360
GAACAAGCCA	AACAAATCCT	TGAATATGGA	GTGCGAGGCA	TCGTTGTTGG	TGGCGCCATT	420
ACTAGACCAA	AAGAGATTAC	AGAACGCTTC	GTTGCTAGTC	TTAAATAA		468

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

ATGACTGCTT	TTCAACAAC	CCCATCTAGT	GTACTTCAAA	CTGGAGCCAT	TTTTCTCTCC	60
ATTATCATTG	AAGCCCTTCC	CTTCGTTCTG	ATAGGAAGTA	TTGTCTCAGG	GCTGATTGAA	120
GTTTATATCA	CACCTGACAA	GGTTTATCAT	TTTCTCCCTC	GAAATCGTTG	GGGGAGAATC	180
TTTTTTGGGA	CCTTTGTCGG	TATACTTTTC	CCCTCCTGTG	AATGTGGAAT	CGTCCCCATC	240
ATCAATCGTT	TTCTGGAAAA	AAAGGTTCCA	AGTTACACGG	CCGTTCCCTT	TCTTGTGACA	300
GCACCTGTTA	TCAATCCCAT	TGTTCTTTTT	GCGACCTATT	CTGCCCTTGG	CAACTCCTTC	360
CATGTCGCCC	TATTACGAGC	TCTGGGTTCC	ATCGTTGTGG	CTGTAATACT	AGGAATTTTT	420
CTAGGATTTT	TCTGGCAAGA	ACCGATTCAA	AAAGAAAATC	GTCTAGCCTG	TCATGAGCAT	480
GATTTTCTC	ACTTAAGTCC	TGCAAAAAAA	GTTTTTCAGG	TCTTTGTGCA	AGCCATTGAT	540
GAGTTTTTTG	ATACGGGACG	TTATTTGGTA	TTTGGCTGTC	TCTTTGCCTC	TGTTATACAG	600
GTTTATGTTT	CGACTCGGAT	TCTGACCTCT	ATCAGTGCGA	CTCCTCTTTT	TGCCATCCTG	660
CTCTTGATGA	TTTTGGCCTT	TCTTCTTTTCG	CTCTGTAGTG	AGGCGGATGC	CTTTATCGGG	720
GCTTCTCTAC	TCTCGAGTTT	CGGTTTGGCT	CCAGTTCTGG	CTTTTCTCGT	CATTGGCCCA	780
ATGCTGGATA	TCAAAAATAT	TCTTATGATG	AAAAATTACT	TGAAAGCACG	ATTTATTAGT	840
CACTTCATTA	CGATTGTGAC	TCTGGTCGTT	TTAGCCTATT	CTCTCTTGAT	TGGAGTCATC	900
CTATGA						906

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TTTTCGTCGT	TGACTTTAAC	GATACCACGG	TCGATACGTC	CTGAAGCAAC	TGTACCACGT	60
CCAGTGATTG	AGAATACGTC	CTCGACTGGA	AGAAGCAATG	GTTTGTGAGT	GTCACGTTCT	120
GGTTCTGGGA	TATACTCATC	AACTGTGTTT	ATCAATTCCA	TAACGATGTC	TTCGTATTTA	180

GAGTCACCTT	CAAGAGCTTT	AAGTGCTGAA	CCTTGGATAA	CTGGAAGATC	GTCACCTGGG	240
AAGTCGTATT	CTGACAATAG	GTCACGGATT	TCCATTTCAA	CCAATTCAAG	CAATTCTTCG	300
TCGTCAACCA	AGTCAACTTT	GTTTCATGAAG	ACGATAAGGT	GTTTAAACACC	AACCTGA	357

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1572 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TTGACAACAC	CAGGGCACGT	TGACTTTACC	TATGAAGTTT	CACGTTTCGT	AGCTGCCTGT	60
GAGGGTGCTA	TTTTGGTGGT	CGATGCGGCT	CAAGGAATTG	AGGCTCAAAC	TCTTGCCAAC	120
GTTTATCTGG	CTTTGGATAA	TGATTGGGAA	ATCATGCCTA	TCATTAATAA	AATTGACCTG	180
CCGGCTGCAG	ATCCGGAGCG	CGTGCGTACA	GAGATTGAAG	ATGTGATTGG	TTTGGATGCC	240
AGTGAAGCAG	TTTTGGCTTC	TGCCAAGGCT	GGTATTGGGA	TTGAAGAAAT	CCTCGAGCAA	300
ATTGTAGAAA	AAGTACCAGC	ACCAACGGGT	GATGTGACGG	CGCCACTTAA	GGCCTTGATT	360
TTCGACTCTG	TTTACGATGC	TTACCGTGGG	GTTATCCCTC	AAGTGCGTGT	CATGGACGGA	420
GTGGTCAAAAC	CTGGTGATAA	GATTTCAGCTC	ATGAGCAATA	GTAAGACCTT	TGATGTGGCC	480
GAAGTCGGTA	TTTTTACACC	AAAAGCGGTT	GGTCGTGATT	TCCTTGCGAC	TGGTGATGTT	540
GGTTACATTG	CGGCGTCTAT	CAAGACGGTT	CAGGATACTC	GTGTGGGTGA	TACCGTTACC	600
TTGGCAACCA	ATCCTGCGGC	AGAACCATTA	CATGGTTATA	AGCAGATGAA	TCCTATGGTC	660
TTTGCGGGTC	TCTACCCAAT	CGAATCAAAC	AAATACAATG	ACCTGCGTGA	AGCGCTTGAA	720
AAAATGCAAC	TGAATGATGC	TAGTCTTCAG	TTTGAACCAG	AAACATCTCA	GGCACTTGGA	780
TTTGGTTTCC	GTTGTGGATT	TCTTGGACTT	CTCCATATGG	ATGTTATCCA	GGAACGTTTA	840
GAGCGTGAGT	TCAATATTGA	CCTCATCATG	ACAGCTCCGT	CTGTTATTTA	CAAAGTTAAT	900
TTGACCGACG	GTGAGTCTAT	GGATGTGTCT	AACCCATCTG	AGTTTCCAGA	CCCAACTAAG	960
ATTGCGACCA	TTGAAGAGCC	TTATGTCAAG	GCGCAAATCA	TGGTACCACA	GGAGTTCGTC	1020
GGAGCAGTAA	TGGAGCTAGC	TCAGCGTAAG	CGTGGGGACT	TTGTGACTAT	GGACTATATT	1080
GATGATAACC	GTGTCAATGT	TATCTATCAA	ATTCCCTCTG	CTGAAATTGT	CTTTGACTTC	1140
TTTGATAAAC	TTAAGTCTTC	GACACGTGGT	TATGCAAGCT	TTGACTACGA	ATTGTCAGAA	1200
TATCGCCCAT	CTAAGCTGGT	GAAAATGGAT	ATCCTTCTCA	ATGGAGATAA	GGTGGATGCC	1260
CTCAGCTTTA	TCGTTACAA	GGACTTTGCC	TACGAACGTG	GGAAACTCAT	CGTTGATAAA	1320
CTCAAGAAAA	TCATCCCTCG	CCAACAATTT	GAAGTTCCAA	TCCAAGCGGC	TATTGGACAC	1380
AAGATTGTCTG	CTCGTACTGA	TATCAAGGCC	CTTCGTAAGA	ACGTAATTGC	TAAATGTTAT	1440
GGTGGTGACG	TTTCTCGTAA	GCGTAAACTC	CTTGAAAAAC	AAAAAGCTGG	TAAGAAACGC	1500
ATGAAATCCA	TCGGATCAGT	TGAAGTTCCG	CAAGAAGCCT	TCCTCAGCGT	CTTGAGTATG	1560
GATGAAGAAT	AA					1572

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

TCATATCGAC CCATACACNG CTGCNGCATT TTCACATTTT CTAAGTTAGA GCATGTTAAG	60
TTTATCGGTC TTACCCACTG TGGACGAATC TGGGAAGGAT GGGGTGTTCC AANAGAACGT	120
ATCATCGTTG TTAAACCAGG TGACCATATT GGAATTAAAA GATATGAAGA TTCATGCAGT	180
AGAATCATT GA	192

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAAGGGCGAC CAATCTACAT CCGTCTTGAA GTGGATAAGA AAGACCGTAT TTGGGGCCTC	60
TTGGCTTATC AAGAAGACTT CCAACGTCTT GCTCGTCCTG CTTACAACAA CATGCAGAAC	120
CAAAACTGGC CAGCCATTGT TTACCGTCTC AAGCTGTCAG GAACTTTTGT TTACCTACCA	180
GAAAATAATA TGCTTGTTT TATTCATCCT AGCGAGCGTT ACGCAGAGCC ACGTTTGGGG	240
CAAGTATTAG ATGCGCGCGT TATTGGTTTC CGTGAAGTGG ACCGCACTCT GAACCTCTCC	300
CTCAAACCAC GCTCCTTTGA AATGTTGGAA AACGATGCTC AGATGATTTT GACTTATTTG	360
GAAAGCAATG GCGGTTTCAT GACCTTAAAT GACAAGTCAT CTCCAGACGA CATCAAGGCA	420

ACCTTTGGCA TTTCTAAAGG TCAGTTCAAG AAAGCTTTAG GTGGTCTTAT GAAGGCTGGT	480
AAAATCAAGC AAGACCAGTT TGGGACAGAG TTGATTTAG	519

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GGAACAAGAC CCAGAAAAGT AGCCTTATTT CTTAAGAATT TTAATAGTTT AAAGCACCTA	60
GCACCTGTTT ATATTGATGA AACAGGAATC GACCGCTATC TCTATCGTCC TTATGCACGG	120
GCTCCTAGAG GGGAGAAAGT CTATGAAAAG ATTAGCGGAC GTCGTTTTGA GCGAACTTCA	180
ATTGTTGCAG GACAAGTAGA CGGAGAGTTT ATAGCTCCCA TGATTTACAA GAAAAGCATG	240
ACAAGCGATT TCTTTGTGGA GTGGTTCAAA ACGCAACTCC TACCTGCTTT GAAGACACCT	300
CATGTTATTG TCATGGGCAA TGCTAGTTTT CATCCCAAGA ACATTTTGGA TGAACCTCTG	360
ATCCAAGATA AACACTTTTT CTTACCTCTA CCACCTTATT CACCAGATTG GAATCCTATT	420
GAGCAAGCTT GGGCTATCTT GAAAAAGAAA GTGACGGATG TATTAAGGGA AGTTTCAACT	480
ATTTTGAAT GTTTGGAATG CTTTTTTAAA ACTAGATGA	519

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

AAAGGAGGAC	CCGCCATGCA	GGATTTCGGGA	ATCCAAGTAC	TCTTTCAAGG	AAATAATCTC	60
CTGAGAATCT	TACAGGGGTT	GGGCGTTACG	ATTGGGATAT	CCATCCTGTC	TGTCCTCTTA	120
TCCATGATGT	TCGGAACAGT	CATGGGAATC	ATCATGACCT	CCCATTCTAG	AATCATACGA	180
TTTTTAACAC	GATTGTATCT	GGAATTTATC	CGTATCATGC	CCCAGCTGGT	GCTACTCTTC	240
ATCGTTTACT	TTGGCTTGGC	TCGAAACTTT	AATATCAATA	TCTCAGGTGA	GACTTCAGCT	300
ATTATCATT	TTACCCTCTG	GGGAACAGCT	GAAATGGGAG	ACTTGGTACG	TGGAGCTATC	360
ACTTCTCTCC	CTAAACATCA	GTTTGAAAGT	GGATAG			396

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CGGCCGGGAC	CATGTATGCT	TTTATCCAGT	ACATCAACCG	CCCTCTTTGA	CCCTTTGATT	60
GAGGTGACGC	AAAACCTTTT	AACACTGCAA	ACGTCTATGG	TTTCTGCAGG	CCGTGTCTTT	120
GCCTTAATCG	ATGAGAGCAC	CTATGAGCCC	CTTCAAGAAA	ATGGGCAAGC	CAAAGTCAAG	180
GAGGGCAATA	TCAGTTTGG	AACATGTGTG	TATCTCGTAT	GA		222

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CCAATCGCTT	TGTTACCTCA	TATGAGAAAA	CACGTGAAAC	GATTCGTTTT	TAATAAAAGA	60
AAAAGATTTT	ATTGTGTGAG	GAGCAGAATC	AAATCTTTTT	CTATAGTTGT	GGGGAGATTT	120
ACTTCATTTT	CTCCTGAGAT	TGAGTTTTTA	CCCAGCCGAT	TTATCCACCA	CCTCAAAACA	180
GTGTTTTATA	CTCTTCGAAA	ATCTCTTCAA	ATCACGTCAG	CGTCGCCTTA	CCGTACTCAA	240
GTACAGCCTG	AGGCTAGCTT	CTTAGTTTGC	TTTTTGATTT	TCATTTAG		288

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATACCTTTGC	CTCTAAAGGA	AATCAAACCA	TCTTTTTTACC	AAATACGCCA	AATGGTGTGG	60
ATGATATCCG	AACACAAATC	TTGTCAGCCC	TTCGCGCTGA	GAAGAAATAA	TAGACTAATA	120
CTCTTCGAAA	ATCTCTTCAA	ACCACGTCAG	CGTCGCCTTG	CCGTATATCT	GCAACCTCAA	180
AACAGTGTTT	TGAGCTGA					198

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...2166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

AAGGAATTGC	CAATGACTTC	TTATAAACGT	ACATTTGTTC	CTCAAATAGA	TGCGAGAGAC	60
TGTGGTGTCTG	CTGCCTTAGC	CTCGATTGCT	AAATTCTATG	GTTTCAGATTT	TTCTCTAGCT	120
CACTTGAGAG	AACTTGCAAA	GACCAATAAA	GAAGGGACGA	CTGCTCTTGG	CATTGTAAAA	180
GCCGCTGATG	AAATGGGCTT	TGAAACAAGG	CCTGTTCAAG	CAGATAAAAC	TCTCTTTGAC	240
ATGAGTGATG	TCCCCTATCC	ATTTATCGTT	CACGTTAACA	AAGAAGGAAA	ACTCCAACAT	300
TACTATGTTG	TCTATCAAAAC	AAAGAAAAGAC	TATCTGATTA	TTGGTGATCC	TGACCCCTTCT	360
GTAAAAATCA	CTAAAAATGTC	AAAAGAACGC	TTTTTCTCTG	AATGGACTGG	AGTAGCTATT	420
TTTCTAGCTC	CCAAACCCAG	CTATCAACCC	CATAAAGATA	AAAAGAATGG	TCTACTAAGC	480
TTCTTCCTC	TGATTTTCAA	ACAAAAATCT	CTCATTGCTT	ACATTGTTCT	CTCAAGCTTA	540
TTGGTCACTA	TTATCAATAT	CGGTGGTTCT	TATTATCTCC	AAGGAATCTT	GGATGAATAC	600
ATCCCAAATC	AGATGAAATC	AACTTTAGGA	ATCATCTCAG	TTGGTCTGGT	TATCACCTAT	660
ATCCTCCAAC	AAGTCATGAG	CTTTTCCAGA	GATTATCTCC	TAACCGTTCT	GAGCCAGAGA	720
TTAAGCATTG	ATGTGATTTT	ATCCTATATT	CGCCATATTT	TTGAACCTCC	CATGTCCTTC	780
TTTGCGACAC	GTCGTACAGG	AGAAATCATT	TCACGGTTCA	CAGATGCTAA	CTCTATTATA	840
GATGCCTTGG	CTTCTACCAT	TCTTTCTCTT	TTTCTGGATG	TTTCTATTCT	GATTCTTGTA	900
GGGGGCGTCT	TACTGGCACA	AAACCCTAAT	CTCTTCCTCC	TTTCTCTTCT	TTCCATTCCCT	960
ATATACATGT	TCATCATCTT	TTCTTTTATG	AAACCTTTCG	AAAAAATGAA	CCATGATGTC	1020
ATGCAAAGTA	ATTCTATGGT	TAGCTCTGCC	ATTATCGAAG	ATATCAACGG	GATTGAAACT	1080
ATAAAGTCGC	TCACGAGTGA	AGAAAATCGC	TATCAAAATA	TAGACAGCGA	ATTTGTAGAT	1140
TATTTGGAAA	AATCCTTTAA	GCTCAGTAA	TATTCATTAT	TACAAACGAG	TTTAAAGCAG	1200
GGAACAAAAT	TAGTTCTGAA	TATCCTTATC	CTATGGTTTG	GCGCTCAATT	AGTCATGTCG	1260
AGTAAAAATTT	CTATCGGTCA	GCTGATTACC	TTTAACACAC	TTTTTCTTAA	CTTTACAACCT	1320
CCTATGGAAA	ATATTATCAA	CCTCCAAACC	AAACTCCAAT	CTGCGAAGGT	CGCTAATAAC	1380
CGTTTGAACG	AAGTCTATCT	AGTCGAATCT	GAATTTCAAG	TTCAAGAAAA	CCCTGTTTCAT	1440
TCACATTTTT	TGATGGGCGA	TATTGAATTT	GATGACCTTT	CTTATAAGTA	TGGTTTTGGA	1500
CGAGATACCT	TAACAGATAT	TAATCTCACG	ATTAAACAAG	GAGATAAGGT	TAGCCTAGTT	1560
GGAGTTAGTG	GTTCTGGTAA	AACAACTTTA	GCCAAAATGA	TTGTCAATTT	CTTTGAACCC	1620
TACAAAGGGC	ATATTTCAT	CAATTATCAG	GATATTAAAA	ACATTGATAA	AAAAGTCTTG	1680
CGCCGTCATA	TTAATTACCT	ACCCCAACAA	GCCTATATCT	TTAATGGCTC	TATCTTGGA	1740
AATTTAACCT	TGGGCGGTAA	TCATATGATT	AGCCAAGAAG	ATATTCTAAG	AGCTTGTA	1800
TTAGCTGAAA	TCCGTCAAGA	CATTGAAAGA	ATGCCTATGG	GCTATCAAAC	TCAGCTCTCT	1860
GATGGAGCTG	GTCTATCAGG	AGGACAAAAG	CAACGAATCG	CTCTCGCTCG	TGCTCTTTTA	1920
ACTAAAGCTC	CTGTTTTAAT	ACTAGATGAA	GCTACTAGCG	GTCTTGATGT	CTTGACTGAG	1980
AAAAAGGTTA	TAGATAATCT	TATATCCCTA	ACTGATAAAA	CCATTCTCTT	TGTAGCCCAT	2040
CGTCTCAGTA	TAGCCGAACG	AACTAACCGT	GTCATTGTTC	TTGACCAGGG	GAAAATCATT	2100
GAAGTTGGTA	GTCACCAAGA	GTTAATGCAG	GCGCAAGGCT	TCTACCATCA	TCTATTCAAT	2160
AAATAA						2166

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GATTCGATGC	CAATGAGAGA	CAGAATTTCA	GCCTTTTTAG	AGGAAAAGCA	GGGCTTGTCT	60
GTCAATTCCA	AGCAGTCCTA	TAAGTATGAT	TTGGAGCAAT	TTTTAGACAT	GGTAGGTGAG	120
CGGATTTCTG	AGACCAGTCT	CAAGATTTAC	CAAGCCCAGC	TAGCCAATCT	AAAAATCAGC	180
GCCCAGAAGC	GAAAGATTTC	GGCCTGTAAC	CAATTTCTAT	ACTTTCTCTA	TCAAAAAGGA	240
GAGGTGGACA	GCTTTTACCG	CTTGGAATTA	GCCAAACAAG	CTGAAAAGAA	GACGGAAAAG	300
CCAGAGATTC	TATACCTAGA	CTCTTTTTTG	CAGGAAAGCG	ACCATCCAGA	GGGCCGCTTG	360
CTAGCGCTCT	TAATCCTAGA	AATGGGGCTC	TTGCCCAGTG	AGATTTTAGC	CATCAAGGTT	420
GCGGACATCA	ATCTGGATTT	TCAGGTGCTG	CGAATCAGCA	AGGCTTCCCA	ACAGAGGATT	480
GTCACCATTC	CCACGGCCTT	GCTTTCAGAA	TTGGAACCCCT	TGATGGGGCA	GACCTATCTT	540
TTTGAAAAGAG	GAGGGAAAACC	CTATTCTCGT	CAGTGGGCCT	TTCGTCAGTT	AGAATCTTTT	600
GTCAAGGAGA	AAGGTTTTC	ATCCTTATCA	GCTCAAGTCT	TACGTGAACA	GTTTATTCTA	660
AGACAAATAG	AAAACAAGGT	CGATTGTGAC	GAAATTGCAA	AAAAATTAGG	ATTAAAAACA	720
GTCCTGACCT	TAGAAAAATA	TAGATAA				747

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GCGGTTTCGC	CAAAAATGGG	GCTTGGAGCG	TATCATTGTT	TTAACTTATC	AAGCCAGTAT	60
TCAGGAGCTG	GTATGGGAGC	AATTCTTGAG	ACACAACGTG	AACTTCGTGA	AGTCTTGAAT	120
GATGGTGTGA	AACCATGTGA	TTTGCATGCG	GAAATTTTGC	CTTCAGGTGG	TGACAAGAAA	180
CATTATCCTA	TCGCCTTTAA	CGCTCTTCCA	CAAATTGATG	TTTTCACTGA	TAATGATTAC	240
ACGTACGAAG	AGATGAAGAT	GACCAAGGAA	ACTAAGAAAA	TTATGGAAGA	TGATAGCATT	300
GCAGTATCTG	CAACATGTGT	GCGTATTCCA	GTCTTGTCAG	CTCACTCTGA	GTCTGTTTAT	360
ATCGAAACAA	AAGAAGTGGC	TCCAATCGAA	GAAGTAAAAG	CAGCTATCGC	AGCCTTCCCA	420
GGTGCTGTTC	TTGAAGATGA	TGTAGCTCAT	CAAATCTATC	CTCAAGCTAT	CAATGCAGTT	480
GGTTCGCGTG	ATACCTTTGT	TGGTCGTATC	CGTAAAGACT	TGGATGCAGA	AAAAGGAATT	540
CACATGTGGG	TTGTTTCAGA	TAACCTTCTC	AAAGGTGCTG	CTTGGAAGTC	AGTTCAGATT	600
GCTGAAACTC	TTCATGAACG	TGGATTGGTT	CGTCCAACAG	CTGAATTGAA	ATTTGAATTA	660

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GCTTTCTCGC CAAACGTAAT TCCTTGTAAT ATTCCCCCAG TTCCATTTTT TCAATCATCC	60
TACCACCTCC TAGCTTTTGC ATATTATATC ATTATTTGTG TTCATTTGTC AAAACATTCT	120
GACACTTTGG TGATTGAAAA AGCCAGCCTT AAGCTGACTC TAAAAGGACC GAGCCTTGTA	180
CAATACAGAA CTCAATCCTC GTTCTAA	207

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...936
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TTGGTGGCGC CAATGGAACC AGCAACGTGC GTGCGGGTAA GCTCTTTGAC ATTCCTGTTT	60
TGGGAACCCA TGCCCATGCC TTGGTACAGG TTTATGGCAA TGACTATGAG GCTTTCAAGG	120
CTTACGCTGC GACCCACAAA AATTGTGTCT TTCTTGTGGA TACCTATGAT ACCCTTCGCA	180
TCGGTGTACC AGCTGCCATT CAGGTGGCGC GTGAGCTGGG TGATCAGATT AACTTTATGG	240

GTGTGCGGAT	TGACTCTGGG	GATATTGCCT	ACATTTCTAA	GAAAGTCCGT	CAGCAACTGG	300
ACGAGGCTGG	ATTTACAGAG	GCTAAGATTT	ATGCTTCTAA	TGATTTGGAC	GAAAATACTA	360
TCCTCAATCT	CAAGATGCAA	AAGGCCAAGA	TTGATGTCTG	GGGTGTGGGT	ACCACAGCTG	420
ATTACAGCCT	ATGACCAGCC	GGCTCTTGGG	GCGGTTTACA	AGATTGTTGC	AATCGAAGAT	480
GAAACTGGTC	AGATGCGCAA	TACGATTAAG	CTGTCTAATA	ATGCGGAAAA	AGTGTCGACG	540
CCAGGTAAGA	AGCAGGTGTG	GCGCATTACC	AGTCGTGAAA	AAGGTAAGTC	AGAAGGTGAT	600
TACATCACTT	ATGATGGTGT	GGATATTAGC	GACATGACAG	AAATCAAGAT	GTTCCATCCG	660
ACCTATACAT	ACATCAAGAA	GACGGTTCGT	AATTTTGATG	CCGTTCCCTCT	CTTGGTGGAT	720
ATCTTCAAAG	AAGGAATATT	AGTTTACAAC	TTGCCTAGTT	TGACTGACAT	TCAGGATTAT	780
GCCCCGTAAG	AATTTGACAA	GTTGTGGGAT	GAGTATAAGC	GTGTGCTCAA	TCCGCAGCAC	840
TATCCAGTGG	ATTTGGCGCG	TGATGTATGG	CAAGATAAGA	TGGACTTGAT	TGATAAGATG	900
CGCAAGGAAG	CCCTTGGTGA	AGGAGAAGAA	GAATGA			936

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

TCACCCAGC	CAAGGTATTG	GATATCCAAT	TTGGCACCAA	CTTTTCTTC	AATGATTTTG	60
TTGGCATTTG	CTAACAAATC	ATCCAAGTTG	TCTGGTTTGT	CACCGATTTG	GTACATTTTG	120
ATAACAGGTT	TGTCACCTGA	ATCAGCAGCT	TTTTTGCTGT	TACCTGTCAA	ATTTCCACAA	180
GCAGCAAGAC	CTGCAGCCAG	AGCGACTACA	CTAGCAGATG	CAAAAGCATA	TTTTTTCCAG	240
TTTTTCATGA	TAAAACTCC	TTTTTTTATT	TTTAACTTA	TAAACAATGT	AATGATCTTA	300
TACTCAATGA	AAATCAAAGA	GCAAACTAGA	AAACTAGCCG	CAGGCTGCTC	AAAGCACTGC	360
TTTGAGGTTG	TAGATAAGAC	TGACGAAGTC	AGTTACATAT	ATCTACGGCA	AGGCGACGTT	420
GACACGGTTT	GA					432

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CCAAGGCAGC	CAACAAACTG	GGCGTCAAGG	TTATTACGGT	CTATGCTTTT	TCATACGGAA	60
AACTGGACCC	GTCCAGATCA	GGAAGTCAAG	TTTATCATGA	ACTTGCCAGT	AGAGTTTTAT	120
GATAATTATG	TCCCGGAACT	ACATGCGAAT	AATGTTAAGA	TTCAAATGAT	TGGGGAGACA	180
GACCGCCTGC	CTAAGCAAAC	CTTTGAAGCT	TTAACCAAGG	CTGAGGAATT	GACTAAGAAC	240
AACACAGGAT	TGATTCTTAA	TTTTGCTCTT	AACTATGGTG	GACGTGCTGA	GATTACACAG	300
GCGCTTAAAGT	TGATTTCCCA	GGATGTTTTA	GATGCCAAAA	TCAATCCAGG	TGACATCACA	360
GAGGAATTGA	TTGGTAACTA	TCTCTTTACC	CAGCATTTGC	CTAAGGACTT	ACGAGACCCA	420
GACTTGATTA	TCCGTACTAG	TGGAGAATTG	CGTTTGAGCA	ATTTCTTCC	ATGGCAGGGA	480
GCCTATAGTG	AGCTTTATTT	TACGGATACC	TTATGGCCTG	ATTTTGACGA	AGCGGCCTTG	540
CAGGAAGCTA	TTCTTGCCTA	TAATCGTCGT	CATCGCCGAT	TTGGAGGAGT	TTAG	594

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 507 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TCTTGTAAGC	CGTGGTCGTT	TCCCTACAGA	AAGCCTTTTA	AGAGTCTTGG	AAAAGATGAC	60
CTTGAAATAA	TAAACAGATC	AATGGTTAAG	GCCAATGTTG	AAGATCTAGC	AAATAACCTA	120
GTTGAAGAAC	TTTCTGGGGG	TCAAAGGCAA	AGAGTATGGA	TAGCTCTAGC	CCTAGCCCAA	180
GATACAAGTA	TCCTACTTTT	AGATGAGCCA	ACTACTTACT	TGGATATCTC	ATATCAAATA	240
GAACTATTAG	ACCTCTTGAC	TGATCTAAAC	CAAAAATATA	AGACAACCAT	TTGCATGATT	300
TTGCACGATA	TAAATCTAAC	AGCAAGATAC	GCTGATTACC	TATTTGCAAT	TAAAGAAGGT	360
AAACTTGTTG	CAGAGGGAAA	GCCTGAAGAT	ATACTAAATG	ATAAACTAGT	TAAAGATATC	420
TTTAATCTTG	AAGCAAAAAT	TATACGTGAC	CCTATTTCCTA	ATTCGCCTCT	AATGATTCCCT	480
ATTGGCAAGC	ACCATGTTAG	CTCTTAA				507

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...348
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

ATCAGTAAGC	CTACACAGAC	ACCTAGCGTA	TTTAAAGTCA	AATCCGTTAT	ATCTGTTATA	60
CCTATTGCTA	AAATATACTG	TAAGCACTCA	AACAATAAAC	TAATCAAGAA	ACCTGTCCCG	120
ACTATTCTTA	AACTAGATAA	ATTAGTTTTT	ATCAAAGGGA	AACAAACACC	TAATGGAATA	180
AAGAAAATCA	GATTAAATAA	CATTTCAGCA	AAAACAATTT	TTCCATCGAC	TATTAGTGGT	240
TCTGAAAATG	GAATCCAATT	GATATACCTT	GGAGCTAAGA	AAAATGCTAT	AAATTCAGGA	300
TTTGTTCCTCA	ACTTAAATAA	GATTCCCCAA	GTTAATAACA	TCAGATAG		348

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

AGAAGGGCGT	TGAACCAGTC	ATTCCAGAAA	CCAAGAGCTG	TTAAGAGCGT	GATGGTTGCG	60
ATACCTGGTA	GTGACAATGG	CAAACAGATT	TGGAAGAAAA	TCCGGGCTTC	ACTGGCACCA	120
TCGATACGAG	CCGATTCTAG	AATGGCTTCT	GGAATGGTCT	TCTTGAAGAA	GGAACGCATC	180
AAGATGATGT	TAAATGGTGA	GAGAAGCATT	GGAACAATCA	AGGCCCAAAC	AGTATCCCCA	240
AGCTGA						246

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 690 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...690
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

CACGCGGAGC	CTGCTCCAAC	TTCTCTTCCC	CCACCCCCCA	TACACCCACG	CTCCCCCTCC	60
AGCAGATCCC	ATCGCAACTT	CTCCCTTTGT	TCCCAAACCC	CGTGGCCTCA	CCACGGCACA	120
CATCCGTGCA	GCCCATATCT	CCCTGCCGAC	ACGGCCCTCC	TCACACCAAC	TGCCCCCCAC	180
TCACCCCACT	CCACCCGTCC	CCGGACCGCC	CCCGCCTCAA	CCCCGGCCAC	CCCACTTCCC	240
TCCACCCCCC	GTTCCCCCGC	ATGCCGCCCC	CCTCCACGCG	GCCAATCCCC	CACCGCGCGC	300
GAGCAACTCC	CCCCCCCCAC	CCCCACCACC	GCCCGCCGCA	CGCCAACCCC	CCCACGCCCC	360
CCCCCGCAGG	AATCCGCGCG	CCCACCCCGG	GCCCACACCG	CACCGGCCTC	ACCGCCCCAC	420
CCCGCCCCCG	CACACCCCCC	CCACTCCGCC	ACCAGCCCAC	ACCGGCCCCC	CTACCACACC	480
CCCAACGAAC	GAGCCGCCCC	GCCCCACGCC	AGCCCCAAAA	CCCCCCCCGC	ACCCACCCCG	540
CCCCGCCGCC	NACCTACCGC	CCATGCTCGC	GACCCCCCGC	ACCGAGCNAG	CCACNNCNG	600
NCCNNNNNNN	NNNTTTCNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNACTA	660
CACAACTGG	CAAGCAGTTG	GCGACCTTGA				690

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

CAATATTTTT	TAAGGGGGGA	CATTTTTATG	TCAGAGCGTA	AATTATTCAC	GTCTGAATCT	60
GTATCTGAGG	GGCATCCGGA	TAAGATTGCA	GACCAAATTT	CAGATGCGAT	TTTGGATGCT	120
ATTTTAGCAA	AGGATCCAGA	GGCGCACGTT	GCTGCTGAAA	CAGCTGTATA	TACTGGTTCT	180
GTCCACGTTT	TTGGTGAAAT	TTCTACAAAT	GCCTATGTGG	ATATTAACCG	TGTGGTTCGT	240
GATACCATTG	CAGAGATTGG	TTATACCAAT	ACAGAATATG	GATTTTCTGC	TGAGACGGTG	300
GGAGTACACC	CATCTTTGGT	GGAACAATCT	CCTGACATCG	CTCAAGGTGT	TAACGAAGCC	360
TTGGAGGTTT	GTGGAAATGC	TGATCAAGAT	CCACTGGACT	TGATTGGAGC	AGGTGACCAA	420
GGGCTCATGT	TTGGATTTGC	AGTAGATGAA	ACAGAAGAGC	TTATGCCATT	GCCAATTGCA	480
CTCAGTCATA	AATTGGTTTC	TCGTCTGGCA	GAACCTCGTA	AGTCTGGAGA	AATTAGCTAT	540
CTCCGTCCAG	ATGCAAAATC	ACAAGTTACA	GTTGAGTACG	ATGAAAATGA	CCGTCCGGTA	600
CGTGTAGATA	CAGTCGTTAT	TTCTACTCAG	CATGATCCAG	AGGCCACTAA	TGAACAAATC	660
CATCAAGATG	TGATTGACAA	GGTCATCAAA	GAAGTTATTC	CATCTTCTTA	TCTTGATGAT	720
AAGACAAAAT	TCTTTATCAA	TCCGACAGGT	CGTTTTGTAA	TCGGTGGTCC	TCAAGGGGAC	780
TCAGGTTTGA	CTGGTCGTAA	GATTATTGTA	GATACTTATG	GTGGCTACTC	TCGTCAATGGT	840
GGTGGTGCCCT	TCTCTGGTAA	AGATGCGACT	AAGGTGGATC	GTTCAGCCTC	TTATGCGGCT	900
CGTATATTG	CCAAGAATAT	CGTTGCAGCA	GGCCTTGCTA	AGAAGGCAGA	AGTGCAGTTG	960
GCCTATGCTA	TCGGTGTTGC	GCAACCTGTT	TCTGTTGCTA	TCGATACTTT	CGGTACAGGA	1020
ACAGTAGCTG	AAAGTCAACT	TGAAAAAGCG	GCTCGTCAAA	TCTTTGACCT	TCGCCCTGCA	1080
GGGATTATCC	AAATGCTGGA	CCTCAAGCGT	CCAATTTACC	GTCAAACATC	GGCTTACGGT	1140
CACATGGGAC	GTACAGATAT	TGATCTTCCA	TGGGAACGTT	TGGATAAGGT	AGATGCTTTG	1200
AAAGAAGCAG	TAAAATAA					1218

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TCATCATGGC	CAAGCAAGGT	GTCGCTTTTT	GCCAAGGAAG	CTGGTGTTTT	AGCGGGACTA	60
ACCGTTTTTC	AAAGGGTTTT	TACCCTATTT	GATGCCGAGG	TGACCTTCCA	GAATCCTCAT	120
CAATTTAAGG	ATGGGGATCG	TTTGACTAGT	GGCGATTTAG	TTTTAGAAAT	CATAGGCTCG	180
GTGAGAAAGT	TCTTAACATG	TGAACGCGTT	GCCTTGAAAT	TTTTACAACA	TTTATCAGGG	240
ATTGCTTCGA	TGACAGCTGC	TTATGTAGAA	GCCTTAGGCG	ATGATTGCAT	TAAGGTATTT	300
GATACTCGAA	AAACTACTCC	TAATTTACGT	CTTTTTGAGA	AATATGCCGT	GAGAGTTGGC	360
GGTGGCTATA	ATCATCGCTT	TAATTTATCA	GATGCTATCA	TGCTAAAAGA	CAATCACATT	420
GCGGCAGTAG	GTAGTGTTCA	GAAGGCAATT	GCTCAAGCGC	GTGCCATATG	CCCTTTTGTG	480
AAAATGGTCG	AGGTGGAAGT	GGAAAGCCTT	GCTGCTGCCG	AAGAAGCTGC	GGCGGCGGGT	540

GCTGATATTA TCATGTTGGA TAATATGTCA TTGGAACAGA TTGAACAGGC CATTACCCTA	600
ATTGCAGGAC GTTCTCGGAT TGAATGTTCT GGAAATATTG ATATGACCAC TATTAGCCGT	660
TTTCGTGGTT TAGCGATTGA TTACGTCTCC AGTGGTAGTT TAACCCATAG TGCTAAGAGT	720
CTTGATTTTT CCATGAAGGG TTTAACCTAC CTTGATGTCT AA	762

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GATCTAGCTT TCGTGATGGA AAGCGATTCT CGTTCGTTTT TTCTTTGTCA TACTCTTCGA	60
AAATCTCTTC AAACCACGTC AGTTTTATCT GAAACTTCAA AGCTGTGCTT TGAGCAACCT	120
GCGACTAGCT TCCTAGTTTG CTTTTTGATT TTCATTGAGT ATCAATTTGA ATGGAAAATG	180
GAAAGTTATC ATCTTGTAAT GAGTTAA	207

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...384
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

CTGCTCAGGC	CTGGAAGTCA	AGGGGTGTGA	TTTGGAGCTT	TAAGTGCTGA	TAAAAAGTTG	60
GATAAGCCTA	ATCTGGAAAA	GTTAATTGCT	GCATCAAAAG	GAATGGAAAT	TGTCCTTTCAC	120
ATGGCCTTTG	ATGAACTAAG	TGATGAAGAT	CAACCGGAAG	CTATTGACTG	GCTCAGTCAA	180
GCCGGTGTCA	CTCGTATCCT	AACTCGTGCT	GGTGTGTCTG	GCGACTCCTT	AGAAAAACGT	240
TTTGTTCACT	ATCACAGAAT	TTTGGAGTAC	GCTAAAGGTA	AAATTGAAAT	TCTACCAGGT	300
GGGGGGATTG	ACCTTGACAA	CCGTCAAACC	TTTATTGACC	AGGTGGGGGT	AACACAATTG	360
CATGGTACTA	AGGTTGTTTT	TTAA				384

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TATTGCGGGC	CCCAAAAAAC	GTCGCAAGAA	TTGAATGTAT	TAAAAAACAC	TTACAATACC	60
TTCCATAAGA	TGGAAGAGTT	GCAGGATGAA	GTCGAAATTT	TATTGGATTT	TTTGGCTGAA	120
GACGAGTCAG	TGCATGATGA	ACTGGTAGCG	CAGTTAGCCG	AAC TTGATAA	GATAATGACC	180
AGCTACGAGA	TGACTTTTACT	CTTGTTCAGAA	CCTTATGACC	ACAACAATGC	CATCTTGGAA	240
ATCCATCCAG	GTTCTGGTGG	TACTGAGGCG	CAGGACTGGG	GTGATATGTT	GCTTCGTATG	300
TATACTCGTT	ATGGTAATGC	TAAAGGCTTT	AAAGTGGAAG	TGTTGGATTA	CCAAGCAGGT	360
GATGAGGCTG	GTATTAAGTC	GGTAACTTTA	TCATTTGAAG	GGCCTAATGC	CTATGGTCTC	420
CTCAAGTCAG	AAATGGGTGT	TCACCGCTTA	GTGCGAATCT	CACCATTGTA	CTCTGCCAAA	480
CGTCGCCATA	CCTCTTTCAC	ATCTGTAGAA	GTGATGCCAG	AATTGGATGA	TACTATTGAA	540
GTGGAAATCC	GTGAAGATGA	TATCAAGATG	GATACCTTCC	G TTCAGGTGG	TGCCGGTGGA	600
CAAAACGTCA	ATAAAGTTTC	AACAGGTGTA	CGTTTAACCC	ACATTCCAAC	TGGAATTGTT	660
GTCCAATCAA	CAGTGGATCG	TACCCAGTAT	GGAAATAGAG	ATCGTGCCAT	GAAGATGTTG	720
CAGGCTAAGC	TCTATCAAAT	GGAGCAAGAG	AAGAAGGCTG	CGGAGGTAGA	TTCTCTCAAA	780
GGTGAGAAAA	AGGAGATTAC	TTGGGGGAAGC	CAAATCCGTT	CTTATGTCTT	CACGCCTTAT	840
ACTATGGTAA	AAGATCACCG	AACTAGCTTT	GAGGTTGCTC	AGGTAGATAA	GGTTATGGAT	900
GGGGACCTAG	ATGGTTTTAT	CGATGCTTAT	CTCAAGTGGC	GAATTAGCTA	A	951

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: *misc_feature*

(B) LOCATION 1...2073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GATTTTAAGT	TAGAAATGAG	ACTGATTTGT	ATGATAAAAT	TTAACAGCCA	TTCGATTCCG	60
ATTCGGCTTA	ATTTATTGTT	TTCAATCGTC	ATTTTACTCT	TTATGACCAT	TATTGGTCGT	120
TTGTTGTATA	TGCAGGTTTT	GAACAAGGAT	TTTTACGAAA	AAAAGCTAGC	CTCAGCTAGT	180
CAGACCAAGA	TTACAAGCAG	TTCAGCCCGT	GGGGAAATTT	ATGATGCTAG	TGGAAAACCT	240
TTGGTAGAAA	ATACGTTAAA	GCAGGTTGTT	TCCTTTACGC	GTAGCAATAA	AATGACGGCT	300
ACAGACTTAA	AAGAAACAGC	TAAAAAGTTA	CTGACTTATG	TGAGCATCAG	TTCTCCAAAT	360
TTGACAGAAC	GCCAGCTGGC	GGATTACTAT	TTGGCTGATC	CTGAAATCTA	TAAAAAACA	420
GTGGAAGCTC	TCCCAAGTGA	GAAACGCTTG	GATTCAGATG	GCAATCGTCT	ATCCGAATCA	480
GAAGTGTATA	ACAATGCGGT	CGATAGTGTC	CAAACAAGTC	AACTAAACTA	TACAGAGGAT	540
GAAAAGAAAG	AAATCTATCT	TTTTAGTCAG	TTAAATGCTG	TTGGAAACTT	TGCGACAGGA	600
ACCATTGCTA	CAGATCCTCT	AAATGATTCT	CAGGTGGCTG	TTATTGCCTC	TATTTCAAAG	660
GAGATGCCTG	GCATTAGTAT	TTCTACTTCT	TGGGATAGAA	AGGTTTTGGA	AACTTCCCTT	720
TCTTCTATAG	TTGGGAGTGT	ATCCAGTGAA	AAAGCTGGTC	TCCCAGCGGA	AGAAGCAGAA	780
GCCTATCTTA	AAAAAGGCTA	TTCTCTAAAT	GATCGTGTAG	GAACCTCCTA	TTTGGAAAAG	840
CAATATGAAG	AGACCTTACA	AGGAAAACGC	TCGGTAAAAG	AAATCCATCT	GGATAAATAT	900
GGCAATATGG	AAAGCGTGGA	TACAATTGAG	GAAGGTAGTA	AGGGAAACAA	TATCAAACCTG	960
ACCATTGATT	TGGCTTTCCA	AGATAGCGTG	GATGCTTTAC	TGAAAAGTTA	TTTCAATTCC	1020
GAGCTAGAAA	ATGGTGAGC	CAAGTATTCT	GAAGGTGTCT	ATGCAGTCGC	CCTTAACCCA	1080
AAAACAGGTG	CGGTTTTGTC	TATGTCAGGG	ATTAAACATG	ACTTGAAAAC	GGGAGAGTTG	1140
ACGCTGATT	CCTTGGGAAC	GGTAACCAAT	GTCTTTGTTC	CAGGTTCCGT	TGTCAAGGCG	1200
GCGACCATCA	GCTCAGGTTG	GGAAAATGGA	GTCTTGTCAG	GAAACCAGAC	CCTGACAGAC	1260
CAGTCCATTG	TCTTCCAAGG	TTCAGCTCCC	ATCAATTCTT	GGTATACTCA	GGCTTACGGT	1320
TCATTCCCTA	TCACAGCGGT	CCAAGCTCTG	GAGTATTCAT	CAAATACCTA	TATGGTCCAA	1380
ACAGCCTTAG	GTCTTATGGG	GCAAACCTAT	CAACCCAATA	TGTTTGTCGG	CACCAGCAAT	1440
CTAGAGTCTG	CTATGGAGAA	ACTGCGTTCA	ACCTTTGGCG	AATATGGCTT	GGGTACTGCG	1500
ACAGGAATTG	ACCTACCAGA	TGAATCTACT	GGATTTGTTC	CCAAAGAGTA	TAGCTTTGCT	1560
AATTACATTA	CTAATGCCTT	TGGGCAGTTT	GATAACTATA	CGCCGATGCA	GTTGGCTCAG	1620
TATGTAGCAA	CTATTGCAA	TAATGGTGGT	CGTGTGGCTC	CTCGTATTGT	TGAAGGCATT	1680
TATGGTAATA	ATGATAAGGG	AGGACTGGGT	GACTTGATTTC	AGCAACTGCA	ACCGACAGAG	1740
ATGAATAAGG	TCAATATATC	CGACTCCGAT	ATGAGCATCT	TGCACCAAGG	TTTTTTATCAG	1800
GTTGCCCATG	GTAAGTAGTG	ATTGACAACT	GGACGTGCCT	TTTCAAATGG	CGCCTTGGTA	1860
TCCATTAGCG	GAAAAACAGG	TACAGCCGAA	AGCTATGTGG	CAGATGGTCA	GCAAGCAACC	1920
AATACCAATG	CGGTGGCCTA	TGCCCCATCT	GATAATCCCC	AAATCGCTGT	TGCAGTGGTC	1980
TTTCCTCATA	ATACCAATCT	AACAAATGGT	GTAGGACCTT	CCATTGCGCG	TGACATTATC	2040
AATCTGTATC	AAAAATACCA	TCCAATGAAC	TAG			2073

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TACAATAAGT TTATGAATAA ACAACAATTT ATTATTATGG CGCTATTTAC AGCTGCTGAG	60
ACCTATTTTTT TCAATGAAGC CTGGATGACT GGCCGCTATA TTATGGCAGC CTTTTGGGCA	120
ATTTTACTCT TTAGAAATTT CCGAGTCAGT TATGTGATGG GCAAAATCGT TGATGTCATC	180
GATCAGCATT TTAATAGGAA AGACTAG	207

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GTCCTCAAGT TGAAGAAGGA GCCTCTGCTC ATCCAGTTGC CCCCAATGTA TGAAGCACTA	60
GAAGTAGCTC CAATGCATCC GACTGGTCCA ACACCAGCTA CAGAACTGT TGATTCATAC	120
CGGGATATGA AGCACCGCAA GAATCTGTTA CAATTTTATA AGAAATATTC TGAGAACAAT	180
ATCTTATCCT TATATATTCC AGCGAGCAGG AGATGGTGTG AGTCCTGCAT TCCCTATCGA	240
TAA	243

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CAAATCTTTA	CGGTTCAAAT	GCACCGAAGG	TCTTTGCACT	TGCTCACAGC	TTGGAACAAG	60
CGCCAGGACT	CAGCTTGGCA	GATACTTTGT	CCCTTCACTA	TGCAATGCGC	AACGAGTTGG	120
CTCTTAGCCC	AGTTGACTTC	CTTCTTCGTC	GTACCAACCA	TATGCTCTTT	ATGCGTGATA	180
GCTTGGATAG	CATCGTTGAG	CCAGTTTTTG	ATGAAATGGG	ACGATTCTAT	GA CTGGACAG	240
AAGAAGAAAA	AGCAACTTAC	CGTGCTGATG	TCGAAGCAGC	TCTCGCTAAC	AACGATTTAG	300

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1725 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TTGAACTTTA	CAAGAGAGGA	GTTAAATAAA	ATGGATAAGT	TAATAATTTT	TATTGAGAAA	60
GGAAAGCCTT	TCTTTGAAAA	ATTATCGAGA	AATATATACT	TAAGAGCGAT	AAAAGATGGT	120
TTTATTTCCA	GTATGCCAGC	AGTATTATTC	TCAAGTATTT	TTATACTAAT	AGCTGCTGTG	180
CCCAATATTT	TTGGGTTTAA	ATGGTCTGAT	GAACAGTTAG	CTTTTATTTT	GAAACCTTAC	240
AACTACTCAA	TGGGAATTTT	AGCTCTCTTA	GTAGCTGGGA	CAACTGCAAA	ATCGTTAACA	300
GATTCAGTTA	ATACACGTAG	TATGGAGAAA	ACCAACCAAA	TCAACTACAT	GTCAACTTTT	360
TTAGCAGCTG	TTGTTGGATT	GTTAATACTG	GCAGCTGATC	CAATTGAAGG	TGGATTGCT	420
AATGGTCTTT	TAGGTACTAG	AGGATTACTT	ACTGCATTTT	TGGCAGCTTT	TATTACAGTA	480
AATATCTATA	AAGTATGTAT	TAAAAATAAT	GTAACCATTA	GA CTTCCTGA	AGAGGTTCCA	540
CCAAATATTG	CACAAGTTTT	TAAAGATGTT	ATTCCGTTTG	CCTTATCTGT	TCTTTCAATA	600
TATGGATTGG	ATTTAATTGT	TAGAAATATT	TTTGGTACAA	ATGTAGCAGA	ATCTGTTGGT	660

AAAATATTAG	CCCCTCTATT	TTCAGCTACT	GATGGTTATA	TCGGTTTAGC	TATTGTATTT	720
GGTGCTTATG	CTTTCTTTTG	GTTTGTGGGA	ATTCATGGGC	CATCTGTTGT	AGAACCCTTA	780
ATTGTAGCTA	TCAGTTATGC	AAATATAGAA	GCTAATGTTT	AGCTTGTGCA	AGCTGGTATG	840
CACGCAGATA	AAATTTTAAA	TCCAGTTACT	CAAACTTTTG	TTGTAACAAT	GGGTGGTACT	900
GGTGCAACAC	TAGTAGTTCC	ATTTATGTTT	ATGTGGTTAT	GTAAATCAAA	AAGAAATAGA	960
ATTGTCGGAC	GTGCGTCTGT	AGTTCCTACT	TTCTTTGGCG	TAAATGAACC	AATCCTATTT	1020
GGTGCTCCAA	TTGTTTTAAA	TCCATATCTC	TTTATTCCGT	TTGTTACTGC	TCCATTATC	1080
AATGTTTGGA	TTATGAAATT	TTTTGTAGAT	GTTCTACAAA	TGAATAGTTT	CAGTATTATT	1140
TTACCTTGGA	CAACACCTGC	TCCAATTGGT	ATTGTTATGG	GAACGGCGCT	GGCTCCATTG	1200
TCATTCGTCT	TGGCTATAAC	TTTAATCATT	ATCGACACTT	TAATCTATTA	TCCATTTGTT	1260
AAAGTTTATG	ACCATCAAAT	TTTAGAAGAA	GAACGGAAAG	GAAACTCTTC	ATCTGAATTG	1320
AAAGAAAAAG	TTGCTGCAAA	CTTCAACACT	GTAAAAGCGG	ATGCTATTCT	TGAAAAAGCG	1380
GGTGTTCGATG	CAGCACAAAA	TACCATCACT	GAAGAAACAA	ATGTCCTCGT	TCTCTGTGCT	1440
GGTGGAGGTA	CAAGTGGACT	CCTTGCAAAT	GCTTTGAATA	AGGCAGCAGC	AGAATACAAT	1500
GTCCCTGTGA	AAGCAACAGC	AGGCGGCTAT	GGTGCTCACC	GTGAAATGTT	GCCAGAGTTT	1560
GATTTGGTTA	TCCTTGCTCC	TCAAGTTGCT	TCAAACTTTG	AAGATATGAA	GGCAGAAACA	1620
GATAAGCTCG	GTATTAAACT	TGCTAAGACA	GAAGGCGCTC	AATACATCAA	ATTAACCTCGT	1680
GATGGAAAAG	GTGCCCTAGC	ATTCTGTACAA	GAGCAATTTC	ATTAA		1725

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGATATTTA	CTATGGCTCA	TGACCAAAGA	GGAGGATCTA	TGAAAGACTT	GTTTTTAAAG	60
AGAAAGCAGG	CCTTTCGTAG	GGAGTGTCTT	GGTTATCTGC	GCTATGTGCT	CAATGACCAC	120
TTTGTCTTGT	TCCTGCTTGT	CCTGTTGGGC	TTTCTAGCTA	CCAGTACAGT	CAACTCTTAC	180
AACATTTTCC	TGAAAATCAT	TGGCCTATCC	TTTTGTTTGT	AG		222

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TCGTCGTTTA	CAGGAGGAAA	TTTAACAGGG	CAATTGACTG	AAAAGATTCA	AGAACATGAA	60
TTAATTAAGA	CTAACCAAGC	AGAGAAAAGT	GTACAGGATG	TTTTGGATAA	TTGTATTGAA	120
AGGGTACAAA	ACAATTCACT	GAAATCAGAT	AGGGTTACTT	CTTTTGAGAC	CCCGTTTGCT	180
CTCTTATTTA	TCTTTGCGAC	TATAGCTGTG	ATGCTAACCT	ATGGGGGTTA	TCGGGTCAGC	240
GCAGGATATA	TATCTGTGGG	AACCTTGGTT	TCGTTTTTGA	TTTACCTCTT	TCAATTACTT	300
AATCCTATTA	GTAATATAGC	TAATTTTGTA	ACTGTTTATT	CTAGGAGCAA	GGGATCTTCA	360
GTTGCACTGG	ATAACTTGCT	TGCAGTTCCT	AAAGAAAAAT	TTGAGGGAGG	AAAATCGGTA	420
TCAGGACAAAG	GGTTGAATTT	TAACCATGTC	TATTTTGGTT	ATGATGAAAA	TCGACCTGTC	480
TTAAAGGATA	TTACTTGTTT	AATTTTCAAG	GGGCAAAAAT	TGCTTTTGTT	GGACCATCTG	540
GATCAGGAAA	ATCAACGATT	GTGCGTTTGT	TAG			573

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 792 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

AAAAGGTTTA	CAAGATGCTG	TAAAACATAC	TCATGGTCAA	CAATGATACA	TTTAACTATA	60
GAATATTGTG	ATAATATTAT	AGATCCATAT	ACAAATTTGG	GAGAGCAACA	AAGAATTGCA	120
AGTGAGCTGG	ATTTGTTAAG	CAAGCTGATT	TTAAGGAGAC	AAGAACAAC	TGAAGAGCTT	180
AATCTACTTG	TAAAATCCCG	ATTTAACGAG	ATGTTTGGGG	AAAATAAAAT	ATTTGAAAGC	240
ATTGATAACT	TATTTGATAT	TATAGATGGT	GATAGGGGCA	AAAATTATCC	TAAATCAGAT	300
GAGTTGTTTA	GTGAGGAGTA	CTGTTTATTT	TTAAATACAA	AGAATGTTAC	TAAAAACGGA	360
TTTTCATTCG	ATACAAAGCA	ATTTATCACT	AAAACAAAAG	ATAAATTACT	TCGAAAAGGC	420
AAACTTGAGC	GTTATGATAT	AGTCTTGACA	ACAAGAGGTA	CTGTTGGAAA	TGTAGCGTAC	480
TACGATGAAT	TAATAAAATA	TAAACATTTA	CGTATAAAAT	CAGGTATGGT	AATATTACGT	540
CCCAAGACAC	CAAATCTAAA	TCAGAAATTT	ATTATCCATG	TTTTAAGAAA	TAATAATTAT	600

AGTCGAGTGA	TATCAGGAAG	TGCTCAGCCT	CAGTTACCAA	TTACAAAATT	AAAAAAAATA	660
CTTCTCCCCC	TCCCCCACT	AGCCCTCCAA	AATGAGTTCG	CAGACTTTGT	AGTTCAGGTC	720
GACAAATCAC	AATTTGCTTG	TGAGATAGCT	ATAAAAGTGT	GGAGAAATAG	CTTGAAATTT	780
AGTATAATAT	AG					792

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATTACTCTTA	CTACAATCTA	TACTGTAGAT	GAACGTGATG	GAACAATTGA	AGAAACTACT	60
TCTCGTCAAA	TTACTAAAGA	GATGGTAAAA	AGACGTATAA	GGAGAGGGAC	GAGAGAACCT	120
GAAAAAGTTG	TTGTTCCCTGA	GCAATCATCT	ATTCCCTTCGT	ATCCTGTATC	TGTTACATCT	180
AACCAAGGAA	CAGATGTAGC	AGTAGAACCA	GCTAAAGCAG	TTGCTCCAAC	AACAGGCTGG	240
AAACAAGAAA	ATGGTATGTG	GTATTTTTAT	AATACTGATG	GTTCCATGGC	AACAGGTTGG	300
GTACAAGTTA	ATGGTTCATG	GTACTATCTC	AACAGCAACG	GTTCTATGAA	AGTCAATCAA	360
TGGTTCCAAG	TTGGTGGTAA	ATGGTATTAT	GTAAATGCAT	CGGGTGAGTT	AGCGGTCAAT	420
ACAAGTATAG	ATGGCTATAG	AGTTAATGAT	AATGGTGAAT	GGGTGCGTTA	A	471

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

ATTATGAAGT	TATTGTCTAT	CGCCATTCCC	AGCTATAATG	CAGCAGCCTA	TCTTCATTAC	60
TGTGTGGAGT	CGCTAGTGAT	TGGTGGTGAG	CAAGTTGGGA	TTTTGATTAT	CAATGACGGG	120
TCTCAGGATC	AGACTCAGGA	AATCGCTGAG	TGTTTAGCTA	GCAAGTATCC	TAATATCGTT	180
AGAGCCATCT	ATCAGGAAAA	TAAATGCCAT	GGCGGTGCGG	TCAATCGTGG	CTTGGCAGAG	240
GCTTCTGGGC	GCTATTTTAA	AGTAGTTGAC	AGTGATGACT	GGGTGGATCC	TCGTGCCTAC	300
TTGAAAATTC	TTGAAACCTT	GCAGGAACCT	GAGAGCAAAG	GTCAAGAGGT	GGATGTCTTT	360
GTGACCAATT	TTGTCTATGA	AAAGGAAGGG	CAGTCTCGTA	AGAAGAGTAT	GAGTTACGAT	420
TCAGTCTTGC	CTGTTTCGGCA	GATTTTTTGGC	TGGGACCAGG	TCGGAAAATTT	CTCCAAAGGC	480
CAGTATACCA	TGATGCACTC	GCTGATTTAT	CGGACAGATT	TGTTGCGTGC	TAGCCAGTTC	540
TAA						543

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1956 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

AAAACGCTTA	CAGGAGAAAAG	GGAGTATATG	GATAATAGAG	AAGCATTAATA	AACCTTTTATG	60
ACGGGTGAAA	ATTTTTATCT	CCAACATTAT	CTAGGAGCAC	ATAGGGAAGA	ACTAAATGGA	120
GAGTATGGCT	ATACCTTCCG	TGTTTGGGCA	CCTAATGCTC	AGGCTGTTCA	CTTGGTTGGT	180
GATTTTACCA	ATTGGATTGA	AAATCAGATT	CCAATGGTAA	GAAATGACTT	TGGGGTCTGG	240
GAAGTCTTTA	CCAATATGGC	TCAAGAAGGG	CATATTTACA	AATATCATGT	CACACGTCAA	300
AATGGTCATC	AACTGATGAA	GATTGACCCT	TTTGCTGTCA	GGTATGAGGC	TCGTCCAGGA	360
ACAGGGGCAA	TCGTAACAGA	GCTTCCTGAT	AAGAAAATGGA	GGGATGGACT	TTGGCTGGCA	420
CGAAGAAAAC	GTTGGGGCTT	TGCTGAACGT	CCTGTCAATA	TTTACGAGGT	TCATGCTGGC	480
TCTTGGAAGA	GAAATCCTGA	TGGCAGTCCT	TATAGTTTTG	CCCAATTGAA	AGATGAACTC	540
ATTCCCTTACC	TAGTTGAGAT	GAACATACT	CATATTGAGT	TTATGCCCTT	GATGTCCAC	600
CCACTAGGTT	TGAGTTGGGG	GTACCAGCTT	ATGGGTACT	TCGCTTTAGA	GCATGCCTAT	660
GGTAGACCAG	AGGAGTTTCA	AGATTTTGTC	GAGGAGTGTC	ATACCCATAA	TATTGGGGTT	720
ATTGTGGACT	GGGTACCAGG	TCACTTTACC	ATCAATGATG	ATGCCTTAGC	CTATTATGAT	780
GGGACACCGA	CTTTTGAATA	CCAAGACCAT	AATAAGGCTC	ATAACCATGG	TTGGGGTGCC	840
CTTAATTTTG	ACCTTGGAAG	AAATGAAGTC	CAGTCCCTTCT	TAATTTCTTG	CATTAAAGCAT	900
TGGATTGATA	TCTATCATTT	GGATGGTATT	CGTGTGGATG	CTGTTAGCAA	CATGCTCTAT	960
TTGGACTATG	ATGATGCTCC	ATGGACACCT	AATAAAGATG	GCGGAAATCT	CAACTATGAA	1020
GGTTATTATT	TCCTTCAACG	CTTGAATGAA	GTTATTAAAGT	TAGAATATCC	AGATGTGATG	1080
ATGATTGCAG	AAGAAAAGTTC	GTCTGCAACC	AAGATTACGG	GAATGAAAGA	GATTGGTGGT	1140

CTAGGATTTG	ACTACAAATG	GAACATGGGC	TGGATGAATG	ATATCCTCCG	TTTCTACGAA	1200
GAAGATCCGA	TTTATCGTAA	ATATGACTTT	AACCTGGTGA	CTTTCAGCTT	TATGTATGTT	1260
TTCAAGGAGA	ATTATCTCTT	GCCATTCTCG	CACGATGAAG	TGGTTCATGG	CAAGAAGAGT	1320
ATGATGCATA	AGATGTGGGG	AGATCGTTAC	AATCAATTCG	CAGGCTTGCG	CAATCTCTAT	1380
ACGTACCAAA	TTTGTCACCC	TGGTAAGAAA	TTGCTCTTCA	TGGGTAGCGA	ATACGGTCAA	1440
TTCTAGAAAT	GGAAATCTGA	AGAACAGTTG	GAATGGTCTA	ACCTAGAAGA	CCCAATGAAT	1500
GCTAAGATGA	AGTATTTTAC	TTCTCAGCTA	AACCAGTTTT	ACAAAGATCA	TCGCTGTCTG	1560
TGGGAAATCG	ATACCAGCTA	TGATGGTATT	GAAATCATTG	ATGCGGATAA	TCGAGACCAG	1620
AGTGTCTTTT	CCTTTATTCTG	TAAGGGTAAA	AAGGGAGAAA	TGTTAGTCTG	TATCTTTAAC	1680
ATGGTACCTG	TTGAGCGGAA	AGATTTTTACA	ATCGGACTAC	CCGTTGCAGG	AATTTACGAA	1740
GAAGTATGGA	ATACTGAGTT	GGAAGAGTGG	GGAGGCGTTT	GGAAAGAACA	TAATCAAACCT	1800
GTTCAAACGC	AAGAAGGACT	ATGGAAAGAT	TATGAGCAGA	CCTTAACCTT	TACCCTACCG	1860
GCTATGGGAG	CAAGTGTATG	GAAAATCAAA	CGTCGCTTGA	AATCTACTAA	AACCGTCACA	1920
AATAAAAACC	AAAAAGGAGT	AGAAAATGAA	AAATGA			1956

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

AGATCTATTA	CCAAGCGAAG	GAAAGATAAA	AAAGCCGAGG	GATTTCTCTG	ACTCTTTACA	60
TATTATTTGT	GGCTCTATAA	TATTGTAGTG	GGTAACCCCC	CTATGGATAT	TATGGAGCCT	120
ATTTTGTGTA	GAAAAAAGT	CCCATATGTA	CCTATAATGA	AAAGCGACAA	AACAACTCAT	180
TAG						183

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

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GTTTAATTAC TTGTATGCGC GCCATCATGG TGGAAACATTT CTCATCCGTA TCGAAGATAC      60
TGACCGTAAA CGCCATGTCG AGGATGGTGA ACGTTCCACA ACTTGAAAAC CTTGCGCTGGT      120
TAGGCATGGA TTGGGATGAA AGTCCAGAAT CACATGAGAA TTATCGCCAG TCTGAGCGTT      180
TGGACTTGTA TCAAAAATAC ATTGACCAAC TATTAGCTGA AGGAAAAGCC TATAAATCTT      240
ACGTTACAGA AGAAGAGTTG GCAGCTGAAC GCGAACGCCA AGAAGTAGCT GGCGAAACAC      300
CACGCTACAT CAATGAATAC CTTGGTATGA GTGAAGAAGA AAAAGCAGCT TACATTGCAG      360
AACGTGAAGC AGCAGGGATC ATCCCAACTG TTCGTTTGGC TGTCAATGAG TCAGGTATCT      420
ACAAGTGGCA TGATATGGTC AAAGGCGATA TCGAATTTGA AGGTGGCAAT ATCGGTGGTG      480
ACTGGATTAT CCAAAAAGAAA GACGGTTACC CAACTTACAA CTTTGCCGTT GCCATCGATG      540
ACCATGATAT GCAAATCTCT CATGTTATCC GTGGAGACGA CCATATTGCT AACACACCAA      600
AACAGCTCAT GGTTTATGAA GCACTTGGTT GGGGAAGCTCC AGAGTTTGGT CACATGACCT      660
TGATTATCAA CTCTGAGACT GGTAAGAAGT TATCTAAACG TGATACTAAT ACACTTCAAT      720
TTATCGAAGA TTACCGAAAAG AAAGGTTACC TTGCAGAAGC AGTCTTTAAC TTTATTGCTC      780
TTCTTG GTTGAACCCAGGT AGTGAAGATG AGATTTTCTC TCGTGAAGAA CTCATTAAAC      840
TTTTTGATGA AAACCGCCTC AGCAAGTCAC CAGCAGCCTT TGATCAGAAA AAACCTAGACT      900
GGATGAGCAA TGATTATATC AAGAATGCAG ACCTTGAAAC CATCTTGAA ATGGCAAAC      960
CATTCCTAGA GGAAGCAGGC CGTTTGACTG ACAAGGCTGA AAAATTAGTT GAGCTCTATA     1020
AACCACAAAT GAAATCAGTA GATGAGATTA TCCCATTGAC AGATCTTTTC TTCTCAGATT     1080
TCCAGAAATT GACAGAAGCA GAGCGCGAAG TCATGACGGG TGANACAGTT CCAACAGTTC     1140
TTGAAGCATT CAAAGCAAAA CTTGAAGCGA TGACAGATGA TAAATTTGTG ACAGAAAATA     1200
TCTTCCCACA AATTAAAGCA GTTCAAAAAG AAACAGGTAT TAAAGGGAAA AATCTTTTCA     1260
TGCCTATTCG TATCGCAGTT TCAGGCGAAA TGCATGGGCC AGAATTACCA GATACAATTT     1320
TCTTGCTTGG ACGTGAAAAA TCAATTCAGC ATATCGAAAA CATGCTAAAA GAAATCTCTA     1380
AATAA                                           1385
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(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAAATAATTA	CTATCCACGA	TAGCAATGAC	GTAAACAGGA	GCGATGTGTT	TGTAGATCTA	60
GTGAGTATCA	CCTTCTCGCT	GATGAATTTT	TTCAAGATTT	TGATTAACCT	GA CTGCACAG	120
GTAAGCCAC	AAGTGATTGA	TGAAAAAATT	CTGATGATGG	ACTTGAATCT	CAATAATTAC	180
TTGAGTACCG	TTATCCAAC	CCGCCAAGAC	GTCTATACTG	GTATAAAAAAT	CCTGCACCGA	240
G TAGGGCATG	GAAGGCAAGA	CATGAATGTT	ACTTCCCTCC	AAAATAGTCA	CATTTTTTGGC	300
TGGCAAGTCC	AGCATATCGC	GGATAAAATTG	ACAAGTGATT	TCTGGGTTGC	TGAAAAATTTT	360
CTTAGCAACC	AAGTCATTGG	TCGGGCTAAT	TCCCAGATGT	CTGAGAATCA	TCCTTTTTCCT	420
CCTTCTATAG	TGAATTGA					438

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAAAAGATTA	CCCAGACCAG	TCTTTGGAAA	GTATCTACCT	TAGTCTTGCT	GGTAGAAAAG	60
AGGAGGTTGC	GGATGCGTCT	CAAGGTCATT	AATAAAATTAG	TTGATATCAA	TATCCTTTTAT	120
TCATCTCAAG	AAGCTAATCT	GGCTAATCTA	CGAAAGAAGC	AGGCTAAGAA	TCCTGGGAAA	180
AAAGTAAATG	TTTCCGCTAG	AGTCCTAAGT	TCTTACATTT	TTTCCAGTCT	CTTGATGCTC	240
ATCTGTTTTA	GTAATATAGC	CTTTCGTTTT	CCTTTTGAGG	AAATGCCAAG	TTTTTTTAGT	300
ACGATGGTTG	CTATTTTACT	GGTGCTGGCC	TTTTCAACTT	CTTTCAC	ATTTTACAAT	360
GTCTTTTATG	AGAGTAAGGA	CCTGGCCTCC	TATAGGCCCT	ATGCCTTTAA	AGAATCAGAG	420
ATTATAATGG	CCAAAGGTC	GTCTGTCC	TTGCCAGCTC	TAACTGGAAT	TGTACCAATC	480
CTAGCTTATT	TTCTGGTCCT	CTACATTAGG	CTAGCACCTT	CTCTGTGGTT	GGGTTTGCCT	540
TTGATGCTAC	TGTCCTTGAC	CTTATTATTT	GTCTCTGTTA	CTTTAGTGAC	GGTAGTGGCA	600
GTACATTTCT	TGGCTCAGAC	TAGGGTCCTC	AGAAAGTATC	AGTCTATTTT	TTCGAATGTG	660
ATGATTGGGA	TAGGAGTTCT	CATACCTTTA	ATATTTATCT	TCTTTCTTCA	GTCGACTTTT	720
GGAAGTATTG	TTGACAAAAGT	TAGAGACATT	CCATTTCTCC	TTTATCCTCT	TCATATCTTT	780
TACAAAATAG	CAGTGAGGCC	TTTTTTCGACA	GAAGCCTTAG	TGGGTCTGCT	CGCTTGGATA	840
GGACTAACTC	TCTTCCTGCT	TTATCTGACC	AAAAAGAAGG	TCCTTCCTCG	TTTTTTATGAC	900
GTGATCCTGC	TTAACAGTGA	GGAGAAGGTC	AAAAAAGAAC	GTCGCAGCAA	GGAGAGGATT	960
TCAACTACTA	AAAAGGGCTT	TTTCCGTATG	GTTTTACGCT	ACCACCTCAC	CCTCTTGGGA	1020
CAGGGGACTG	GCGTGATTAC	AGTGCTTTTT	ACAAGTGCTT	TCCTTCCTTA	TCTCATGATG	1080
ATCAGTCTGA	TTTCCAAAAT	CCGAGATTCT	CAGATAGTTC	CAGACATTCA	TCCTCCATAC	1140
TGGTTACCCT	TGTTTTTTGT	AGGAGTGTTT	ATAGCAGTTG	TCAATAACAA	TATCACCAGC	1200
CTGCATTCAA	TTGCCTTGTC	CTTGGAGAGG	GAAAAATGTTG	ATTTTCTTAA	GAGTTTACCC	1260
TTTGACTTTG	CTCGTTATGT	GAAAGTGAAA	TTTTGGATTA	TCTTTGCTGT	TCAGTCCTTT	1320
TTACCAGTTC	TGACTTTGCT	TGGTCTTTCT	CTATATCTAG	GCTTGCCCAT	CATTTTCGATG	1380
ATTTACCTTC	TTGTAGTCTG	GATCATTGCC	AGTGTCATCC	TTTCTTGCCA	CCATTACTTT	1440

AAGGACGTTA	AAAATCTGTC	AACAAATTGG	AGTAGCATT	CGGACCTGGT	GAATCGTTCA	1500
AATGGCATAG	TCGCCATAGT	TTTATTGTTT	ATTTATAGTG	CAATCCTGAT	GGCCCTTGTA	1560
ATTGGGAGCA	TATTCTTGGT	TCAGTCTCTC	TCCACTATCC	TTGCCATCAG	CTTGGGAGTA	1620
GGAGCTCTTA	TCCTCCTGCT	TGCTCTTGCT	ATTTTGGCT	ATCATTATTA	CCTGTCACGC	1680
ATATTGGCAG	AAATAGAAAA	AAGATGA				1707

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACTTTCTA	CCAGGTTTTT	TAAAAGCATA	ATTGTTAGTT	GTAGTCATTT	ATTATTCTTC	60
AAAGAAAAAT	GGTGGGGCGA	ATTTTTTCAG	TTCTTCAAAG	CACTTTTGAG	CAGTATCTGC	120
ATCTTCACAG	ATGATAAGAC	AGACATCATT	ACCACAAAGG	GTAGCGATAG	CGTCAGGGAA	180
GCTCAAAGTA	TCAATGATAG	AACCAAAGGA	TTGAGCCAGT	CCAGGAAGGG	TTTTTAG	237

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

CGGTTTGAGT	TTGCTGGCTT	TACGTGGAGT	TTGTGCTTGA	GGATATATCT	TCATGGGCCC	60
TTGATAATCA	CTGTCAGTCA	AGATTTTACC	AGCTTGTCGG	ATATTTCTGC	GACTCATTTT	120
GAACAACTTC	ATATCATGAC	AATAGTTCAC	AGTGATATCC	AAAGAAACAA	TTCTCCCTTG	180
ACTTGTGACA	ATCGCTTGAG	CCTTCATAGC	GTGGCATTTC	TTTTTACCAG	AATAATTTCG	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

CGACTTGAGT	TTGCTGGATT	TACGTGGAGT	TTGTACTTGA	GGATATATCT	TCATGAGTCC	60
TTGATAACCA	CTGTCAGCCA	AGATTTTACC	AGCTTGTCGG	ATATTTCTGC	AACTCATTTT	120
GAACAACTTC	ATATCATGAC	AATAGTTCAC	AGTGATATCC	AAAGAAACAA	TTCTCCCTTG	180
ACTTGTGACA	ATCGCTTGAG	CCTTCATAGC	GTGGCATTTC	TTTTTACCAG	AATCATTCGC	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CGGCTTGAGT	TTGCTGGATT	TACGTGGAGT	TTGTGCTTGA	GGATATATCT	TCATGAGCCC	60
TTGATAACCA	CTGTCAGCCA	AGATTTTACC	AGCTTGTC	ATATTTCTGC	AACTCATTTT	120
GAACAACTTC	ATATCATGAC	AATAGTTCAC	AGTGATATCC	AAAGAAACAA	TTCTCCCTTG	180
ACTTGTGACA	ATCGCTTGAG	CCTTCATAGC	GTGAAATTC	TTTTTACCAG	AATGATTCGC	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

CGGCTTGAGT	TTGCTGGATT	TACGTGGAGT	TTGTGCTTGA	GGATATATCT	TCATGAGCCC	60
TTGATAACCA	CTGTCAGCCA	AGATTTTACC	AGCTTGTC	ATATTTCTGC	AACTCATTTT	120
GAACAACTTC	ATATCATGAC	AATAGTTCAC	AGTGATATCC	AAAGAAACAA	TTCTCCCTTG	180
ACTTGTGACA	ATCGCTTGAG	CCTTCATAGC	GTGGCATTTT	TTTACAAGAA	TAATTCGCTA	240
ATTCTTTTTT	AG					252

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

CGGCTTGAGT	TTGCTGGATT	TACGTGGAGT	TTGTGCTTGA	GGATATATCT	TCATGGGCCC	60
TTGATAACCA	CTGTGAGCCA	AGATTTTACC	AGCTTGTCCTG	ATATTTCTGC	GACTCATTTT	120
GAACAACTTC	ATATCATGAC	AATAGTTCAC	AGCGATATCC	AAAGAAACAA	TTCTCCCTTG	180
ACTTGTGACA	ATCGCTTGAG	CCTTCATAGC	GTGAAATTC	TTTTTACCAA	AATCATTCGC	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GTTGGTTCTA	CCTGCAAAAG	ATTACCAGGC	AAGCCGACAT	TCACTGATTT	AATCGAAATG	60
CCTGCCTTTT	CTTCCGCTTG	GGAAATGGCT	GACTTGATAG	CAGTTGCTGC	TGTATCAATA	120
TCAACAATAA	TTCCATCCTT	TACACCTTTA	CTTTTGGCAT	TACTCACGCC	AATTACATTT	180
AATTCACCAT	TTCTCTGCTC	GGCCACAAGC	ACCTTGACAG	AGCTTGTTCC	AATATCTAGA	240
CCTGTAAAAA	AGCCTTCTCT	AGCCATTACA	TCGCTTCCTC	TCTATCTTCC	AAGTTTCGCA	300
CTTCGTATTA	TTCCATAG					318

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TACACCTCTA	CTTCTAAAAC	ATTGTTAGAA	ATCGATTTGA	CTGTCCTGAT	TGATTGTGCC	60
TATTATTATT	TCATTTTACT	ATACTCTGTT	AATTTATATG	AGTTTAAACC	GATTTCATCT	120
TTAACCTCGA	GTAAAGCAGT	TTCAAATATT	TGTTTAAGAG	TTTTTGATTG	TTTACAATTA	180
ACCGACAAAC	TTTCTGATAA	AATATGTACA	ACTTCTGAGA	CTGAATAA		228

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TACACCTCTA	CTTCTAAAAC	ATTTTTAGAA	ATCGATTTGA	CTGTCCTGAT	CGATTGTGCC	60
TGTTCTTGTT	TCATTTTACT	ATATAGATCG	CATTCGAAAG	AATTCGTTCC	AAAATTGCTT	120
GGTTCGTTCT	TCTCTTGGAC	GAATAAGAA	TTGATGGGCA	TTATTTTTTT	CAACAATTTT	180
CCCACTGTCT	ATAAAAATAA	CATGATGGGC	TACATCTCTA	GCAAAACCTA	TCTCATAAAG	240
CTGATCAAAA	ACTCAATCTG	A				261

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

TACACATCTA	CTTCTAAAA	ATTGTTAGAA	ATCGATTTGA	CTATCCTGAT	CTATTTGTCC	60
TGTTCTTATT	TCATTTCACT	ATATCTCAAA	TTGAGTATGA	CGAAGTGCGC	TCCCATGTCC	120
TGGGAACGCA	CTTTCTTCAT	ATTTTTTCATA	TTCTTGAATC	CATCGATAAA	GACTATTGGG	180
ATGAATTTTT	AA					192

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

CCAACTGAGT	TTTCTATCAT	TCTACGAGGT	AACATGAAAT	CATTTTTTAAA	AACATATCGA	60
ACCTATTTTA	TTTCTTTCAT	CATTCCCTGTA	GTGATTATGT	CTGGAGTATA	TCTATCTCAA	120
GGTATCTACT	GGAATAGCGA	CAACTCTCCT	CTATTAGGAG	ATGGCTTTCA	TCAATACGTT	180
ATTTTTGATA	TAGCCTTACG	AAATATCCTA	CATGGAAATA	GTAGTCTGTT	TTACACCTTT	240
ACAAGTGGTC	TAGGGCTAAA	CTTCTATGCC	CTATCTAGTT	ATTACTTGGG	TAGTTTTCTC	300
GCGCCTCTGG	TTTACTTTTT	TGATCTAACG	AATATGCCAG	ATGCTATCTA	TCTGACAACT	360
CTCTTAAAA	TTGGATTGAT	TGGTCTGTCA	ACCTTTTTTA	GTTTGAATAA	ATTGTTTCAA	420
TCTATCCCTC	AGACTTTAAA	ACTAGCCTTA	TCTACTTCCT	ATGCTCTGAT	GAGTTTCACT	480
GTCAGTCAAT	TAGAGATAAA	AACCTGGCTA	GATGTTTTTA	TCTTGATTCC	TTTAATTATA	540
ACTGGTTTAC	ATCTACTGAT	AACTGAAAAG	AACTCCTAT	TGTACTTTAC	AAGTCTGTCA	600
ATCTTATTTA	TTCAAAATTA	TTATTTTGGA	TATATGACAG	TATTGTTTCT	TATTTTCTGG	660
TATCTCTGTC	AAATTTTCGTG	GGACTTTAAG	ACTCGAAAAT	CATCTGTTCT	TGATTTTCATA	720
GTTATCTCCT	TTTTAGCTGG	TATGGCTAGT	TTGATTATGA	CTCTTCCCAC	TCTATTTGAT	780
TTACAGACAC	ATGGGGAAAA	ATTGACTGAA	GTTACAAAGT	TTCAAACCTGA	AAGTAGCTGG	840
TATCTTGATC	TCTTTGCTAA	GCAATTCATT	GGTTCCTTTG	ACACAACAAA	GTATGGGGCC	900
ATCCCAATGA	TTTTTGTTGG	ACTACTTCCC	TTTATTTTGA	CCATTTTATT	TTTTACGCTG	960
AAATCTATTA	AGTTTCACGT	GAAACTCATA	TATGTAATAT	TCTTTGCATT	TCTAATTGCA	1020
AGCTTTTACA	TAGAAGCTCT	TGACTTATTT	TGGCAAGGCA	TGCATACTCC	AAACATGTTT	1080
TTACATCGCT	ATGCTTGGAT	TTTCTCTACC	TTGTAAATTT	ACACAGCAGC	AGAAGTCTTA	1140
AAGCGTCTGA	AAGAACTTAA	AGTCTGGAAT	TTTTTAGTTT	CGCTTTTTTCT	TGTAGTAGCA	1200
GGATTTTTAG	CTACCATCTA	TCTAAAATCG	CATTATTCCT	TTTTAACAGA	TTTGAATATT	1260
CTGCTTACTC	TTGAATTTTT	GGTTGTCTAT	TCTCTTTTAC	TCCTTGCACT	TATCAAAAAG	1320
TTTATATCTG	TGAATCTATT	TGCCATTCTA	ATCTCTTTAT	TTATACTGGT	TGAAATGAGT	1380
TTAAATGCTT	CATCTCAAA	GGACGGAATT	GCTAAGGAAT	GGGGATTGTC	TTCTCGAAGT	1440
GCTTATAGTC	GAGATATCCC	AGCTATGGAA	TCTTTCTCAA	CATATATTGG	AAATCAATTT	1500

ACTCGTACTG	AAAAACTACA	AACTCAGACA	GGAAATGACA	GTATGAAATT	CAACTACAAT	1560
GGAATCTCTC	AATTTTCATC	TGTTTCGAAAT	CGTTCATCAA	GCTCTACTTT	AGATAAACTT	1620
GGTTTTAAAT	CCTCTGGGAC	TAATCTCAAT	CTCCGATATG	CAAATAATAG	TATTTTGGCT	1680
GATAGTTTAT	TTGGTATCCA	GTACAATATC	TCAGACAGTC	CTATTGATAA	GTATGGCTTT	1740
AAAGATATCT	ATCAAAAAGA	TAATCTTACC	CTATATGAAA	ATCAATACTC	TCTTCCGATT	1800
GCAGTTGCTA	GTCAATCTGT	TTACAATGAT	GTCAAGTTCA	ATGAACATAC	CTTGGATAAT	1860
CAGGCCTCAT	TTTTAAATCA	ACTTGCTAAC	GTCAATTTTG	ATTATTTTTC	TCCAATACCT	1920
TATGAAAAAA	CAGAAAAAAT	AGAAAAATACT	AATGATTTGA	TTAGTGTCAC	AAGTTCTTCA	1980
AATGAAGATG	CAGCAATCCA	GTATCAAATT	GAAGTTCCAG	AAAACAGCCA	AGTTTATCTC	2040
TCTTTCATAA	ACCTTCACTT	TTCTAACGAT	AAACAAAAGA	AGGTTGACAT	CCTTGTAAT	2100
GGTGAAAAAA	AGACTTTTAC	AACTGATAAT	GTCTTCTCCT	TCTTTAATCT	AGGATATACT	2160
AAAGAGAAAA	AAACTTTCAA	TATCAATGTT	AGTTTCCCTG	GAAATTCACA	AGTATCATTT	2220
GAATCTCCTA	CCTTCTATCG	TTTAGATACC	AAAACTTTCA	CCGAGGCAAT	TCAAAAAATT	2280
AAAGAACAAC	CTGTCACAGT	ATCAACTTCT	AAAAACAAGG	TTTTTGCTAC	ATATGATGTC	2340
CAACAAGATA	CATCTATTTT	CTTCACCATT	CCTTATGACA	AAGGTTGGTC	TGCCTACCAA	2400
GATGGTAAGA	AAATAGAAAT	TAAACAAGCT	CAAACTGGAT	TTATGAAAGT	TGACATTCCC	2460
AAGGGGAAAAG	GAACATTATC	ACTTTTCCTT	ATTCCCTATG	GTTTTATTAC	TGGAGCAATC	2520
TGTTCCTTTA	CTTCTCTCTT	ACTATTTGGA	ATCTATAATC	ACAGACGAAA	GTCATCTAAG	2580
GCATAA						2586

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

AGGATTCCTA	CCTTATTTCA	CAACGATATT	AACGAGTTTA	GTTGGCTCAA	ACAGTTTGGG	60
AAACTGTTTG	AGGTTGGAAA	TCAGCAAATA	AATTGGTTAT	TTTACAACAA	TATTAACCAA	120
TTTATTTGGT	ACACTAATCA	CTTTCACGAT	TTCCCTTACCG	TCAATTTCTG	CTTTGACTTT	180
TTCATCCGCT	AG					192

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

ATGATCGAGT	TTGAAAAACC	AAATATAACA	AAAATTGATG	AAAATAAAGA	TTATGGCAAG	60
TTTGTAATCG	AACCAC TTGA	ACGTGGCTAC	GGTACAAC TC	TTGGTAACTC	TC TTCGTCGT	120
GTACTTCTAG	CTTCTCTACC	AGGAGCAGCT	GTGACATCTA	TCAACATTGA	TGGTGTGTTA	180
CATGAGTTTG	ACACAGTTCC	AGGTGTTTCGT	GAAGACGTGA	TGCAAATCAT	TCTGAACATT	240
AAAGGAATTG	CAGTGAATC	GTACGTTGAA	GACGAAAAAA	TCATCGAACT	GGATGTTGAA	300
GGTCCTGCTG	AAGTAACAGC	TGGTGACATT	TTGACAGATA	GCGATATTGA	AATTGTAAAT	360
CCAGATCATT	ATCTCTTTAC	AATTGGTGAA	GGTTC TTTCTC	TAAAAGCGAC	TATGACTGTT	420
AACAGTGGTC	GTGGATATGT	ACCTGCTGAT	GAAAATAAAA	AGGATAATGC	ACCAGTTGGA	480
ACACTTGCTG	TAGATTCTAT	TTATACACCA	GTTACAAAAG	TCAACTATCA	AGTGGAACCT	540
GCTCGTGTAG	GTAGCAATGA	TGGTTTCGAC	AAATTAACCC	TTGAAATCTT	GACAAATGGA	600
ACAATTATTC	CAGAAGATGC	TTTAGGGCTT	TCAGCACGTA	TTTTGACAGA	ACATCTTGAT	660
TTGTTTACAA	ATCTTACTGA	GATTGCTAAG	TCAACTGAAG	TGATGAAAGA	AGCTGATACT	720
GAATCTGACG	ACCGTATTTT	AGATCGTACG	ATTGAGGAAC	TGGACTTGTC	TGTGCGTTCA	780
TACAACTGTT	TAAAACGTGC	CGGTATCAAT	ACTGTGCATG	ATTTGACAGA	AAAATCTGAA	840
GCAGAGATGA	TGAAAGTACG	AAATCTTGGA	CGCAAGAGTT	TGGAAGAAGT	GAAACTCAAA	900
CTCATTGATT	TGGGTC TTGG	ATTAAAAAGAT	AAATAA			936

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

TGTGAAACTA	CAAGCGATTT	ACTTTATGGA	AGGAATAGAA	TGACAAAGGT	TGTTTTTGAA	60
GAAAAATACT	ATCCAGCTGT	AAAAGAAATG	GTTTATCGAA	CTCGTTTGGC	CAACGGATTG	120
ACAGTTGCTC	TTTTGCCTAA	AAAGGAATTT	AAAGAGGTTT	ACGGGAGTGT	CACTGTACAG	180

TTTGGTTCGG	TAGATACGTT	TGTCACAGAA	GTTGACGGAG	ATGTAAAAACA	ATATCCTGGA	240
GGAATTGCTC	ATTTTCTTGA	ACATAAATTA	TTTGAGAGAG	AAGATTCTAG	TGATTTGATG	300
TCGGCTTTTA	CGAGTCTAGG	TGCAGATAGT	AATGCCTTTA	CAAGCTTTAC	AAAAACAAAC	360
TATCTTTTTT	CAGCAACGGA	TTATTTTTTA	GAAAAATTTAG	ATTTACTTGA	TGAATTGGTA	420
ACATCAGCAC	ACTTTACTGA	AGCTTCCATT	CTGACAGAGC	AGGATATTAT	TCAGCAAGAA	480
CGAGAAATGT	ACCAAGATGA	TCCAGATTCT	TGTTTATTCT	TTTCAACTTT	AGCGAATTTG	540
TATCCTGGTA	CACCTTTAGC	AACTGATATA	GTTGGAAGTG	AGGAGTCCAT	TTCCCAAATC	600
AATCTAACTA	ATTTGCAAGA	AAATTTTACA	AAGTTTACAA	AACCTGTAAA	CATGTCTCTG	660
TTTTTAGTTG	GTAATTTTGA	TGTGGAGCGA	GTACAGGACT	ATTTTGAAAAG	CAAAGAAGCTG	720
AAAGATTTCAG	ATTTTCAGGA	AGTAGCAAGA	GAAAAAGTTGT	TTTTACAGCC	TGTAAAGCTA	780
ACAGATAGTA	TGAGAATGGA	AGTATCTTCT	CCCAAACTAG	CGATTGGAGT	TAGAGGTAAG	840
CGAGAAGTTT	CTGAAGCGGA	TTGCTATCGA	CATCATATTT	TATTAAAATT	ATTGTTTTGCA	900
ATGATGTTTG	GTTGGACTTC	GGATCGTTTT	CAAAAAATGTT	ATGAATCAGG	TAAAATTGAT	960
GCGTCCTTAT	CTCTGGAAGT	TGAAATAACA	AGTCGCTTTC	ATTTTGTCAT	GTTGACAATG	1020
GATACGAAAAG	AGCCAGTTGC	TTTGTCTCAT	CAATTTAGGA	AGGCTATTCT	TAATTTTACA	1080
AAGGATTTAG	ATATTACAGA	GGAACATTTA	GATATTATCA	AAAGAGAGAT	GTTTGGCGAA	1140
TTTTTCAGTA	GCATGAACTC	TCTTGAATTT	ATTGCAACGC	AATATGATGC	TTTTGAAAAAT	1200
GGTGAGACAA	TTTTTGATTT	GCCGAAAATT	TTACAGGAAA	TTACTTTAGA	GGATGTCCTT	1260
GATGCTGGAC	ATCATTTAAT	AGATGATGGT	GACATAGTTG	ATTTTACAAAT	ATTCCCATCG	1320
TAG						1323

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

AAACAGACTA	CGTACAGGCT	TGCACAGGTT	GGGGTGCAGC	CTTATCGACA	AGTACATGCT	60
CACTCAACAG	GTAACCGCAA	CTCAACCGTA	CAGAATGAAG	CGGATTATCA	CTGGCGGAAA	120
GACCCAGAAAT	TAGGTTTTTT	CTCGCACGTT	GTCGGAAACG	GTCGCATCAT	GCAGGTAGGA	180
CCTGTGAACA	ACGGAAGTTG	GGATGTTGGG	GGCGGTTGGA	ATGCTGAGAC	CTATGCAGCG	240
GTTGAACTGA	TTGAAAGCCA	TTCAACTAAG	GAAGAGTTTA	TGGCTGACTA	TCGCCTCTAT	300
ATCGAATTGC	TACGCAATCT	AGCGGACGAA	GCAGGCTTGC	CGAAGACTCT	TGATACAGAC	360
GACTTGGCAG	GTATCAAGAC	GCATGAATAC	TGTACCAATA	ACCAACCAAA	CAACCACTCA	420
GACCACGTTG	ACCCTTATCC	ATATCTTGCA	AGTTGGGGCA	TTAGCCGTGA	ACAGTTTAAG	480
CAAGACATCG	AAAACGGCTT	GAGCGCTGCA	ACAGGCTGGC	AGAAAAATGG	CACTGGCTAC	540
TGGTACGTAC	ACTCAGACGG	CTTTTATCCA	AAAGATAAGT	TTGAGAAAAAT	CAACGGTACC	600
TGGTATTATT	TCGATGGCTC	AGGCTATATG	CTTTCAGACC	GCTGGAAGAA	GCACACAGAC	660
GGTAATTGGT	ACTGGTTTCA	CAACTCAGGC	GAAATGGCCA	CAGGCTGGAA	GAAAAATCGCT	720
GAGAAGTGGT	ACTATTTTGA	TGTAGAAGGT	GCCATGAAGA	CAGGCTGGGT	CAAGTACAAG	780

GACACCTGGT	ACTACTTAGA	CGCTAAAGAA	GGCGCCATGG	TATCAAATGC	CTTTATCCAG	840
TCAGCGGACG	GAACAGGCTG	GTACTACCTC	AAACCAGACG	GTAGCATGGC	AGACAAGCCA	900
GAGTTCACAG	TAGAGCCAGA	TGGCTTGATT	ACAGTTAAAT	AA		942

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1254
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

AATAAGACTA	CTATGAAAAA	AATATTTTTTA	ACTTTGTAA	CTGTCTCTCT	TTTAGGGGGT	60
GCTTCTACTG	CTGTTGCTCA	AGATTTTACC	ATTGCCGCTA	AACATGCGAT	TGCTGTTGAG	120
GCAAATACTG	GTAAAAATCT	CTATGAGAAG	GATGCAACGC	AACCTGTCGA	AATTGCTTCC	180
ATAACAAAAT	TGATTACTGT	TTATCTGGTC	TATGAAGCTT	TGGAAAACGG	AAGTATTACC	240
CTCTCCACTC	CTGTAGATAT	TTCTGATTAT	CCTTATCAAT	TGACGACAAA	TTCTGAAGCC	300
AGTAATATTC	CTATGGAGGC	CCGTAATTAT	ACTGTGCAAG	AGTTGCTTGA	AGCAACTCTG	360
GTATCTAGTG	CCAACAGCGC	CGCTATTGCC	CTAGCTGAGA	AAATTGCTGG	CTCAGAAAAA	420
GATTTCTGTCG	ATATGATGCG	GGCAAACTC	TTGGAAATGGG	GAATTCAGGA	TGCCACTGTT	480
GTCAATACGA	CAGGTCCTTA	CAATGAAACT	CTAGGGGATA	ACATTTACCC	AGGTTCTAAA	540
AAAGATGAGG	AAAAATAAGCT	TAGTGCTTAT	GATGTCGCTA	TCGTTGCTCG	CAACCTCATC	600
AAAAAATACC	CACAAGTCTT	AGAAATCACC	AAAAAACCTT	CTTCTACTTT	TGCTGGGATG	660
ACAATCACTT	CAACCAACTA	CATGTTAGAA	GGTATGCCTG	CTTACCGTGG	TGGTTTTGAT	720
GGGCTAAAAA	CAGGAACAAC	AGATAAGGCT	GGAGAGTCTT	TTGTTGGTAC	TACTGTCGAA	780
AAAGGCATGA	GAGTCATCAC	AGTTGTTTTA	AATGCAGATC	ATCAAGACAA	TAATCCTTAC	840
GCTCGATTTA	CAGCTACATC	TTCCCTAATG	GATTATATTT	CTTCTACATT	TACACTTCGC	900
AAAATCGTTC	AACAAGGCGA	TGCCATATCAA	GATAGCAAAG	CCCCTGTACA	AGATGGAAAA	960
GAAGATACAG	TAACTGCAGT	GGCTCCAGAG	GATATCTATC	TAATCGAACA	GATTGGGAAT	1020
CAATCTTCCC	AATCTGTTCA	ATTCACACCT	GATTCCAAAG	CAATCCCAGC	ACCACTTGAA	1080
GCTGGAACAG	TGGTTGGCCA	TTTGACTTAT	AAAGACAAGG	ACTTGATTGG	TCAAGGTTAC	1140
ATCACCACAG	AGCGCCCTAG	TTTCGAAATG	GTAGCAGACA	AGAAAATTGA	AAAAGCCTTC	1200
TTCTTAAAAA	TTTGGTGGA	TCAGTTTGTG	CGCTTTGTTA	ACGAGAAATT	ATAA	1254

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

CTACATTATA CCAGATTTGG AGAAAATATG TTAGAAATTA AAAACCTGAC AGGTGGCTAT	60
GTTTCATGTTT CTGTTTTGAA AGATGTGTCC TTTACTGTTG AAAGTGGGCA GTTGGTCGGT	120
TTGATTGGTC TCAATGGTGC TGGGAAATCA ACGACGATCA ATGAGATTAT CGGTCTGTTG	180
GCACCTTATA GTGGCTCCAT CAATATCAAT GGCCTGACTC TGCAAGGAGA TGCGACTAGC	240
TACCGCAAGC AGATTGGCTA CATTCTGAG ACGCCTAGTC TGTATGAGGA ATTGACCCTC	300
AGAGAGCATA TCGAAACGGT TGCTATGGCT TACGGTATTG AGCAAAAAGT GGCTTTCGAA	360
CGAGTAGAGC CCTTGTTAAA AATGTTCCGT TTGGACAGAA ATTAG	405

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

AAAAACTATA CACCAGAGCA ACAAAAACTC CATGATCAAT TTGAAGCAGA AGCAACGGAA	60
GATGCTAAAA AACAAAGCGA TATTGTGTTG AATGTTGACC AGGATTTTCAT GAGCATATCT	120
AAGTCTAATA AAAGTGGTTC AGACTGGAAG AAACTTTCA CAGTGAGGAC AACCAATAGG	180
CTAGCAAATG ACTTGAATAA TGTCTTGAAA CAGGCTGATA AAGATACTCC TAATACCCCA	240
ACTTGGCTAA ACTCAGCTGC TTCTAAAGCT AAAGATGATG ACAGAGCATA TAAACTACTG	300
AAGACTCTTA TACCAGGAGA AAATTACCTA TCATGTTAA	339

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TCACTATATA	CGAGAATTC	GCTATTGTTA	TGGACCCATA	CAGGCGAATC	ATTTTTCTTA	60
ATAGCTGGTG	GATGTAATAC	TGAGTGGATG	AACGTCTTTT	TAGAAGAGCT	TTCACAAGCT	120
TATCCAGATG	ATTACCTTTT	ATTCGTTATG	GACAATGCTA	TATGGCATAA	ATCAAGTACC	180
TTAAAGATTC	CGACTAATAT	TGGCTTTGCA	TTTATTCCTC	CGTACACACC	AGAGATGAAC	240
CCCATTTGAAC	AAGTGTGGAA	AGAGATTCGT	AAACGTGGAT	TTAAAAATAA	AGCCTTTCAA	300
ACTTTGGAAG	ATGTCATGAA	TCAACTTTAA				330

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...348
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

CTTGGAGAGT	TGTCGATACC	GCTAAGGCAG	TCTTCAACGT	TGATAACTAC	AAAGAATATC	60
TTTCATTGCA	ATGTGATAGC	GCCCTCCGTA	ATATTGTCCG	CATCTATCCT	TACGATGTGT	120
CTCCTAATGT	GGATACTACG	GGTGAACGGC	AAGCAAATGA	AAGTAGTCTC	CGTGGCTCTA	180
GCGAAATTGT	TGCTAACCGT	ATTCGTGAAA	AAATCCAAAG	TCGTGTTGAA	GATGCTGGCT	240
TGGAAATCCT	TGAAGCACGT	ATCACTTACC	TACCTAATGC	TCCAAAAATT	GCTGCCGTTA	300
TGCTTCAACG	CCAACAAACA	TCTGCCATTA	TTGATGCACG	AAAAATAA		348

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TTTCAATATA	CCATAACTGT	TCCTAGTCAA	CCTGCAAGCC	CTGTCCCAGC	TCCAAGCTCA	60
GCTCCGACTC	AAGATCCTAG	AGTGGTAGCA	AGCGCTTCGG	CTAGCTCAAC	GAGCACACAA	120
GCTCAAGAGC	AAGTTGACAA	GTCTGAACTT	CGTGCCTTGA	GTCAAGAGTT	AGACCAACGC	180
TTGAAAGCTT	TGGCAACAAT	ATCTGATCCG	AAAATCGATG	CAACCAAGGC	TGTCCTCCTA	240
GATGCTCAAA	AAGCTCCGGA	AGATAGTGCC	TTGACAGAGT	AA		282

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GCAAGATATA	CAAGATTTTA	TTATAAAAGC	TTTTCTTTTA	GTGAACTGAT	AGGTATTTTC	60
TTAGCAAACG	ATAAAGTTTT	AGGGCCGATA	CAATCAATTG	CCTATTCATT	AAATAAGATA	120
AATACAACCA	AAGATTTAAG	GAAACCGTTT	TTAAAATACT	TAAGTGGAGA	GAAGAATTTT	180
ATAGACGCTG	AACATGATAA	TAACGGACTG	TATACTTCAT	CAATAGATGT	GATACACATG	240

AAAGATGTTG	TATATTCTAT	TACACCAGAA	AATAAAATTAA	GTATTGACTT	CTCATTTAAG	300
TCACCATTTA	GGGTATTATT	AACAGGAACT	TCGGTAGTGT	GGAAAACAAC	GATTTTAAAT	360
TTAATTAATG	GTTCTTTAAA	GCCACAAAAA	GGTTATGTAA	ATTTGTTATC	ACATGGGAAA	420
AAGAGTTCAG	ATTCAATACC	AACAGTTGAT	CAGACACCAT	ATATTTTTGA	CACTACTATT	480
CGTGAGAACG	TAACTTTATT	TCAAAATGAA	TATTTTTTCAG	ATGATCAGAT	AATTGAGGTG	540
TTAAAAAAGG	TAAATCTATA	TGAAGAATTA	GAAAAGATAG	ATATACTAAA	TTATCAATGT	600
GGTGAAAAATG	GTAGTAATTT	GTCTGGAGGT	CAAAAACAAA	AAATAGCTTT	AGCTAGAGCT	660
CTGATTAGAA	ATAATAAAGT	GTACTTATTT	GACGAAATAT	CAGCTAATTT	AGATAATGAT	720
AATTCAAATTT	CCATACATGA	TATTCTGTTC	AATTTAGGTA	TTTCATTTAT	TGAAGTTTCA	780
CATCATTATG	ACTTAAATGA	CAAGAGATAC	ACTGATATAT	AA		822

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

ACAAAGTATA	CTAGTAATCC	TTTCTGTGGA	GTTCTGGTTG	GTATTGGGAT	GA CTGCTCTA	60
ATTCA GTCTA	GTTCTGGTGT	AACAGTTATC	ACAGTCGGCC	TGGTCAGTGC	CGGTCTCTTA	120
ACCTTACGTC	AGGCTATCGG	GATTGT CATG	GGTGCTAATA	TTGGGACAAC	TGTCACATCC	180
TTTCTCATCG	GTTTTAAATT	AGGTA ACTAT	GCCCTACCTA	TGCTCTTTAT	CGGTGCCGTC	240
TGTCTCTTTT	TTACAAAAAA	TCGGACAGTC	AATAATATCG	GACGCATCCT	CTTTGGTGTG	300
GGTGGTATCT	TTTTTGCCCT	CAATCTCATG	AGCGGCGCAA	TGGCTCCACT	CAAGGATTTA	360
CAGGTCTTTA	AGGACTATAT	GATTGAGCTA	AGTAAAAATC	CTGTTTTTGGG	TGTCCTTTGTC	420
GGTACTGGCT	TGACCTTGCT	AATTCACGCT	TCTTCGGCTA	CCATTGGGAT	TTTACAAAAC	480
CTCTACGCCG	GCAATCTAAT	TGACCTACAG	GGAGCTTTGTC	CGGTTCTATT	TGGTGACAAT	540
ATCGGGACAA	CCATTACAGC	CATCATTGCC	TCTTTAGGGG	CTAATATTGC	AGCTAAACGG	600
GTAGCAGGAG	CTCATGTTGC	CTTCAACGTT	ATCGGAACAG	TCGTCTGCGT	TATTTTTCTA	660
GTTCCTTTTA	CTGTCCTGAT	TCATTGGTTT	GAAGCTACGC	TAAATCTAGC	ACCGGAAATG	720
ACCATCGCCT	TTGCTCACGG	AACCTTTAAT	ATTACCAACA	CCATTGTCCA	ATTTCCATTT	780
ATCGGAGCTC	TGGCTTACTT	TGTAACCAAG	ATTATTCCTG	GAGAGGACGA	GGTTGTCAAA	840
TACGAACCCT	TATATCTTGA	TGAACATTTT	ATCAAACAGG	CCCCATCTAT	CGCTCTAGGA	900
AATGCTAAGA	AAGAGCTCTT	GCACTTAGGA	AACTACGCTG	CTAAAGCCTT	TGACCTTTCC	960
TATAAGTACA	TCATTGACTT	GGATGAAAAA	GTTGCTGAAA	AAGGGCATAA	AACCGAAGAA	1020
GCAATTAACA	CCATCGATGA	GCAATTAACA	CGTTATCTCA	TTGCCCTTTC	AAGCGAAGCT	1080
CTCAGCCAAA	AAGAAAAGTGA	AGTGCTTACC	AATATCCTTG	ATTCCCTCCCG	TGATTTGGAA	1140
CGGATTGGAG	ACCACACGGA	GGCTCTACTC	AATCTGACTG	ACTATCTTCA	ACGGAAAAAT	1200
GTTGAATTTT	CTGATGCCGC	CTTGAAAAGAA	TTAGAGGAAG	TTTACCGCCA	AACTAGTGAC	1260
TTTATCAAAG	ATGCTCTGGA	TAGTGTGGAA	AACAATGATA	TTGAAAAAGC	ACGCAGTCTT	1320

GTAGAACGTC ATGAAGCAAT CAATAAGATA GAACGTGTTC TCAGAAAAAC CCACATCAAA	1380
CGCCTCAACA AAGGCGAATG TTCAACACAA GCTGGGGTCA ACTTTATCGA CATCATCTCA	1440
CACTACACTC GTGTATCAGA CCACGCTATG AACCTTGCTG AAAAGGTTTT TGCAGAACAA	1500
ATCTAA	1506

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

TTCTTTTCATA CCAACGTCTT TCTAACTGAT AATAGTCCTT TTTATTATAT CAAAAAAGC	60
CCCCTGAGTC ACTCTAAAAC GNGACTGGAA AGCATTTGGG AATTCTTTAG ACAGAGATTC	120
TCAGTTTTAG CGGCAAAATT GGGTCAGGAT AAAGAAAAAA GCCCTATTAA AGGCTTTTTTA	180
GGATGTTTAC ATCCACCCTG A	201

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1254
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ATCATGGAGT	TAGTGCAATG	AATTTCAACA	CATTTTATCC	AATCAAAAAA	GTTTAAAACA	60
AACAAAATTA	CCGTGCGTTT	TACCGCTCCA	TTATCCCTTG	ATACGATTGC	AGGTCACATG	120
TTGAGTGCAA	GTATGCTAGA	GACTGCTAAT	CAGATGTACC	CCACTTCTCA	AGATTTGAGG	180
AGACACTTGG	CCAGTCTATA	CGGTACAGAT	ATGTCAACCA	ATTGTTTCAG	AAGAGGGCAA	240
AGCCACATTA	TAGAATTGAC	ATTTACCTAT	GTTTCGTGATG	AGTTTTTAAG	TAGGAAAAAC	300
GTGCTAACCT	CTCAGATTTT	GGAACCTGTA	AAAGAAACTC	TTTTTTCACC	CGTAGTAGTT	360
GATAATGGGT	TTGATCCGGC	CTTATTTGAA	ATTGAGAAAA	AACAATTGCT	AGCAAGTTTA	420
GCAGCTGATA	TGGATGATTC	TTTTTATTTT	GCACATAAAG	AATTGGATAA	ATTGTTTTTT	480
CATGATGAAC	GTCTTCAATT	GGAATATAGT	GATTTACGAA	ATCGTATTTT	AGCTGAAACT	540
CCACAAAGTT	CTTACTCTTG	TTTCCAAGAA	TTTTTAGCCA	ATGATCGAAT	AGATTTCTTT	600
TTCTTAGGTG	ATTTTAATGA	GGTTGAAATT	CAAAATGTAT	TAGAATCATT	TGGCTTTAAA	660
GGTCGAAAAG	GAGATGTGAA	GGTTCAGTAT	TGTCAACCTT	ATTCTAATAT	CCTTCAGGAA	720
GGTATGGTTC	GGAAAAATGT	GGGACAATCC	ATTTTGAAT	TAGGTTATCA	TTACCGTTCT	780
AAATATGGTG	ATGAACAACA	TTTACCCATG	ATTGTAATGA	ATGGTTTACT	TGGTGGATTT	840
GCTCACTCTA	AGCTCTTTAC	AAATGTCCGT	GAAAATGCTG	GATTAGCTTA	TACCATTTCA	900
AGTGAGCTTG	ATTTATTTAG	TGGATTCTTG	AGGATGTATG	CTGGTATCAA	TCGAGAAAAT	960
CGTAACCAGG	CTCGTAAAAAT	GATGAATAAT	CAACTGCTTG	ATTTAAAAAA	AGGTTATTTT	1020
ACAGAGTTTG	AGTTAAATCA	GACCAAGGAA	ATGATTCTGTT	GGTCGTTGTT	ACTTTCTCAA	1080
GATAATCAAT	CTTCATTGAT	TGAACGTGCT	TATCAAAATG	CCTTATTTGG	AAAATCTTCA	1140
GCAGACTTTA	AAAGTTGGAT	TGCAAAGCTT	GAACAAATTG	ACAAAGATGC	TATTTGTAGA	1200
GTAGCTAATA	ATGTGAAACT	ACAAGCGATT	TACTTTATGG	AAGGAATAGA	ATGA	1254

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

CAATCGGAGT	TCCAAGTCAA	CGGAAGTAGA	TGGTTTTTAG	AAATGAGAAA	TATCGGACAA	60
GCTGGTAAAA	TCTTGGCTGA	CAGTGGTTAT	CAAGGGCTCA	TGAAGATATA	TCCTCAAGCA	120
CAAACTCCGA	GGAAATCAAG	TAAACTTAAG	CCATTAACTC	TTGAAGATAA	AGCCTGTAAT	180
CATGCGCTAT	CTAAGGAGAG	AAGCAAGGTT	GAGAATATCT	TTGCCAAAGT	AAAAACGTTT	240
AAAATGTTTT	CAACAACCTA	TCGAAATCAT	CGTAAACGCT	TCGGATTACG	AATGAATTTG	300
ATTGCTGGTA	TTATCAATCA	TGAAGTAGGA	TTCTAG			336

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TTTCAACATA CTATAAAATC AGGCAATACA ACGGCTAAAA AGTTTGAGTT TATCGAAATA	60
CCAGTGCAAA AACTGAAAAA AGCGATTTAT AAAGCTCATC TCAAAGATTC AGATGACTTT	120
AGACCAGAAA CATCCACACC AAATCTTTTT GAAAGCTGTT TGAAGCTTTG TCCTTGCTTT	180
CTTAGTTCAT AG	192

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CATTGGCATA CATGTTTGTT AGAAGACGGA TTACAAACGG AGGTATTTGT AATGTTAGAA	60
TCTAAAAAAA CAACTCGATA TGTATTTTAT GTCTATCTGA TGTTATTAAC TTGGGGAATC	120
TTATTTAAGT TTGAAACAAA TCCTGAATTT ATAGCATTTT TCTTAGCTCC AAGGTATATC	180
AATTGGATTC CATTTTCAGA ACCACTAATA GTCGATGGAA AAATTGTTTT TGCTGAAATG	240
TTATTTAATC TGATTTTCTT TATTCCATTA GGTGTTTGTT TCCCTTTGAT AAAAATAAT	300
TTATCTAGTT TAAGAATAGT CGGGACAGGT TTCTTGATTA GTTTATTGTT TGAGTGCTTA	360
CAGTATATTT TAGCAATAGG TATAACAGAT ATAACGGATT TGACTTTAAA TACGCTAGGT	420
GTCTGTGTAG GCTTACTGAT TTATCAAATT TTTATAAGAG TGTTCAAATC ACAGACTAGA	480
AAATGGATCA ATATCTTAGG TATGCTTAGC CTGTTGTTTT CTTATCTTGT TTTACTGTTA	540
CTGCATTTAA TTGGTGTTTA A	561

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 624 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: *misc_feature*
 - (B) LOCATION 1...624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TTAAAGGAGT	TTCATATGTC	AAACGAAAAA	AACACAAACA	CTAACGTAGA	AAAGAAAGAT	60
GCTACTGTTG	TAGCTCACGA	AATCAAAGGG	GAAGTTACTT	ACGAAGATAA	AGTTATCCAA	120
AAAATCATTG	GTCTTTCACT	AGAAAACGTT	TCAGGTCTTT	TGGGAATCGA	TGGTGGTTTC	180
TTCTCAAATC	TTAAAGAAAA	AATCGTTAAC	AGCGATGACG	TAACAAGTGG	TGTTAACGTA	240
GAAGTTGGTA	AAACACAAAGT	TGCAGTTGAC	TTAAACGTTA	TTGTTGAGTA	CCAAAAAAT	300
GTTCCAGCTT	TATATTCAGA	AATCAGAGAA	ATCGTATCTT	CAGAAGTTGC	TAAAATGACT	360
GACTTGGAAT	TTGTTGAAAT	CAACGTAAAC	GTTGTGACAC	TCAAACTAA	AGAACAGCAT	420
GAAGCAGACT	CAGTAAGCCT	TCAAGATCGC	GTATCTGACG	TTGCTGAATC	AACAGGAGAA	480
TTCATTTCAG	AACAATTCGA	AAAAGCTAAA	TCTGGTCTTG	GATCTGGTTT	CTCAACTGTT	540
CAAGAAAAAG	TTAGCGAAGG	TGTAGAAGCT	GTAAAGGTG	CAGCAAATGG	TGTAGTATCT	600
CACGAAAACA	CTCGTGTAAT	CTAA				624

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: *misc_feature*
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

ATAAAGGAGT	TAATCATGAA	GGTAGTAAAC	TTGTATGATT	TGAAACAAAT	GGGAAATAAA	60
GGTGGTTGTA	CCATCCAATT	GATTCATCAC	TTTCCTTTTG	GTATGGGCTT	AGGACATCTC	120
AAAAAAGACT	ACATTGAATT	TAAACGTGTT	GGTATCTTTG	ATGGGAAAGC	AGTAGAAGTT	180
ACTCTTCGAG	AACCTTATTC	GAGAGATCTA	CTGCAGGTTG	TCAAGTCAAT	AAAGTAA	237

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TATAATAATA	CCACCTTTTT	TTACGTTTTT	TATAAATGTA	GAAAATATTC	ACATTTACCT	60
AGGAGGAACA	ATATGAGATG	GGATTATGGA	CAGATTTTTA	AAGAAATTCG	AAAGTCAAAA	120
GGATTGACCC	AACAAGATGT	ATGTGGACAA	GTCATACATC	GGACAACTCT	AACAAATATT	180
GAACACGGTA	AAGTTATTCC	CAGTTTTGAA	AACATGGTAT	TTCTTCTTGA	ACAAATTGAT	240
ATGAGCTTGG	CAGAATTCAA	GTATATATGC	AACGAATACC	ATCCTAGTAA	AAGGCGAGAT	300
ATTATTGTAG	AGAGCCAAAA	TCCGTCTACT	TTTCAAGATA	CTAGAAAAAT	GGTTGAACTC	360
ACTGAGAAAT	GTCAAAAATA	TCTTAAGACA	CATCACGATG	TTCTTATTCA	AAATATCTAT	420
CGTCATACAA	AAATTGTCAC	AGAGTTACGA	ACTAAAAGGAT	TCAAAAACAA	CCACGTCTTG	480
AAAGATTTGT	CTGAAGAAAT	TTGGGACTAT	CTTGAACCTA	TGGATACATG	GTACATTAGT	540
GATTTGAAAT	TGCTTGGAAC	CATTCTCTTT	TTCTTTCCCT	CTGAAAATCT	TCCCCTTCTT	600
ATTGATAGAA	TTATGAAAAC	CATCGAGAAA	TATAAATACT	TCCGAGAAAC	AAAAGTATTT	660
TTATCATCTT	TTTAGCCAA	TCTCTCCACT	GTATATTTC	ACATCATTTA	TTCAAAGAAT	720
GTGAAACAAT	CACCCTACAA	CTTTTGGTAT	TAG			753

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

CCGAATAATA CTGGTTCATT GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG	60
TTTTTAGAGA CAGCATTGCG ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT	120
CCACTACCAC CCATTAAAGC GAATGTTTGT ATTTGTGATA GGTTGATGAT GTGTGGAATG	180
GCTTGTCAT TATTTGCTGC AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTTCT	240
AGGATGGCAC TGTA	255

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

TACTCAAATA CCAAGACTGG AAAAGCCAAA TCCGCAAAGT TTCGTCCTAG TTTTTTTAAT	60
CTAAAAAGTT TGGTTAGGAT AATGCAGACG ACTAAGGTCA GTATCAATAA TAAAATAGAT	120
GCTAATTTCA TTAAATCAT ACCCATATTG TATCATAAAA AAAGGCTAAT GGAAACGAGA	180
AACAGAGGAA TTTATAGGAA AGTCAGGCTT TTGAGATTGT GGGTGATTTT TGTTATAATG	240
AAAGTTATAA AATCTTATAA TACCTTGAAT GATTATTATC GAAAACCTTT TGGAGAAAAG	300
ACTTTTAAAG TCCCTATTGA TGCGGGATTT GACTGTCCCA ATCGTGATGG AACTGTGGCT	360
CATGGAGGCT GTACTTTTTG TACGGTTTCC GGTTCCTGGAG ATGCCATTGT GGCACCAGAT	420
GCGCCTATCC GTGAGTAA	438

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

TATCCAAATA	CTCCAGTGAG	GCATAAACCG	CCATGGACAA	GGTATCCTCC	TCATAAAGGC	60
GCCAAGGACT	CTCTGCAGGA	ACTACCTTAC	AGGTCACCTC	CACCTCCAAA	AGAGGCAGGG	120
AAATGGCAGG	ATAACCGTAA	ACGACCGCAT	GTTCCCCTAT	TAAAATTATC	TTACTATGTG	180
CCTGACCGAC	ACCAACTTTT	TTTGTCAATTT	TTTCCTTTTA	CTAGACGAAA	AAACGTCTTA	240
TTTTTCATAC	AAGTATTAAT	TCTTTCCTAT	CTATTTTATT	ATATTTTCAC	AAAAAAAGCG	300
ATTGTTTCCA	TTCACAATCG	CTTCTTTCAT	TACCGAACCC	ATTCACCATT	ATAG	354

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

ACGGAAAATA	CTATGTTTAC	CTTAAAGATG	CGGCCCATGC	GGACAATATT	CGGACAAAAG	60
AAGAGATTAA	ACGTCAGAAG	CAGGAACACA	GTCATAATCA	TAACTCAAGA	GCAGATAATG	120
CTGTTGCTGC	AGCCAGAGCC	CAAGGACGTT	ATACAACGGA	TGATGGGTAT	ATCTTCAATG	180
CATCTGATAT	CATTGAGGAC	ACGGGTGATG	CTTATATCGT	TCCTCACGGC	GACCATTACC	240
ATTACATTCC	TAAGAATGAG	TTATCAGCTA	GCGAGTTAG			279

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GTTATGAATA	CAGTGAAAAA	TAAGCAAGAA	ATCTTAGAGG	CTTTTAGAGA	AAATCCAGAT	60
ATGATGGCCA	TTCTGACGAT	CATCCGAGAC	CTTGGTCTGA	AAGACTCGTG	GTTGGCAGCA	120
GGTTCGTCA	GAAATTTTCAT	TTGGAATCTT	TTGTCAGACA	AATCCCCCTT	TGATCATGAA	180
ACAGATATAG	ATGTGATTTT	CTTTGATCCA	GATTTTCTT	ATGAGGAAAC	CTTATTACTG	240
AAGAAAAAGC	TGAGAGAGGA	TTTTCCTCAG	TACCAGTGGG	AATTGAAAAA	TCAGGTCTAT	300
ATGCATCAGC	ACAGTCCTCA	CACTGCTTCC	TATACCAGTT	CTCGTGATGC	TATGAGTAAG	360
TATCCAGAAC	GGTGACGGC	AGTTGGACTG	CGCTTGAATG	AAGAATCAGA	TTTTGAACTC	420
TATGTACCTT	ATGGTTTGGA	GGATATTTTG	AATTTTCAAG	TTCGTCCAAC	TCCTCATTTT	480
TTAGAAAATG	AAGACCGAAT	GGAACTCTAT	CAAACACGTT	TATCCAAGAA	AAATTGGCAG	540
GAGAAATGGA	AAAATTTGAT	TTTTAAAAAT	ACTTAA			576

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

ACTATGAATA	CAAATCTCAA	GCCCAAACCTT	CAGCGTTTTG	CTTCTGCGAC	TGCCTTTGCC	60
TGTCCTATCT	GTCAAGAAAA	TCTGACTCTG	TTAGAGACTA	ATTTCAGTG	CTGCAACCGT	120
CATTCTTTTG	ACTTGCGCAA	ATTTGGCTAT	GTCAATCTAG	CACCTCAAAT	CAAGCAATCT	180
GCTAACTATG	ACAAGGAAAA	TTTTCAAAAC	CGTCAACAAA	TCCGTAGAAG	CCGGCTTTTA	240
CCAAGCTATC	TTAGATGCTG	TATCTGA				267

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

AGTGGTGATA	CTATGAAGAT	TAGTAAGAGG	CACTTATTAA	ATTATTCCAT	CTTGATTCCC	60
TACTTACTTT	TATCTATTTT	GGGCTTGATT	GTGGTCTATT	CGACCACCAG	TGCTATTTTA	120
ATTGAAGAAG	GCAAGAGCGC	CTTGACGTTG	GTTGCGAAAC	AAGGAATCTT	TTGGATTGTT	180
AGTTTGATAC	TGATTGCCTT	AATTTATAAA	TTGAGACTAG	ATTTTTTGAG	AAATGAGCGA	240
CTAATCATTT	TAGTTATATT	AATAGAAATG	CTTTTATTGT	TCTTGGCTCG	TTTTATTGGT	300
ATTTTCAGTAA	ACGGGGCATA	CGGTTGGATT	TCGGTTGCAG	GAGTAACTAT	TCAGCCAGCT	360
GAGTACTTAA	AAATCATTAT	TATTTGGTAT	TTAGCTCACC	GATTCTCCAA	ACAGCAAGAA	420
GAAATAGCTA	CTTATGATTT	TCAAGTTTGT	ACTCAAAATC	AATGGCTTCC	CCGTGCTTTT	480
AATGATTGGC	GATTCGTTCT	CCTAGTTCTG	ATTGGAAGTT	TGGGAATTTT	CCCTGATTTA	540
GGAAATGCGA	CTATTTTAGT	CTTGGTTTCC	TTGATTATGT	ATACAGTTAG	TGGAATCGCT	600
TATCGCTGGT	TTTCAACCAT	TCTGGCGCTC	GTATCTGCCA	CTTCTGTCTT	TGTCTTGACC	660
ACTATCAGCC	TAATCGGTGT	TGAGACCTTT	TCAAAAATTC	CAGTATTTGG	CTATGTAGCC	720
AAGCGCTTTA	GTGCCTTTTT	TAATCCTTTT	GCCGATCGTG	CTGATGCAGG	TCACCAGTTA	780
GCTAATTCCT	ATTTTGCCAT	GGTCAATGGT	GGTTGGTTTG	GTCTAGGTCT	TGGAAACTCG	840
ATTGAAAAAC	GAGGTTATTT	GCCAGAAAGT	CATACAGACT	TTGTCTTTTC	TATCGTGATT	900
GAAGAATTTG	GCTTTGTTGG	TGCCAGTCTT	ATTTTAGCTC	TCTTGTTTTT	CATGATTTTG	960
CGGATTATCT	TGGTCGGTAT	CCGAGCGGAG	AATCCTTTCA	ATGCCATGGT	TGCACTCGGT	1020
GTCGGAGGGA	TGATGTTGGT	TCAGGTATTT	GTCAATATCG	GAGGGATTTC	GGGCTTGATT	1080
CCATCTACAG	GAGTGACTTT	CCCTTTCTTA	TCCCAGGGTG	GAAATAGTCT	TCTAGTCTTA	1140
TCAGTGGCAG	TAGCCTTTGT	CTTAAATATT	GATGCCAGTG	AAAAACGCGC	TAAGTTGTAC	1200
CGAGAATTGG	AAAATCAACC	AATGAACCTT	CTGTTGAAGT	AG		1242

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

TTGATAGATA	CGAAAAACAA	CTTAGTTATG	CAGAGCCAAT	TTTATGATGG	AGAATTAAGG	60
GAATTAACAG	AACAAATTCT	TAATTCGGTT	ACAGGAGATG	AGAAAAAGAT	TATAGAATTT	120
TTTAGAGATT	CAATCTTTAA	CTTCAATTTT	TTATATAGAA	AATTAGAAAC	TATTAATGAA	180
TTATTTGATG	AAATTCGTGA	AGAGCATGAA	AGCTATAGAA	GAGGAGGATG	GTCTGCTAAT	240
AATCATCTAT	TTAATGCGGA	GTTTACAGTA	AAAAATCTTT	ATAACTTTTT	AAAATTAAAT	300
TGTTTTATGT	TTGAACATTA	TAAGATTTAT	AAATCAATCA	TTAATAGATA	TTTAGAAATA	360
TTATTACTCA	GTTATGATAA	TTCATATGTA	AACCCTGACT	CAAGTATTTT	CGATAGAACA	420
TCTTCTTGGC	TTAAAAATCT	TGATTTGGAT	GATGTTAAAT	TAATTC'TTCC	GAATATAGAT	480
TTTAAGGTTG	TAAATTTATA	TTTTAGAAAC	TATTCATTTG	GTAAAATAAA	AATTACTGAG	540
GAAGCGAAA	ACTACTTGTT	GAATCGAATT	ACTTATCTTC	AAGAAAGACT	TGAAATTACT	600
GAAGATGAAA	ATCTTCGAGA	GCTTAAAAAT	ATGCTAATTT	TTCTTCCCCT	TGTTGATGAT	660
ATTGACATAG	AAAAAGTAAT	AGAAATTTTA	AATAATCAAA	CAC'TGTATTA	TAATTGGAGC	720
GAGGAATTTA	GGAGAA'TTAT	TAAAATTGTC	CTCGATAATA	TGGATGTTAT	TGATAAAGAT	780
TCATTGAAAT	CTAAGATAAT	TGGGATTGTA	AATAAACATT	TAAATGAAAT	TTTGGAGAAA	840
AATTTTCTT	TATATAATTC	AGTGTATCCG	CTCTATTAC	AGTTACTAGA	ATACTGCTCA	900
ACTGATCAGG	AAACTGCAAT	AATAGTACTC	GAAAAATTTA	ATACAGATAT	TTTAAGAATA	960
AAATATAAAA	ATGATGATAT	AAAAAATATC	ATAGAATATT	CTGACTTGAT	ATGTCACTTA	1020
TTTAAGTATT	TTGAAAAGGA	TATTAAGAT	GACATTTTAG	ATACTCTAAA	AGTTTATGAA	1080
GAATCAGAAA	ATATTATTTA	CCATAAAGTA	ATTGATTTGA	TGAGTTATAA	TGTC'TATGAT	1140
TTTCCTCAGA	TACAAAATAA	AATCTACCAT	TATTTGATTA	AAAGAATTAA	TGATAAAAGA	1200
GTTGAGGGGG	TTAAAACTTT	CCCAGACCCA	AGAGAAAAGT	CTGTATCAGA	TTTATACAAC	1260
TTAAGTAGAA	AAGGATATTT	TTCTGATTTT	GAGATTTTAA	AAGATATTGA	AGAAGATATT	1320
CGAGGACTTT	ATCCTGAAGT	AGATTGGACC	TGGTTCCATG	ATAGAAGTGA	TGATGTTATC	1380
CATCGTCTAC	TAGAACATAG	AACTCCCAAT	AATATTAAAA	CTTATTTTTC	AAAAAATGAA	1440
GAAGATAATA	AATTGATTAA	TGAGTATATT	TTAAAAGCTT	TCGATGAGGA	TAAATTAATA	1500
CTTAAGAAAT	AA					1512

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ACTGGAGATA CAGCCTTGCA CTCACAAAGA CAGCAGATCT TTCTTTTGCA AAAACAAAT	60
GACCTGTTTG ATGAATTAGC CATTCAAGCT GAATCTAGAC ATAGCTTTT AAAAAGGAA	120
AATCCTACTT ACTTAGAATC CAAGGATAGA TATCTATTGT TCACTCATT CCCGAACAGT	180
TTTTTCTATA TTTTTTGCAT ACGATATTGC CGAAATGATT GA	222

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

GAATTGGATA CTAAGATAGG TATAAGTAAA AACACCATTA GAAATTATGA AAAAAGGGTT	60
AGGTCTACTA AGAAAAATAC TATATTTGAC TTAGTTAAAG TATTCAGTAG CTTGATTGAT	120
GCCCTCTTTT CTCCAGTTCA AAAGGATTCT CCTAGCGATA TCCAATCTAT CTACGACCAA	180
CGGGCACCAC CCAGACAAGG TAAAGTTCTG ACCTATGCCG AGAGGCAACT GTATGATCAG	240
AAAAACGAAG TATCGTAA	258

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

CAGATGGATA	CGATTGAAAA	TCTCATTATT	GCGATTGTGA	AACCCTTAAT	TTCACAACCA	60
GATGCCTTAA	CTATCAAGAT	TGAGGATACA	CCAGAATTTT	TGGAATATCA	TTTGAATCTT	120
GATCAAAGCG	ATGTGGGTCG	TGTAATCGGT	CGTAAGGGTC	GCACTATTTT	TGCGATAAGA	180
ACGATTGTCT	ACTCTGTCCC	AACTGAATAC	AAAAAAGTAA	GAATCGTTAT	TGACGAAAAA	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

AGGATTGGTA	CGTATCAAAT	GATCGATATT	CAAGGAATCA	AAGAAGCCCT	TCCCCACCGT	60
TATCCTATGC	TTCTAGTGGA	CCGTGTCTTG	GAGGTGAGCG	AGGATACCAT	TGTTGCTATC	120
AAAAATGTGA	CCATCAACGA	GCCTTTCTTT	AACGGCCACT	TTCCTCAATA	CCCAGTTATG	180
CCAGGTGTTT	TGATTATGGA	AGCCTTGGCG	CAAAGTGGCG	GTGTGTTGGA	GTTATCAAAA	240
CCTGAAAAATA	AAGGAAAACT	GGTCTTTTAC	GCTGGTATGG	ATAAGGTTAA	GTTCAAGAAG	300
CAAGTTGTAC	CAGGCGACCA	ATTGGTTATG	ACAGCGACTT	TTGTAAAACG	TCGTGGCACC	360
ATAGCTGTGG	TTGAAGCAAA	GGCTGAAGTG	GATGGCAAGC	TTGCAGCCAG	TGGTACCCTT	420
ACTTTTGCAA	TTGGGAACTA	A				441

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

AAAGAAGGTA	CTCATATGAT	TAAATATAGT	ATCCGTGGTG	AAAACCTAGA	AGTAACAGAA	60
GCAATTCGTG	ATTATGTAGT	TTCTAAACTC	GAAAAGATCG	AAAAGTACTT	CCAACCAGAA	120
CAAGAGTTGG	ATGCCCCGAAT	TAACTTAAAA	GTTTATCGTG	AAAAAACGGC	TAAAGTGGAA	180
GTAACGATTC	CGCTTGGATC	TATTACTCTC	CGCGCAGAAG	ATGTATCTCA	AGATATGTAT	240
GGTTCAATTG	ACCTTGTAAC	TGATAAAATT	GAACGTCAGA	TTCGTAAAAA	TAAAACAAAA	300
ATCGAGCGTA	AAAAATAAAA	TAAGGTAGCA	ACTGGTCAAT	TATTTACAGA	TGCTTTGGTG	360
GAAGATTCAA	ATGTTGTCCA	GTCTAAAGTT	GTTTCGTTCAA	AACAAATTGA	TTTAAACCA	420
ATGGATTTGG	AAGAAGCAAT	TCTACAAATG	GATTTATTGG	GGCATGATTT	CTTTATCTAT	480
GTAGATGTTG	AAGATCAGAC	AACCAATGTG	ATTTATCGTC	GTGAGGATGG	TGAAATTGGT	540
TTGTTAGAGG	TTAAAGAATC	TTAA				564

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 837 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TGGCTATTCA	CTTTACCGAG	CAGTTCAGGC	TGCCAAAGAA	AAAGGGGAAG	GAAAGATTTT	60
TCTTGGAAG	ATAAATTTGA	ATTTGCTAAA	GAGCTTGTTA	AGAAAGCAGG	TCAGTACATT	120
CTTGACCATA	TGCAGGAAGA	CTTGCGTGTT	GAAACCAAGT	CCTCTCCAAC	AGATTTGGTG	180
ACCAGACTGG	ACAAAGAAGT	TCAGGAACTC	TTGGTTGGTG	AGATTTTGTC	CCGTTATCCT	240
GAGGATAAGA	TTTGTGCTGA	AGAAGGTTGT	CTGCGAGCCT	CGGTTCAAGA	GGGCAAGGTT	300
TGGGTCATTG	ATCCCATTGA	TGGTACCAAT	AATTTTGTAG	CCCAGCAGGA	AGATTTTGCT	360
GTTATGATGG	CTTATTTTGA	AAATGGTCAG	GGACAGTTTG	GTCTGATTTA	TGATGTGGTC	420
AAAGGGGATT	GTTACCACGG	TGGTGGGGAA	TTTCCAGTTT	GTCTAAATGA	TAGGTCCCTA	480
GCTCCTTTTA	AAACTAAACC	ACTTGGAGAT	TTTCTCATTG	CAGGGAATAG	TGGTATGCTG	540
GAAACCAATG	AATGGGGGCT	GGCTGATTTG	AGCCGATCGG	TTCTTGGTGT	TCGTGTCTAT	600
GGAAGTGCGG	CCATTAGTTT	TGCCAAGATT	TTGTCAGGGC	GTTTGTTGAC	CTATCTCACT	660
TATCTGCAAC	CATGGGATTA	TGCCGCAGCT	AGTATTTTAG	GGGAAAGTCT	GGGCTATCGG	720
GTTGTGACCC	TTTTTGGTGA	AGCTCCTGAT	TTTCAAACCA	GACAGCCGGT	CATGATGGTG	780
CCTCTTGAGA	TGCAGGAGGA	AATTCAGTCC	TATATTTACG	AAAGGAAAAG	AACTTAA	837

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...966
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

AAGAGGTTCA	CTATGAGTGA	GATCGAAATT	ATTAACGCCA	AAAAAATCTA	CCACGATGTC	60
TCTGTTATTG	AGAATTTGAA	CATTACAATT	CCAAAAGGAA	GTCTCTTTAC	CCTTCTTGGA	120
GCTTCAGGAT	GTGGGAAAAC	GACCCTTCTT	CGTATGATTG	CAGGTTTCAA	CAGTATCAAA	180
GATGGAGAAT	TTTACTTCGA	TGATACAAAA	ATCAATAATA	TGGAACCCAG	CAAACGCAAT	240
ATCGGGATGG	TTTTCCAAAA	CTACGCTATT	TTCCCACATT	TGACTGTCCG	AGACAACGTT	300
GCTTTTGGTC	TTATGCAAAA	GAAGGTTCCT	AAAGAAGAAT	TGATTCAACA	GACCAACAAG	360
TATCTTGAAC	TCATGCAAAAT	TGCTCAATAT	GCGGATCGAA	AGCCCGATAA	ACTCAGTGGT	420
GGACAACAAC	AACGTGTCAC	CTTGGCATGC	GCCTTAGCGG	TTAATCCAAG	TGTTCTCCTC	480
ATGGACGAGC	CACTTAGTAA	TCTGGAGGCC	AACTTCGCT	TGGATATGCG	TCAAGCCATC	540
CGAGAAATCC	AACACGAAGT	GGGAATTACA	ACTGTTTATG	TAACCCACGA	CCAAGAAGAA	600
GCCATGGCTA	TTTCAGACCA	AATTGCTGTT	ATGAAAGATG	GGGTGATCCA	ACAAATCGGC	660
CGACCAAAAG	AACTCTATCA	TAAACCAGCT	AATGAGTTTG	TGGCAACCTT	TATCGGACGC	720
ACAAATATTA	TCCCTGCCAA	TCTTGAAAAA	CGGAGCGACG	GCGCTTATAT	CGTCTTTTCA	780
GATGGCTATG	CCCTTCGAAT	GCCAGCTCTT	GATCAGGTTG	AGGAGCAAGC	TATTCATGTA	840
AGCATTCGTC	CCGAAGAGTT	TATCAAAGAT	GAATCTGGAG	ATATTGAAGG	AACTATTAGT	900
GATAGCGTCT	ATCTTGGACT	AAATACGAAG	TATTTTCATTG	AGACAGGTTT	TGCCTCAAAA	960
ATTAA						966

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

AAATTCTGGT	TTCATCCTCT	CCTCTTTCTA	GCTATTGACC	AAATGGGCGT	AAAAGCCACC	60
CTGTGCAAGC	AAATCAGCAT	GCTTTCCTTC	TTCGACAATC	TTGCCCTGAT	CCAAGACAAC	120
TACCTTCTCT	GTCCGCTCAG	CAATAGTCAA	GCGGTGAGCA	ATGAAAAATCA	AGGTCTTGTC	180
CAAAGCCATG	AGATTATCGA	CAATCCGCTT	CTCTGTCAAA	ATATCCAAAC	TGCTAGTCGC	240
CTCATCCAAA	ATCAAGACCG	GCGCATCTGT	CAAGAGAGCA	CGCGCCAAAG	CGATTCTCTG	300
ACGTTGACCA	CCTGA					315

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1194 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GTGAGTATCA	CAATAACGCT	AAGAAAGTGG	CAAGCTGAAG	CGATTAAAAG	AAGTGAACAT	60
TTATCTAATG	GAATCTTTTT	AGAGGCTCTT	GGGGGCAGAG	GCAAAACTAT	CTGTGCACTT	120
GCTATTGCAA	AACATAAAAA	AGCTAAAAAA	ATCATCATCA	CAAACAATCG	ACTAGCTATT	180
CTGAATGGTT	GGATAGATGC	AGTCAAGTTT	ATGAATTTTG	ATAAAGGTGT	TGAGATTATC	240
ATTCAGACAG	ATAGATATCT	TCAAAATCAA	GTCAAAAAGG	GGCATAAATT	AGATTGTGAT	300
GTGCTGATAG	TAGACGAATG	GCAGAATATG	TCTTCTGACA	AACAAGTGGC	CTTATATCGC	360
AAAATAAAGC	GAAAAATACAC	GATAGGTCTT	TCAGCGACAC	CAATTTCGGAA	AAAAGGACAA	420
AATTTCTATC	CGCTTGAAAA	AACGGTATTT	GGTTGGGCAA	CCCCAAATAA	TAAATTTGAC	480
TGGCAAAAGA	CTCATGGAAA	AATGGTCTAT	GATCCATTTA	GCTATTCAAA	AGAGAAGTGG	540
GAAGATTTTC	AAAATTATGA	AAGTTATATC	TCGAGCTTGC	CTAATTTCTT	CCGCTGGGAA	600
GAGATTGAAG	GAATTGAGAA	TGCAGTTGAG	AATAACGGTT	TTGAGATTAA	GTTTTACCAA	660
AAGAGAGTCG	CCTCTGGCAA	TCCAGAAAAA	CTTGCAGAAT	TTAGAAAAC	AAATCTTGTA	720
ACAGTGGACG	GCAAACTG	AATGGCCAAG	CAATCGTTTG	GAAGAAAGAC	CTTTGAACGC	780
TACCTTAATC	AAACAGGCGT	AGCAGTCGAT	TTTCCAAAAT	TAAAGCCAGT	AAATGCGGAT	840
ACGCCATTGA	TGTTACAAC	TGACGGTTTA	ATCGAACGAG	CACCACACGA	TATGTTGATT	900
GTCAGTAAAT	CTAAGCAGAT	TGTCAACGTC	ATTAGCGAGC	GCCATCCTGA	AATTGGAATC	960
TGGACGGGCG	ATATTCAAGA	AGGACTTTAT	AAGAAATTCG	TGGTTGCTAC	TAGTCAAGTG	1020
TTAGGTGTCG	GAGTAGACGG	CTTGCAACAC	AAATACCAAA	CTATTGTCGT	ATTGGATCCA	1080
GTAGAAGAAG	GTTCTGGAGA	ATATGATGAT	TATCGACAAT	TGCTCTGGCG	CATAACAGGA	1140
AGTCGTCAGC	AGCATGATGT	AAATGTAATT	GAATTTTATT	ATAAAGAAAAG	TTAA	1194

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

CGCCGCTGGT	TGAAGACAAA	AACAGAGGAG	TGCTTTATGA	AAGCCTATAC	TTATGTTAAA	60
CCAGGACTTG	CTTCTTTTGT	TGATGTAGAC	AAACCAGTTA	TTCGCAAGCC	AACAGACGCT	120
ATTGTGCGTA	TTGTAAAAAC	CAC TATTTGT	GGAACAGACC	TCCATATTAT	CAAAGGGGAT	180
GTTCC TACTT	GCCAAAGTGG	TACCATTCTT	GGCCACGAAG	GGATTGGGAT	TGTTGAAGAA	240
GTTGGGGAAG	GAGTTTCCAA	CTTCAAAAAA	GGTGACAAGG	TCTTGATTTT	TTGCGTCTGT	300
GCCTGTGGTA	AATGCTACTA	CTGTAAAAAA	GGAATTTATG	CTCACTGTGA	AGACGAAGGG	360
GGCTGGATTT	TCGGTCACTT	GATTGATGGT	ATGCAGGCTG	AATATCTACG	TGTCCCTCAT	420
GCAGATAATA	CTCTTTACCA	TACTCCAGAA	GACTTGTCAG	ATGAAGCTTT	GGTTATGCTG	480
TCAGACATTC	TGCCTACTGG	ATATGAAATT	GGTGTCTTAA	AAGGGAAAGT	AGAACCTGGT	540
TGCAGCGTAG	CCATTATTGG	TTCAGGTCCA	GTTGGATTGG	CTGCTCTTTT	AACAGCCCAA	600
TTCTATTAC	CAGCTAAATT	GATTATGGTA	GACCTAGACG	ATAACCGCTT	GGAAACTGCC	660
CTATCATTCG	GTGCGACTCA	TAAGGTTAAT	TCTTCAGACC	CTGAAAAAGC	CATTAAAGAA	720
ATTTATGATT	TGACAGATGG	TCGTGGTGTG	GATGTCGCTA	TCGAAGCTGT	TGGTATTCCCT	780
GCAACATTTG	ATTTCTGTCA	AAAGATTATC	GGTGTAGACG	GAACGGTTGC	CAACTGTGGT	840
GTGCATGGTA	AACCAGTTGA	ATTCGATTTA	GATAAACTTT	GGATTCGCAA	CATCAATGTA	900
ACAACTGGTT	TGGTATCTAC	AAATACGACT	CCACAATTGT	TGAAAGCACT	TGAAAGTCAT	960
AAGATTGAAC	CGGAAAAATT	GGTAACTCAC	TATTTCAAAC	TCAGTGAAAT	TGAAAAAGCC	1020
TACGAAGTCT	TCAGTAAGGC	AGCAGACCAC	CATGCCATTA	AGGTCATTAT	CGAAAAACGAT	1080
ATCTCAGAAG	CCTAA					1095

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GCGTTATGGT	TTTGTCTCTAA	CGAGTTGGGT	GGGGGGATGA	TTTTGGCAGG	TTTGTCTTAGC	60
AATGTCCTCT	CGCCGGTTTA	TGAGCTTTCC	TTTACTCTTG	ATATTTGGAG	TATCTTGATT	120
TGCCTCATTA	TCGCTTCTT	TGGAACGGCT	TTTGCTTTTT	TCATTTCCAT	GAAGGCTGTG	180
TCCTTGTTT	CTCCTTGGT	GGGTTTCCG	CTTACTCAGT	GCGCAGTGAA	CCTCTCTCTT	240
CTGCTCTCTT	GA					252

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GGGCCTTCCA	CNGAACTACG	TTTTGAGTTG	GCGCGCCTTG	TTGAAATTTG	CCAACCAANG	60
AAAATATCCC	TTGGGATGGT	TCTTGGCAAT	GCAAGCAATA	TCATCGTTTCG	TGATGGTGGG	120
ATTTCGTGGAT	TTGTCATCTT	GTGTGACAAG	CTCAATAACG	TTTCTGTTGA	TGGCTATACC	180
ATTGAAGCAG	AAGCTGGGGC	TAACTTGATT	GAAACAACCTC	GCATTGCCCT	CCGTCATAGT	240
TTAACTGGCT	TTGAGTTTGC	TTGTGGTATT	CCAGGAAGCG	TTGGCGGTGC	TGTCTTTATG	300
AATGCGGGTG	CCTATGGTGG	CGAGATTGCT	CACATCTTGC	AGTCTTGTA	GGTCTTGACC	360
AAGGATGGAG	AAATCGAAAC	CCTGTCTGCT	AAAGACTTGG	CTTTTGGTTA	CCGCCATTCA	420
GCTATTCAGG	AGTCTGGTGC	AGTTGTCTTG	TCAGTTAAAT	TTGCCCTAGC	TCCAGGAACC	480
CATCAGGTTA	TCAAGCAGGA	AATGGACCGC	TTGACGCACC	TACGTGAACT	CAAGCAACCT	540
TTGGAATACC	CATCTTGTGG	TTCCGTCTTT	AAGCGTCCAG	TCGGGCATTT	TGCAGGTCAG	600
TTAATTTTCA	AAGCTGGCTT	GAAAGGCTAT	CGTATCGGTG	GCGTAGAAGT	GTCAGAAAAG	660
CATGCAGGAT	TTATGATCAA	TGTCGCAGAT	GGAACGGCCA	AAGACTACGA	GGACTTGATC	720
CAATCGGTTA	TCGAAAAAGT	CAAGGAACAC	TCAGGTATTA	CGCTTGAAAG	AGAAGTCCCG	780
ATCTTGGGTG	AAAGCAAGTA	G				801

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

AGCAATTCCA	CTTCTGCTTT	TTCTTTACCG	ACAGCAGCAA	CGATTTCTTC	TTGGAAGGCA	60
ATCAATTCTT	TGACAGCTTC	GTGCCCTTTA	AGGAGCGCTT	CCAACATGAT	TTCTTCTGAC	120
AATTCTTTGG	CACCAGACTC	TACCATGTTG	ACAGCGTGCT	TGGTTCCAGC	TACTGTCAAT	180
TCAAGAAGAG	ATTGCTCTGC	TTGTTCTTGA				210

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

TTAAATTCCA	CATCATCAAA	AAAATTCACC	TTATTCTTAA	TAATGAATAT	TTCGTTAAAT	60
AAACATATAT	ATAAATATTT	CAATATCCTT	TCAATATCAT	CCTCTAAATT	CTCCTCAATA	120
TTTTGTATCA	GCCCATTTAC	AATCTTACTT	AAAAAAGATA	AGCTCTTTAT	CTCTAAAATT	180
AAATATTTTC	ATACAACTGT	TGTATCGAGA	AATATATAA			219

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

AAATGCTCCA	CACCTAGCTC	ATCTGGGGAT	CAGTCACGTC	TGGATGCCAC	CAGCCTTCAA	60
GGAACCAACG	AAAAAGATGT	CGGCTATGGG	GTCTATGACT	TATTTGACTT	AGGAGAGTTC	120
AACCAAAAAG	GGACTGTCCG	CACCAAGTAT	GGTTTCAAAG	AAGACTATCT	TCAAGCCATT	180
CAAGCCCTTA	AAGCGCAGGG	AATTCAACCT	ATGGCCGATG	TAGTTCTCAA	CCACAAGGCT	240
GCTGCTGATC	ACAGGGAAGC	CTTTCAGGTT	ATTGAAAGTG	ATCCTGTAGA	CCGTACAGTT	300
GAACTTGGAG	AACCCTTCAC	CATCAATGGC	TGGACTAGTT	TTACCTTCGA	TGGTCGCCAA	360
GATACCTACA	ATGACTTCCA	CTGGCACTGG	TACCACTTCA	CAGGTACAGA	CTATGATGCC	420
AAACGCCGTA	AATCCGGGAT	TTACCTAATC	CAAGGAGACA	ACAAGGGCTG	GGCTAACGAG	480
GAATTGGTCG	ATAACGAAAA	CGGAAACTAC	GACTACCTCA	TGTATGCCGA	CCTAGACTTT	540
AAACATCCTG	AAGTCATCCA	AAACATCTAT	GACTGGGCTG	ATTGGTTCAT	GGAAACGACT	600
GGTGTAGCTG	GTTTCCGTTT	GGATGCCGTT	AAGCATATTG	ACTCTTTCTT	TATGCGCAAC	660
TTCATCCGCG	ATATGAAGGA	AAAATACGGT	GACGATTTCT	ATGTTTTTGG	TGAATTTTGG	720
AACCCAGACA	AGGAAGCCAA	TCTGGACTAT	CTCGAAAAAA	CGGAAGAACA	CTTTGACCTT	780
GTCCGATGTT	GTCTCCACCA	GAATCTCTTT	GAAGCCAGTC	AAGCTGGCGC	AAACTATGAC	840
CTTCGTGGCA	TTTTTCACAGA	TAGCCTGGTT	GAATCAAGC	CTGACAAGGC	TGTGACTTTT	900
GTCGACAACC	ACGATACCCA	ACGAGGACAA	GCCCTTGAGT	CTACCGTTGA	AGAATGGTTC	960
AAGCCAGCAG	CCTATGCCCT	CATTTTGTTA	CGCCAAGACG	GCCTTCCATG	TGTCTTTTAC	1020
GGAGACTACT	ATGGGATTTT	AGGCCAGTAT	GCTCAAGAAG	ATTTCAAAGA	AATCCTTGAC	1080
CGCCTCCTAG	CCATCCGAAA	AGACTTGGCC	TATGGAGAAC	AAAATGACTA	CTTTGACCAT	1140
GCTAACTGTA	TCGGTTGGGT	ACGTTCAAGT	GCTGAAAATC	AATCCCCAAT	CGCAGTCCTT	1200
ATCTCAAATG	ACCAAGAAAA	CAGCAAGTCA	ATGTTTGTCT	GTCAAGAATG	GACTAATCAA	1260
ACCTTTGTAG	ATTTACTTGG	TAACCACCAA	GGTCAAGTTA	CAATTGATGA	GGAAGGTTAT	1320
GGACAATTCC	CTGTCTCAGC	TAGATCCGTA	AGTGTCTGGG	CAGTCAATAC	CATCTAA	1377

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1536 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

CGGACTACCA	CTCTACGCCG	CTCTAACACG	CGGAGCCTGC	TCCAAC TTCT	CTTCCCCC	60
CCCCCATACA	CCCACGCTCC	CCCTCCAGCA	GATCCCATCG	CAACTTCTCC	CTTTGTTCCC	120
AAACCCCGTG	GCCTCACCAC	GGCACACATC	CGTGCAGCCC	ATATCTCCCT	GCCGACACGG	180
CCCTCCTCAC	ACCAACTGCC	CCCCACTCAC	CCCAC TCCAC	CCGTCCCCCG	ACCGCCCCCG	240
CCTCAACCCC	GGCCACCCCA	CTTCCC TCCA	CCCCCGTTTC	CCCCGCATGC	CGCCCCCCTC	300
CACGCGGCCA	ATCCCCCACC	GCGCGCGAGC	AACTCCCCC	CCCCACCCCC	ACCACCGCCC	360
GCCGCACGCC	AACCCCCCCA	CGCCCCCCCC	CGCAGGAATC	CGCCGCCCCA	CCCCGGGCCC	420
ACACCGCACC	GGCCTCACCG	CCCCACCCCG	CCCCCGCACA	CCCCCCCCAC	TCCGCCACCA	480
GCCCACACCG	GGCCCCCTAC	CACACCCCCA	ACGAACGAGC	CGCCCCGCCC	CACGCCAGCC	540
CCAAAACCCC	CCCGCCACCC	ACCCCGCCCC	GCCGCCNACC	TACCGCCCAT	GCTCGCGACC	600
CCCCGCACCG	AGCNAGCCAC	NNCNGNCCN	NNNNNNNNNT	TTTCNNNNNN	NNNNNNNNNN	660
NNNNNNNNNN	NNNNNNNNNN	NNACTACACA	AACTGGCAAG	CAGTTGGCGA	CCTTGACTTT	720
GCTAACGACC	GTA TGCCTA	CATGATGGAA	TGTCTTAATC	TGGTCTTTGT	AGAGGAACAG	780
CCTGTCCTTC	TCTACTGTCC	ACAAGGATTG	GATAAGAAAAG	TTCTAGACTA	CGATAATATC	840
TTTCCAAATA	TGTATAAGAT	TGGGGCTTCC	TTTGACCCTA	AAAATGCCAA	AATGGTAGAT	900
GTGTCTCAAC	TTCAAAACAT	GGATTACGGT	TTCGAAGCCT	ATGCAACTCA	AGCCTTCAAC	960
GCTCCTGATG	GGCGTGCTCT	AGCAGTTAGC	TGGCTTGGTT	TGCCAGATGT	TTCTTACCCA	1020
TCTGACCGTT	TTGACCACCA	AGGAACCTTC	TCTTTGGTCA	AGGAACTCAC	TATCAAAGAC	1080
GACAAGCTCT	ACCAGTATCC	AGTCGCTGCT	ATTAAGGACC	TTCGTGCTTC	TGAAGAAGCC	1140
TTCTCAAACC	GTTTCCAAAC	CAAGAACACT	TACGAAC TTG	AACTCAACTT	GGAAGCTAAT	1200
AGCCAGAGCG	AGATTGTCTT	ACTTGCTGAT	AAAGAAGGTA	AGGGACTTTC	AATCAACTTT	1260
GACCTTGTA	ACGGTCAAGT	GACAGTGGAT	CGTAGCCAGG	CTGGAGAACA	GTATGCCCAA	1320
GAATTTGGGA	CAACTCGTTC	TTGCCCTATC	GAGAATCAGG	CTACTACTGC	TACAATCTTC	1380
ATCGATAACT	CTGTCTTTGA	AATTTTCATC	AATAAAGGAG	AAAAAGTATT	TTCTGGTCGT	1440
GTCTTCCCAC	ATGCGGACCA	AAATGGTATC	CTGATCAAAT	CTGGAAACCC	AACTGGAAC T	1500
TACTATGAAT	TAGATTATGG	TCGCAAAACT	AACTGA			1536

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1650 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

ATATATTACA	CATATAGGAG	AAAAATATTG	CTTACAGTAT	CTGATGTTTC	ACTACGTTTT	60
AGTGATCGCA	AACTTTTTGA	TGATGTCAAT	ATCAAATTTA	CAGAAGGAAA	TACTTACGGA	120
TTAATCGGTG	CTAATGGTGC	CGGAAAATCA	ACCTTTTTTA	AAATTTTAGC	TGGAGATATC	180
GAACCTACTA	CTGGTCACAT	CTCTCTTGGT	CCAGATGAAC	GTCTCTCTGT	TCTTCGTCAA	240
AATCACTTTG	ACTACGAAAG	TGAACGTGCC	ATTGATGTCG	TTATCATGGG	AAATGAAAAA	300
CTTTATAGCA	TCATGAAAAG	GAAAGATGCT	ATCTACATGA	AGGAAGATTT	CTCAGACGAG	360
GACGGGGTTC	GTGCTGCCGA	ACTCGAAGGA	GAGTTTGCCG	AACTTGGAGG	TTGGGAAGCA	420
GAGAGTGAAG	CCTCTCAACT	ACTTCAAAAC	CTAAACATTC	CAGAAGAATT	ACACTACCAA	480
AACATGAGCG	AATTGGCCAA	CGGTGAAAAA	GTAAAGGTTT	TCCTCGCCAA	AGCACTTTTT	540
GGTAAACCAG	ATGTTCTTCT	CTTGGACGAG	CCTACTAACG	GTTTGGATAT	CCAATCGATT	600
ACTTGGTTAG	AAGACTTCTT	AATTGACTTT	GATAACACAG	TTATCGTAGT	ATCCCACGAC	660
CGTCACTTCT	TAAACAAAAGT	TTGTACTCAC	ATGGCCGACC	TTGACTTTTG	AAAAATCAAA	720
CTCTATGTCG	GAAACTACGA	CTTCTGGAAG	GAATCTTCTG	AGCTTGCTGC	TAAATTGCTA	780
GCAGACCGTA	ATGCTAAAGC	AGAAGAAAAA	ATTAAACAAT	TGCAAGAATT	CGTTGCTCGT	840
TTCTCTGCCA	ATGCTTCTAA	GTCAAGGCAG	GCAACATCAC	GTAAGAAAAT	GCTTGATAAG	900
ATTGAGCTAG	AAGAGATTGT	ACCATCTAGT	CGTAAATATC	CATTTATCAA	CTTTAAAGCG	960
GAACGTGAGA	TTGGTAATGA	TCTCTTGACA	GTAGAAAAATC	TAAGTGTAAA	GATTGATGGT	1020
GAAACTATCT	TGGATAATAT	TAGTTTCATC	TTGCGTCCAG	ATGATAAGAC	AGCACTTATT	1080
GGACAAAATG	ATATTCAAAC	GACTGCATTA	ATTTCGTGCA	TCATGGGAGA	TATTGACTAT	1140
GAAGGAACTG	TCAAGTGGGG	AGTTACAACT	AGTCAATCTT	ACCTACCAAA	AGATAACTCA	1200
GCTGATTTTG	CAGGAGGAGA	ATCAATTCTT	GACTGGTTGC	GTCAATTTCG	AAGTAAAGAA	1260
GATGATGACA	ATACTTTTCT	ACGTGGTTTC	CTCGGCCGTA	TGCTCTTCTC	TGGAGATGAA	1320
GTTAACAAAC	CTGTAAATGT	CTTGTACGGG	GGAGAAAAAG	TTCGTGTCAT	GCTTTCAAAA	1380
CTCATGCTCT	TAAAATCAAA	TGTCCTTGTA	CTTGATGATC	CAACAAATCA	CTTGGACTTG	1440
GAATCTATCT	CAAGCTTGAA	TGATGGATTG	AAAAACTTTA	AAGAATCAAT	CATCTTTGCC	1500
AGCCATGACC	ACGAATTTAT	TCAAACCTTG	GCTAACCATA	TCATTGTCTT	ATCTAAAAAT	1560
GGCGTCATTG	ACCGTATCGA	TGAAACCTAC	GATGAATTCC	TAGAAAATGC	AGAAGTACAA	1620
GCAAAAGTTA	AAGAACTTTG	GAAAGACTAA				1650

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

CTGAACTACA	CCCCAAAAGT	TAGACAGAAA	AAATCTAACT	TTTGGGGTGT	TTTTATTATG	60
AAATTAAGTT	ATGATGATAA	AGTTCAGATT	TATGAACTTA	GAAAACAAGG	ATATAGCTTA	120
GAGAAGCTTT	CAAATAAAAT	TGGGATAAAC	AATTCTAATT	TTAGGTACAT	GATTAAATTG	180
ATTGATCGTT	ACGGAATAGA	GTTCGGCAAA	AAAGGAAAAA	ATCGTTACTA	TTTTCCTGAT	240
TTAAAACAAG	AAATGATTTA	TAAAGTTTGA				270

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

TTTCAATACA	CTGTAACATG	TGATGAAAAT	GCCAGTAATG	ATACCGAGAA	AAAAGCTGAG	60
AAACTTTTCC	CAGCTTTATT	TGTTATAGTC	AAAGCGAATG	ACTTGTTCCT	GTGCATCTAC	120
ATGAGCATGG	ACCCCAAAGG	GTACAATTGC	TCTTGGAGTT	GCGTGGCCGA	CATTCAGATT	180
ATAGACAATC	GGGATATTGT	TGTCAATGAT	ATCCAATAG			219

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

ATTCAATACA	CTATAGACTG	TAATCAAACA	ACGATTTGGC	GAAATGTAAA	AAAATATGAG	60
GAGTTCGGAC	TCGACTCTCT	CCTTCAAGAA	ACACGTGGTG	GTCGTAACCA	TGCATATATG	120
ACGGTTGGGG	AAGAGAAAAGC	CTTTCCTTGCC	CGCCATTTGA	AGGCTACAGA	GGCAGGAGAA	180
TTTGTTACAA	TTGATGCCTT	ATTTCAAGGCT	TATAAAAAGG	AGTTAGGTCG	TTCCCTACACA	240
CGTGATGCCT	TCTATCAACT	GTTGAAGCGC	CATGGTTGGC	GAAATATTAT	GCCACGTCCA	300
GAACATCCTA	GGAAAACAGA	CGCTCAAACC	ATTGTCGCGT	CTAAAAATAA	AATCTCAATT	360
CAAGAAGAAA	AGAAAGCGCT	TTAA				384

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GAAAGGTACA	CTATTATGAA	AGGTATTATT	CTTGCAGGCG	GCTCAGGTAC	CCGCCTGTAC	60
CCACTTACTC	GGGCTGCGTC	AAAACAGCTG	ATGCCGTTT	ATGATAAACC	TATGATTTAT	120
TATCCGTGT	CGACATTAAT	GTTGGCTGGA	ATTAAAGATA	TTTGTATTAT	CTCAACTCCT	180
CAAGATTTGC	CCCGGTTTAA	GGACTTGCTC	TTGGATGGTT	CCGAATTTGG	GATCAAGCTT	240
TCCTATGCGG	AACAACCTAG	TCCCGATGGA	CTTGCTCAGG	CTTTTCTTAT	CGGTGAAGAA	300
TTTATCGGTG	ACGATAGTGT	TGCCTTGATT	TTGGGCGACA	ATATCTATCA	TGGACCTGGT	360
TTGAGCAAAA	TGCTTCAAAA	GGCAGCCCAG	AAAGAGAAAAG	GTGCGACTGT	TTTTGGCTAC	420
CAAGTGAAGG	ATCCAGAGCG	TTTTGGTGTG	GTCGAGTTTG	ATACAGACAT	GAATGCCATT	480
TCCATAGAAG	AAAAACCAGA	GAATCCTCGC	TCCAACATATG	CCGTGACCGG	TCTGTATTTT	540
TATGATAATG	ATGTTGTAGA	AATTGCTAAA	GGTATTAAAC	CAAGTGCACG	TGGCGAGTTA	600
GAAATTACAG	ATATCAACAA	GGCTTACCTA	AATCGTGGTG	ACCTTTCTGT	TGAGCTGATG	660
GGGCGTGGTT	TTGCCTGGTT	GGATACGGGA	ACCCATGAAA	GCCTGCTAGA	AGCTTCTCAG	720
TATATCGAAA	CAGTTCAACG	GATGCAGAAAT	GTTCAAGTTG	CAAACTTGGA	AGAAATTGCC	780
TATCGCATGG	GCTATATCAG	TTGTGAAGAT	GTGCTCGAGT	TGGCGCAACC	TCTGAAGAAG	840
AATGAATACG	GACAATATTT	GCTCCGTTTG	ATTGGAGAAG	CATAG		885

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AGGAGACACA	CAATGACATT	TTTAAACAAA	ATCCATGAAA	CTGCTACTTT	CCTGAAAGAA	60
AAGGGAATTG	CAGCCCCTGA	GTTCCGGTCTA	ATCCTTGGAG	CAGGACTTGG	AGAATTGGCA	120
GAAGAAATCG	AAAATCCAGT	TGTAGTAGAC	TATGCTGAGA	TTCCAAACTG	GGGCCGTTCA	180
ACAGTAGTCG	GTCATGCTGG	TAAATTGGTA	TATGGTGAAC	TGGCAGGTCG	CAAGGTCTTG	240
GCTCTTCAAG	GTCGTTTCCA	TTTCTATGAA	GGGAATCCTC	TGGAAGTGGT	GACTTTCCCA	300
GTTCGTGTGA	TGAAAGTTCT	TGGATGTGAA	GGTGTTATTG	TAACCAATGC	AGCTGGCGGT	360
ATCAGATTTG	GTCCTGGTAC	CTTGATGGCT	ATCTCAGACC	ATATCAACAT	GACGGGGCAA	420
AATCCATTGA	TGGGTGAAAA	CTTGGATGAC	TTTGGCCCAC	GTTTCCCAGA	TATGTCTAGG	480
GCCTACACAC	CAGAATACCG	TGCCACTGCC	CATGAAGTGG	CTAAAAAACT	TAATATCAAG	540
CTTGATGAAG	GTGTCTATAT	CGGAGTTACT	GGTCCGACTT	ATGAAACACC	AGCAGAAATT	600
CGTTCCCTATA	AGACACTGGG	AGCAGATGCA	GTTGGTATGT	CTACGGTTCC	TGAAGTTATC	660
GTGGCAGCCC	ACTCTGGCTT	GAAAGTTCTG	GGAATTCAT	GTATCACTAA	CTTTGCGGCT	720
GGTTTCCAAG	AAGAACTCAA	TCACGAAGAA	ATTGTAGAAG	TGACTGAACG	TGTTAAAGGT	780
GATTTCAAAG	GCTTGCTTAA	AGCGATTCTT	GCTGAATTGT	AA		822

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAGGAAAACA	CAATGGCTAA	AGTATGTTAC	TTTACAGGTC	GTAAGACTGT	ATCAGGAAAC	60
AACCGTTTAC	ACGCGATGAA	CCAAACAAAA	CGTGCCGTAA	AACCAAACCT	TCAAAAAGTT	120
ACTGTTCTTA	TCGATGGTAA	ACCTAAAAAA	GTTTGGGCTT	CAGCTCGTGC	TTTGAAATCA	180
GGTAAAGTTG	AACGCGTTTA	A				201

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AGAGGAAACA	CCTCAAGATC	TTTATCAGGA	GGACAGTACA	TGTCACAAGA	AAAATACATC	60
ATGGCCATTG	ACCAGGGAAC	TACAAGTTC	CGTGCCATCA	TTTTCAACAA	AAAAGGGGAA	120
AAGGTTAGCT	CGAGTCAAAA	AGAGTTTACT	CAGATTTTCC	CTCAAGCAGG	TTGGGTTGAG	180
CACAATGCCA	ATGAAATTTG	GAACTCTGTT	CAGTCAGTTA	TTGCGGGTGC	TTTCATCGAA	240
AGTGGTGTCA	AGCCAAATCA	AATCGAGGCA	ATCGGGATTA	CCAACCAACG	TGAAACAACG	300
GTTGTCTGGG	ATAAGAAAAC	AGGACTTCCT	ATCTACAATG	CTATCGTTTG	GCAGTCACGC	360
CAGACAGCAC	CTTTGGCTGA	GCAACTAAAA	AGCCAAGGTT	ATGTGGAAAA	ATTCCATGAA	420
AAGACTGGTT	TGATTATTGA	TGCTTACTTC	TCTGCTACCA	AGGTTCTGTT	GATTTTGGAT	480
CATGTAGAAG	GTGCTCAAGA	GCGAGCAGAA	AAAGGGGAAT	TGCTCTTTGG	TACTATCGAT	540
ACTTGGTTGG	TTTGGAATTT	GACTGACGGT	GCGGCTCACG	TGACTGACTA	CTCAAATGCA	600
GCTCGTACCA	TGCTTTATAA	CATTAAAGAA	CTCAAATGGG	ATGATGAGAT	TTTGGAATTC	660
CTTAACATTC	CGAAGGCTAT	ACTTCCAGAA	GTTCGTTCTA	ACTCCGAAAT	CTACGGCAAG	720
ACAGCTCCAT	TCCATTTCTA	CGGTGGAGAG	GTGCCAATCT	CAGGTATGGC	TGGGGACCAA	780
CAAGCAGCCC	TCTTTGGACA	GTTGGCTTTT	GAGCCAGGTA	TGGTTAAGAA	TACTTATGGA	840
ACAGGCTCTT	TCATCATCAT	GAATACTGGG	GAAGAGATGC	AGTTGTCCTG	AAACAACCTC	900
TTGACAACCA	TTGGTTACGG	AATCAACGGT	AAGGTTTATT	ATGCCTTGGA	AGGTTCTATC	960
TTCATCGCAG	GAAGTGCTAT	TCAGTGGCTT	CGTGACGGTC	TTCGCATGGT	TGAAAATTCA	1020
CCAGAATCTG	AAAAATACGC	TCGTGATTCT	CACAACAACG	ATGAAGTTTA	TGTCGTTCCA	1080
GCCTTTACAG	GTCTAGGCGC	TCCATACTGG	AACCAAAATG	CTCGTGTTTC	CGTCTTTGGT	1140
TTGACTCGTG	GAACAAGCAA	AGAAGACTTT	ATCAAGGCGA	CTTTGCAATC	TATTGCTTAT	1200
CAAGTGCGTG	ACATCATCGA	CACCATGCAA	GTGGATACTC	AGACTGCCAT	TCAAGTATTG	1260
AAGGTGGATG	GTGGTGACAG	CATGAACAAC	TTCTCATGTC	AGTTCCAGGC	GGATATTTTA	1320
GGCATTTGATA	TTGCACGTGC	TAAAAACTTG	GAAACAACAG	CTCTAGGAGC	GGCCTTCCTA	1380
GCAGGTTTAT	CAGTAGGGTA	CTGGAAAAAC	TTGGACGAGT	TGAAACTCTT	GAACGAGACA	1440
GGAGAACTCT	TTGAGCCATC	TATGAATGAA	TCTCGCAAGG	AACAACCTCT	CAAGGGCTGG	1500
AAGAAGGCTG	TGAAAGCAAC	TCAAGTCTTT	GCGGAAGTAG	ACGACTAA		1548

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AAAATGAACA CAGAACAGCT TAACCAAGCC TTACAAATGA CAATTAGTGA AATGTCAACA	60
ACTTCAACAA ATTTCGATGAT TACAAGTAAT ATCTTGAGTA TTCAGTTGAA TGAGCAAAGG	120
GAAGAGAATC AAAGACTTCA AGCACGAGTG GATGAGCTGG AAGCTCTGCT TGATGAACAA	180
ACTAAACCAG CAGACAAAGG AGAATAG	207

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CTGAACTGCA CCCCAAAAGT TAGACAGAAA AAATCTAACT TTTGGGGTGT TTTTATTATG	60
AAATTAACTT ATGATGATAA AGTTCAGATC TATGAACTTA GAAAACAAGG ATATAGCTTA	120
GAGAAGCTTT CAAATAAAAT TGGGATAAAC AATTCTAATA TTAGGTACAT GATTAAATTG	180
ATTGATCGTT ACGGAATAGA GTTCGTCAAA AAAGGAAAAA ATCGTTACTA TTCTCCTGAT	240
TTAAAACAAG AAATGATTAA TAAAGTCTGA	270

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

ATGAACTGCA	CCCCAAAAGT	TAGACAGAAA	AAATCTAACT	TTTGGGGTGT	TTTTATTATG	60
AAATTAACCTT	ATGATGATAA	AGTTCAGATC	TATGAACTTA	GAAAAACAAGG	ATATAGCTTA	120
GAGAAGCTTT	CAAATAAATT	TGGGATAAAT	AATTCTAATA	TTAGGTACAT	GATTAAATTG	180
ATTGATCGTT	ACGGAATAGA	GTTTCGTCAA	AAAGGAAAAA	ATCGTTACTA	TTCTCCTGAT	240
TTAAAACAAG	AAATGATTCA	TAAAGTCTTA	CATGAAGGCT	GGACTAAAGA	TAGAGTTTCT	300
CTTGAATACG	GTCTCCCAAG	TCGTACGATA	CTTCTTAACT	GGCTAGCACA	ATACAGAAAA	360
AACGGGTATA	CTATTGTTGA	GAAAACAAGA	GGGAGAGTAC	CTAAAATGGG	ACGTAAGCCA	420
AAAACGAGAC	CTGAAGAGAG	AACAGAATTA	GAACGTCTTC	AAGCAGAAAA	TGAGTACCTG	480
AGAGCGGAGA	AGGCCATCCT	AAAAAAGTTA	AGAGAACTCC	GATTGAAGGA	GGAAAAAGAG	540
AAAGAAGAAA	GACAGAAATT	GTTCAAGAAT	TAA			573

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

ATGAACTGCA	CCCCAAAAGT	TAGACAGAAA	AAATCTAACT	TTTGGAGTGT	TTTTATTATG	60
AAATTAACCTT	ATGATGATAA	AGTTCAGATC	TATGAACTTA	GAAAAACAAGG	ATATAGCTTA	120
GAGAAGCTTT	CAAATAAATT	TGAGATAAAC	AATTCTAATC	TTAGGTACAT	GATTAAATTG	180
ATTGATCGTT	AA					192

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

TTCATATGCA	CGATGCCAGT	GTCAAGGATG	TGGTGCTCAA	CCAGCATCCT	CAGGATATTG	60
ACAGTTTGGG	GTACTAGCAT	GATCAAGCGA	AAAAC TTATT	GGAAGGACTT	AATTCAGTCC	120
TTCACAGGCT	CCAAGGGGCG	TTTTTTATCC	ATCTTGATCC	TGATGATGTT	GGGATCTCTA	180
GCCTTAGTAG	GCCTCAAAGT	AACCAGTCCC	AACATGGAGG	CGACAGCTAA	TGCTTATTTA	240
ACAAC TGCTC	AAACCTTGGA	TTTGGCAGTC	ATGTCTAACT	ATGGCTTGGA	TCAAGCAGAC	300
CAAGAAGAAC	TAAAACAGAC	GGAGGGCGCA	GAGGTCGAGT	TTGGCTATTT	GACAGATGTG	360
ACTATGGATA	ATGGGCAGGA	TGCCATTCCG	CTGTACTCCA	AACCAGAGCG	AATTTCAACC	420
TTTCAGCTAA	GAAAGGGACG	ACTTCCTCAG	TCAGACAAGG	AAATCGCTTT	GGCCACTCAT	480
TTGCAAGACC	AATACAGCGT	GGGACAGGAG	ATTAGTTTTA	AAGAAAAAGA	AGAGGGTCAT	540
TCCTCTTTAA	AAGACCATAC	TTATACCATT	ACTGGTTTTG	TGGATTCTGGC	TGAAATCCTC	600
TCCCAGCGAG	ATATGGGCTA	CGCAGGAAGT	GGAAGTGGGA	CTCTGGCAGC	CTATGGGGTG	660
ATTTTACCTA	GTCAATTTGA	TCAGAAAGTC	TACAATATAG	CTCGTTTGAA	ATATCAAGAT	720
TTAGCAGGTT	TAAATGCCTT	TTCATCAGCT	TATGAAGAAA	AATCCAAGCA	ACATCAGGAA	780
GAGCTTGAAC	AAATTTTATC	AGATAATGGC	AAGGTACGTC	TGCAACTTTT	GAAAAAGAA	840
GGACAAGAGT	CTCTAGACAA	GGGGCAAGAG	ACCTTGACA	AGGCTCAGAC	TAATTTGCAG	900
GAAGGCAAGC	GTCGTTTAGC	AGCTGCTCAA	GCTCGTATAC	AGGCTCAAGA	AAGTCAACTA	960
GCCTTGTTTC	CTCAAGTTCA	GAGAGAGCAG	GCTAGTGCTC	AACTTACCCA	AGCCAAGCAG	1020
GAATTGGGCA	AGGAAGAGGC	CAAAC TAAAG	CAAGCTGAAC	AAAATCTAGC	CCAAGAAAAG	1080
GAAAAATTAG	AAAAACATCA	GCAAGTCTTG	GACGATTTGG	CGGAGCCAAG	GTATCAGGTC	1140
TATAATCGTC	AGACCATGCC	AGGTGGTCAG	GGCTATCTTA	TGTATAGCAA	TGCTTCATCC	1200
AGTATTCGAG	CAGTGGGCAA	TATCTTTCCT	GTGGTACTTT	ATGCCGTAGC	AGCCATGGTG	1260
ACATTTACGA	CCATGACTCG	CTTTGTAGAC	GAAGAGCGAA	CTCATGCAGG	GATTTTAAAG	1320
GCCTTGGGTT	ATCGTAGTAA	GGATATTATC	GCCAAGTTTC	TCCTTTATGG	ACTAGTAGCT	1380
GGGACTGTCT	GAACGGCTCT	AGGTAGTATA	CTTGGTCATT	ATTTGCTAGC	CAGTGTAATT	1440
TCAAGTGTC	TTACAAAAGG	CATGGTGGTG	GGAGAACTC	AGATTCAAGT	CTATTGGACC	1500
TATAGCTTAC	TAGCTTTTGT	CTTGAGCTTG	TTGGCGAGTG	TGTTATCAGC	CTATCTGGTG	1560
GCTTGAGGG	AACTTCATGA	CGAAGCAGCC	CAGCTTCTAC	TTCTTAAACC	TCCTGTCAAA	1620
GGAGCTAAAA	TCTTATTGGA	GCGTATCGGT	TTTATCTGGC	GTCGTCTCAG	TTTTACTCAT	1680
AAGGTAACAG	CCC GCAACAT	CTTTCGTTAT	AAGCAGAGAA	TGTTGATGAC	AATCTTTGGT	1740
GTGGCAGGTT	CTGTAGCTCT	GCTCTTTGCA	GGTTTGGGAA	TCCAATCTTC	TGTAGCAGGA	1800
GTTCCGCTTA	AACAGTTTCA	ACAAATCCAA	CAGTATCAGA	TGCTTGTCTC	TGAAAATCCT	1860
AGTGCGACCA	ATCAGGACAA	GGTAGAGCTA	GCAGAAGTGT	TGAAAGGGCA	GGAGATACTA	1920
GCCTACCAGA	AAATCTATTCT	TAAAACGCTA	GACAAGGATT	TCAAAGGCAA	GGCTGGTCTT	1980
CAAAACATTA	CTCTTATGAT	GATAGAGAAG	GAAGATTTGA	CTCCCTTTAT	CCATCTTCAA	2040

CATCATCAGC	AGGAGCTGAC	ATTAAAAGAT	GGCATCGTTA	TTACAGCTAA	ACTCGCCCAG	2100
CTGGCAGGTG	TCAAGGTTGG	GCAGACTTTA	GAAATTGAAG	GTAAGGAACT	AAAGGTCGCT	2160
GCTATTACTG	AGAACTACGT	TGGTCACTTT	ATTTATATGA	GTCAGGCTAG	CTATGAGCAA	2220
CTTTACGGAC	AGCTACCCCA	AGCCAACACT	TATCTGGTCT	CATTAAGGGA	TACCAGTGCA	2280
ACTAGTATCG	AAAGTCAGGC	GGGCTTGCTT	ATGAATCAAT	CTGCGGTGTC	CAGCGTTGTC	2340
CAAAATGCTT	CAGCCATTCT	ACTCTTCGAC	TCTATCGCTA	GCTCACTCAA	TCAGACCATG	2400
ACCATCTTGG	TCATCGTATC	GGTTCTATTA	GCTATTGTCA	TCCTTTACAA	TCTGACCAAT	2460
ATCAACGTAG	CTGAGAGAAT	CCGTGAACCT	TCCACTATCA	AGGTTCTTGG	TTTTCATAAT	2520
AATGAAGTCA	CCCTCTACAT	TTACCGTGAG	ACGATTGTGC	TGTCCCTTGT	GGGAATCGTA	2580
CTTGGTCTGA	TAGCTGGTTT	CTATTTACAC	CAATTTTGA	TTCAAATGAT	TTCGCCTGCG	2640
ACTATTCTCT	TTTATCCGCA	GGTAGGCTGG	GAAGTCTATG	TAATCCCAGT	GGCAGCAGTA	2700
AGCTTCATTT	TGACCTTGCT	TGGTTTCTTC	GTCAATTATT	ATCTGAGAAA	GGTTGATATG	2760
TTAGAAGCCC	TGAAATCTGT	AGAGTAA				2787

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AAAACTAGCA	CCCTTCTTTT	ACTGTCTACT	GTAGCCCTAG	CTGGGTGTAG	CAGCGTCCAA	60
CGCAGTCTGC	GTGGTGATGA	TTATGTTGAT	TCCAGTCTTG	CTGCTGAAGA	AAGTTCCAAA	120
GTAGCTGCC	AATCTGCCAA	GGAGTTAAAC	GATGCTTTAA	CAAACGAAAA	CGCCAATTTT	180
CCACAATAT	CTAAGGAAGT	TGCTGAAGAT	GAAGCCGAAG	TGATTCTCCA	CACAAGCCAA	240
GGTGATATTC	GCATTAAACT	CTTCCCTAAA	CTCGCTCCTC	TAGCGGTTGA	AAATTTCTCT	300
ACTCACGCCA	AAGAAGGCTA	CTATAACGGT	ATTACCTTCC	ACCGTGTCAT	CGATGGCTTT	360
ATGGTCCAAA	CTGGAGATCC	AAAAGGGGAC	GGTACAGGTG	GTCAGTCCAT	CTGGCATGAC	420
AAGGATAAGA	CTAAAGACAA	AGGAACTGGT	TTCAAGAACG	AGATTACTCC	TTATTTGTAT	480
AACATCCGCG	GTGCTCTTGC	TATGGCTAAT	ACTGGTCAAC	CAAACACCAA	TGGCAGCCAG	540
TTCTTCATCA	ACCAAACTC	TACAGATACC	TCTTCTAAAC	TCCCTACAAG	CAAGTATCCA	600
CAGAAAATTA	TCGAAGCCTA	CAAAGAAGGT	GGAAACCTTA	GTCTAGATGG	CAAACACCCA	660
GTCTTTGGTC	AAGTGATTGG	CGGTATGGAT	GTTGTGGATA	AGATTGCTAA	AGCCGAAAAA	720
GATGAAAAAG	ACAAGCCAAC	TACTGCTATC	ACAATCGACA	GCATCGAAGT	GGTGAAAGAC	780
TACGATTTTA	AATCTTAA					798

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AAAAATAGCA	CCACGCTCAC	AATTTCTTCT	AATCGCCTCA	GCTTCAATAT	TTCTTACTTT	60
CCAATAGACT	TCCTGCGAAA	CAAAATATGG	TATAGTAGTT	CTATGAATGA	TGAAGCAAGT	120
AAACAATAA	CTGATGCACG	ATTTAAGCGT	CTTGTTGGTG	TTCAGCGCAC	GACTTTTGAA	180
GAGATATTAG	CTGTATTAAA	AACAGCTTAT	CAACTTAAAC	ACGCAAAAGG	TGGACGAAAA	240
CCTAAATTAA	GCCTAGAAGA	CCTTCTTATG	GCCACTCTTC	AATATGTGCG	AGAATATCGA	300
ACTTATGAAC	AAATTGCGGC	TGATTTTGGT	ATTCACGAAA	GCAACTTAAT	CCGTCGGAGC	360
CAATGGGTTG	AAGTAACTCT	TGTTCAAAGT	GGTGTTACGA	TTTCAAGAAC	TCCTCTCAGT	420
TCTGAGGACA	CGGTAATGAT	TATTGATGCG	ACGGAAGTAA	AAATCAATCG	CCCTAAAAAA	480
AGAATTAGCG	AATTATTCTG	GTAA				504

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAGCAAGGCA	CGCTAAGCTT	GGTAAACTGC	GAGCCGCTAG	AAGCTTATCG	TCAACTGGAA	60
GAAGCTGCAC	TTGTTGGATG	TTGGGCGCAT	GTGAGAAGGA	AGTTTTTTGA	AGCGACCCCC	120
AAGCAAGCAG	ATAAATCATC	TTAGGAGCT	AAAGGATTAG	CCTATTGTGA	TCAGTTATTT	180
TCCTTGGA	GAGACTGGGA	GGCTTTGCCA	GCTGATGAAC	GA	ACTACAGAA	240
GAGCTCCAAC	CCCTAATAGA	AGACTTCTTT	GCTTGGTGCC	GCCGTCAGTC	AGTTTTAGCA	300
GGTTCAAAAC	TAGGAAGGGC	AATTGAATAC	AGCCTCAAGT	ATGAAGAAAC	CTTTAAGACC	360

ATTTTGAAAG ACGGACATCT GGTCCCTTTCC AATAATCTAG CTGAATGCGC CATTAAATCA	420
TTGGTTATGG GACGGAGTAA AAGAGTCCAG TGGACTCTTT TAGCCTAA	468

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

ATACTGGGCA CAAGCCAAGA TATTTTATT AGTTTGGCTA GTGACAATCT TGTGCTGTTC	60
TTCGTTGATT TCCTTGATAT CCAAAAGAAC CAAGTCAGTG ACAGCCATGA GTTTGTCAAA	120
CTTCTCAAGG TAACGTGGTT TATTACGGAA AGGAAGAGCA CAGGTATCCA AGGTACAGTG	180
GATTCCTTGT TCCTTAGCCT TGGTGAAGAG AGCAATCAGG AAATCAATCT GCAAGAGAGC	240
TTCTCCTCCA CTGACTGTAA TCCCACCCTT ATTTCCCCAG AAACCACGGT AGCGCAAGGC	300
CTCTGTCAAG ACATCATCTA CCGTCCGTTC ACGTGA	336

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

AAGAACAGGT TGAAGATCAA GACCATGATT TCTATGGTAG CCAATTTGAT AACCAAATCG	60
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AGAATTCCAA	AGCCTTTAGC	TTTTTCAGCTA	CGGGTAAACT	CGCTGGAGAT	TATGATATCC	120
AACTCATTTGG	CAACTTCAAC	CAAGAAAAATG	CAGTTGCTGC	TGGACTTGCT	TGTCTCCGTC	180
TCGGAGCAAG	TCTTGAGGAC	ATCAAAAAAAG	GCATCGCTGC	AACCCGCGTT	CCTGGTCGTA	240
TGGAAGTCCT	CACTCAGAAA	AATGGAGCCA	AGGTCTTCAT	CGACTATGCC	CACAATGGGG	300
ATAGTCTGA						309

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1212
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GGTGGCTTAA	CGGACAGTCA	AAGGAGAAAT	CATATGACAC	AACATCTTAC	TGCTGAAACT	60
CTTCGCAAAG	ACTTCTTGC	TGTTTTTGGT	CAAGAAGCAG	ACCAAATTTT	CTTTTCACCA	120
GGTCGTATCA	ATTTGATTGG	TGAACACACA	GACTACAACG	GTGGGCACGT	TTTTCCCTGCT	180
GCTATTTCTT	TGGGAACTTA	CGGTGCAGCT	CGTAAGCGTG	ACGACCAAGT	CTTGCGTTTC	240
TACTCAGCTA	ACTTTGAGGA	CAAGGGCATT	ATCGAAGTGC	CTCTCGCTGA	CCTCAAGTTT	300
GAAAAAGAGC	ACAACCTGGAC	CAATTATCCA	AAAGGTGTCC	TTCATTTCTT	GCAAGAAGCT	360
GGGCACGTGA	TTGACAAAGG	TTTTGATTTT	TATGTTTATG	GGAATATCCC	AAATGGTGCT	420
GGTTTGCTCT	CTTCAGCATC	CCTTGAACCTC	TTGACAGGGG	TAGTGGCAGA	GCATCTCTTT	480
GATTTAAAAAT	TAGAGCGTCT	CGATTTGGTT	AAAAATCGGAA	AACAAACAGA	AAATAACTTT	540
ATCGGAGTAA	ATTCTGGCAT	TATGGACCAA	TTTGCTATTG	GTATGGGGGC	TGACCAACGT	600
GCTATTTACT	TAGATACCAA	TACTTTAGAA	TACGACTTGG	TGCCACTTGA	TTTGAAGGAC	660
AATGTCGTTG	TTATCATGAA	CACCAACAAA	CGCCGTGAAT	TGGCGGACTC	TAAATACAAT	720
GAACGTCGTG	CTGAGTGTGA	AAAAGCAGTG	GAAGAATTGC	AAGTTGCCTT	GGATATTGAG	780
ACCCTGGGTG	AATTGGACGA	GTGGGCCGTT	GACCAATATA	GCTATCTGAT	TAAAGATGAA	840
AATCGTTTGA	AACGTGCTCG	CCATGCTGTG	CTTGAAAACC	AACGTACCCT	TAAAGCTCAA	900
GCAGCCCTTC	AAGCAGGTGA	TTTGGAACA	TTTGTCGTT	TGATGAATGC	GTCACACGTT	960
TCTCTGGAGC	ATGATTATGA	AGTAACTGGT	TTGGAATTGG	ATACTCTTGT	TCACACAGCT	1020
TGGGCACAAAG	AAGGAGTTCT	CGGTGCTCGT	ATGACAGGGG	CTGGTTTTGG	TGGCTGTGCC	1080
ATTGCCTTGG	TTCAAAAAAG	TACTGTTGAG	GCCTTTAAGG	AAGCTGTAGG	CAAACACTAC	1140
GAGGAAGTAG	TTGGATACGC	TCCAAGCTTC	TATATCGCTG	AAGTTGCAGG	TGGCACTCGC	1200
GTCCTTGACT	AG					1212

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

AAAACATTAA CAAATATAGT TGGTAAATCA TTAGGACCTA AATCAGCTGT TAGATTCGGA	60
GAAGCTTTAT CCTATATTGA AGGTCCTCTT CGCAGAATAA ATGAGACGAT AGATGGCGGT	120
TTATATCAAA TAGAGCAAAT GATTGCATCT GGATTGAAAG AATCGGGTTT AAATGACTGG	180
ACTGCGAAAA CTTTAGCTTC AGCTATTCGT GGGATATTAG ATGTACTTAT TTAG	234

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

TGGAAATTAA CGACAGTAGC CTTGCATCTG TCAAAACGGC TATTCAGGAC GTGTTGGAGG	60
GCAGATGAAA TGATTGATAT TCATTCGCAC ATTGTCTTTG ATGTAGATGA TGGTCCCAAG	120
TCAAGAGAGG AAAGTAAGGC TCTCTTGACA GAAGCCTACA GGCAGGGGGT GCGAACCATT	180
GTCTCTACCT CTCACCGTCG CAAGGGCATG TTTGAAACTC CAGAAGAGAA GATAGCAGAA	240
AACTTTCTTC AGGTTGCGGA AATAGCTAAG GAAGTCGCGA GTGACTTGGT CATTGCCTAT	300
GGGGCTGAAA TTTACTACAC GCCAGATGTT TTGGATAAGC TGGAAAACAA TCGGATTCCG	360
ACCCTCAATA ATAGTCGTTA TGCCTTGATA GAGTTTAGTA TGAACACTCC TTATCGCGAT	420
ATTCATAGTG CTTTGAATAA AATATTGATG TTGGGAATTA CTCCCGTCAT TGCCACATA	480
GAGCGTATG ATGTTCTTGA AAATAATGAA AAACGCGTTC GAGAGCTGAT CGATATGGGC	540
TGTTACACGC AAATAAATAG TTCACATGTC CTCAAAATCCA AACTTTTTTG AGAACCTTAT	600
AAATTCATGA AAAAAAGAGC GCAGTATTTT TTGGAGCGTG ATTTGGTTCA TATCATTGCA	660
AGTGATATGC ATAATGTGGA CGGCAGACCC CCCCATATGG CAGAAGCATA TGACCTTGTT	720

TCCCCAAAAT ACGGAGAAGC GAAGGCTCAG GAACTTTTTTA TAGACAATCC TCGAAAAAATT	780
GTAATGGATC AACTAATTTA G	801

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 948 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ACATCCCTAA CACTAAAATT CCTTTCCCAG CTCTTGCTGA ACGCGATAAC GACGATATCC	60
GTTTCGGTCT TGAACAAGGT ATCAACTTCA TCGCAATTTC ATTTCGTACGT ACTGCAAAAG	120
AATGTGAACG AAGTTCGTGC AATCTGTGAA GAAACTGGAA ACGGACATGT TCAATTGTTC	180
GCTAAAATCG AAAACCAACA AGGTATCGAT AACTTAGACG AAATTATCGA AGCAGCTGAT	240
GGTATTATGA TTGCTCGTGG TGATATGGGT ATCGAAGTAC CGTTCGAAAT GGTTCAGTT	300
TATCAAAAAA TGATTATCAA GAAAGTCAAT GCTGCAGGTA AAGTTGTTAT CACTGCAACA	360
AACATGCTTG AAACAATGAC TGAAAAACCA CGTGCAACTC GTTCAGAAAGT ATCAGACGTA	420
TTCAACGCTG TTATCGACGG AACTGACGCT ACAATGCTGT CAGGCGAGTC TGCAAACGGT	480
AAATACCCAC TCGAGTCAGT AACTACAATG GCTACAATCG ACAAGAACGC TCAAGCTCTT	540
CTTAATGAAT ACGGACGTCT TGATTTCAGAT TCATTTGAGC GTAACCTCTAA GACAGAAGTA	600
ATGGCTTCTG CTGTTAAAGA TGCTACTAGC TCAATGGATA TCAAATTGGT TGTAACCTTT	660
ACTAAGACAG GTCATACTGC ACGTTTGATT TCTAAATACC GTCCAAATGC TGACATCTTA	720
GCATTGACAT TTGACGAATT GACAGAACGT GGCTTGATGT TGAACGGGG TGTATCCCA	780
ATGTTGACAG ATGCTCCATC TTCAACTGAC GATATGTTTCG AAATCGCTGA ACGTAAAGCG	840
GTAGAAGCAG GTCTCGTTGA GTCAGGCGAT GATATCGTTA TCGTTGCTGG TGTGCCAGTA	900
GGAGAAGCTG TTCGCACAAA CACAATGCGT ATCCGCACAG TACGTTAA	948

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

AAAACGAGGT TAGAAGAGAT GATTTTTTGAT ACACATACAC ACTTGAATGT AGAAGAATTT	60
GCAGGTCGTG AGGCAGAAAG AATTGCCTTG GCTGATGAGA TGGGTGTGAC ACAGATGAAT	120
ATTGTTGGTT TTGATATACC GACGATTGAG CGTGCCTTGG AGTTGGTAGA TGAGTATGAG	180
CAGCTCTATG CGACTATTGG TTGGCATCCT ACAGAAGCTG GTATTTATAC AGTAGGAAGT	240
TGA	243

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AAAAAGAGGT TTTATATGTT AAGTTCAAAA GATATAATCA AGGCTCACAA GGTCTTGAAC	60
GGTGTGGTTG TGAATACTCC ACTGGATTAC GATCATTATT TATCGGAGAA GTATGGTGCT	120
AAGATTTATT TGAAAAAGA AAATGCCCAG CGTGTCGCT CCTTTAAAAT TCGTGGTGCC	180
TATTATGCCA TTTCCCAGCT CAGCAAGGAA GAACGTGAAC GTGGGGTAGT CTGCGCTTCT	240
GCGGGAAATC ATGCGCAGGG AGTAGCCTAT ACTTGTAATG AAATGAAAAT TCCTGCTACT	300
ATCTTTATGC CCATTACTAC GCCACAACAA AAGATTGGTC AGGTTCGCTT TTTTGGTGGG	360
GATTTTGTAA CTATTAAACT AGTTGGAGAT ACCTTTGATG CCTCAGCCAA AGCAGCTCAA	420
GAATTTACAG TCTCTGAAAA TCGTACCTTT ATTGATCCTT TTGATGATGC TCATGTTCAA	480
GCAGGTCAAG GAACAGTTGC TTATGAGATT TTAGAAGAAG CTCGAAAAGA ATCGATTGAT	540
TTTGATGCTG TCTTGGTTCC TGTGGTGGT GCGGCTCTCA TTGCCGGGGT TTCTACCTAT	600
ATCAAGGAAA CAAGTCCAGA GATTGAGGTT ATCGGAGTAG AGGCGAATGG AGCGCGTTCC	660
ATGAAAGCTG CCTTTGAGGC TGGAGGTCCA GTAAACTCA AGGAAATTGA TAAATTTGCT	720
GATGGGATTG CTGTGCAAAA GGTAGGTCAG TTGACCTATG AAGCAACTCG TCAACATATT	780
AAAACTTTGG TAGGTGTCGA TGAGGGATTG ATTTCTGAAA CCTTGATTGA CCTTTACTCT	840
AAGCAAGGGA TAGTCGCAGA ACCTGCTGGA GCGGCTAGTA TCGCCTCTTT AGAGGTTTTTA	900
GCTGAATATA TTAAGGGGAA AACCATTTGT TGTATCATTT CTGGAGGAAA TAATGATATC	960
AACCGTATGC CAGAAATGGA AGAGCGTGCC TTGATTTATG ATGGTATCAA ACATTACTTT	1020
GTGGTCAATT TCCCACAACG TCCAGGAGCT TTGCGTGAGT TTGTAAATGA TATCCTGGGG	1080
CCAAATGATG ATATCACACG TTTTGAGTAT ATCAAACGAG CTAGCAAGGG AACAGGCCCA	1140

GTATTAATTG GGATCGCTTT AGCAGATAAG CATGATTATG CAGGTTTGAT TCGTAGAATG	1200
GAAGGTTTTG ATCCAGCTTA TATTAACCTA AATGGTAATG AAACGCTTTA TAATATGCTT	1260
GTCTGA	1266

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

CACTCTATAA CTATTTATTA TCTTATCAAA AAGGAGAATC ATAACATGGA TAAGAAACAA	60
AACCTAACTT CATTTCAAGA ACTAACAACCT ACCGAACTCA ACCAAATTAT AGGTGGAGGA	120
TGGTGGGAAG ATTTCTTATA TAGATTTAAT ATAATTGAAC AAAAAAATAC AAAAGGATTT	180
TATCAGCCAA TACAACTATA A	201

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...345
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GCCAATATAA CTAAAAAAG GAGAAATACA ATGGCAAAAG CAATTACAGA TGCAACATTC	60
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GAACAAGAAA	CAAAAGACGG	TTTGGTCTTA	GTAGACTTCT	GGGCAACTTG	GTGTGGTCCA	120
TGTCGTATGC	AAGGTCCAAT	CTTGGACAAA	TTGTCTGAAG	AACTTTCAGA	AGATGTCTTG	180
AAAATCGTTA	AAATGGACGT	TGATGAAAAT	CCAAACACAG	CTCGTGCTTT	TGGAATCATG	240
TCTATTCCAA	CTCTTCTCTT	CAAAAAAGAC	GGCCAAGTTG	TCAAACAAGT	TGCAGGTGTT	300
CACACAGCAG	AACAAATCAA	GGCCATCATT	GCTGAATTGA	GCTAA		345

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...537
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

AAACGTATAA	CATCTCCTAA	AGATGTGTCA	GCACAAATTA	CGATTAACCA	TAAAAAAGCG	60
CGCTATGTTT	GGATTGAGCT	AGAAGGCTAT	AATGCCCTCA	GTCTTGCAGA	AGTTGAAGTT	120
TTCCGCTTTA	TAGCTACGAA	TGGTGAAACG	GCGATACAAG	TTTCTAAGCC	AGTTCAACCA	180
ATCAGTCAGA	CTCCTGTGAA	GGATAAAACA	TTGACAATTC	AACACAGTGG	AGCTTACATT	240
GCCCGCTACT	CCATAACTTG	GGAAGAAGTT	CCAGTAGATA	AAGATGGAAA	CCAAGTTGTT	300
CGTAGTCATT	CTTGGGAAGG	AAACGGTCGC	AACCAGACTG	CAGGTTTTGT	CCTCAACCTC	360
CCAATCAAAG	AAAAATATGAG	AAATCTGCGA	GTTAAGATTG	AGAAAAAGAC	AGGTCTACTA	420
TGGAATAGAT	GGCAACAAT	CTATGAAAAC	AGACCAATTT	TAGCTCAACC	TCACCGTAAA	480
ATTACCCATT	GGGGTACGAT	ATTGAATTC	AAGGTGAGTG	ACGATGATGT	CTTGTA	537

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAAAGGAGGT	TAGAAGAGAT	GATTATTACA	AAAATTAGCC	GTTTAGGAAC	TTATGTGGGA	60
GTAAATCCAC	ATTTTGCAAC	ATTAATAGAT	TTTCTAGAAA	AAACAGGACT	AGAAAATTTA	120
ACAGAAGGTT	CGATTGCTAT	CGATGGTAAT	CGATTGTTTG	GGAATTGCTT	TACTTATCTA	180
GCAGATGGTC	AAGCAGGGGC	TTTCTTTGAA	ACACACCAAA	AATATTTGGA	TATTCATTTA	240
GTTTTGGAAA	ACGAAGAAGC	CATGGCTGTT	ACATCGCCGG	AAAATGTAAG	CGTTACCCAA	300
GAATATGATG	AAGAGAAAGA	TATTGAATTA	TACACAGGGA	AAGTGGAACA	GTTGGTTCAT	360
TTGAGAGCTG	GCGAATGCCT	CATCACTTTT	CCAGAAGATT	TACATCAACC	CAAGGTTCGT	420
ATAAATGATG	AACCTGTGAA	AAAAGTTGTC	TTTAAAGTTG	CGATTTCTTA	A	471

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

TCTCATTCAA	CTACTTGCAA	ATGCCCTTGT	TTGGGGTGTC	TTGGCACCAC	TTGGAGATGT	60
TGTGATTTAT	CAAGAAGCGG	CAGAAAAAGT	ATTTGCACAA	GGGATTGTTG	CGGGAATTGC	120
CAATGGTGTA	TCTGTAGCTA	TTGCAGGAAC	TCTTCTCTTA	CTTGCCTATG	CAGGAACCCA	180
AACTCGTGCA	GGAAGTTTGA	AAAAGGACTA	ATACTCAATG	AAAATCAAAG	AGCAAACCTAG	240

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAAAAATTC	CTAGGCGG	AC	GTGGAAC	CCCA	CTTTTGT	CCCA	AACTGT	CAAA	GGGGGG	ACTG	60	
ATGGGAAAA	TCATCGGA	AT	CACTGGG	GGGA	ATTGCCT	CAG	GTAAGT	CAAC	TGTGAC	AAAT	120	
TTTCTAAAA	ACCAAGGG	CT	TTCAAG	CAGT	GGATTG	CCGA	CGCAGT	GTTC	CACCAAC	TAC	180	
AGAAAACCT	G	GTGGTC	GTCT	GTTTGAG	GCT	TTAGTAC	AGC	ACTTTGG	GCA	AGAAAT	CATT	240
CTTGAAAAC	G	GAGAACT	CAA	TCGCCCT	CTC	ATAGCTA	GT	TCATCTT	TTT	AAATCCT	GAA	300
GAGCAAAAA	AT	GGTCTA	ATCA	AATTCA	AGGG	GAGATT	TATCC	GTGAGGA	ACT	GGCTACT	TTG	360
AGAGAACAG	T	TGGCTCA	GAC	AGAAGAG	ATT	TTCTTC	CATGG	ATATTCCC	CT	ACTTTTT	TGAA	420
CAGGACTAC	A	GCGATTG	GTT	TGCTGAG	ACT	TGGTTG	GTCT	ATGTGG	ACCG	AGATGCC	CAA	480
GTAGAACG	CT	TAATGAAA	AG	GGACCA	GTTG	TCCAAAG	ATG	AAGCTGA	GTC	TCGTATG	GCA	540
GCCCACTGG	C	CTTTAGAAA	AA	AGAAAAG	AT	TTGGCC	CAGCC	AGGTTCT	TGA	TAATAAT	GGC	600
AATCAGAAC	C	AGCTTCTT	A	TCAAGTG	CAT	ATCCTT	CCTTG	AGGGAGG	TAG	GCAAGAT	GAC	660
AGAGATTAA												669

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

ACATTATCA	CTGACAGT	AG	AAGAAGA	AAAA	AATGCTG	GCA	GAAATCA	AAAG	AAAA	CAAAGA	60	
ATAAAGG	GAGA	AACCTAT	GCA	AGTAAT	CAAA	CGTAATG	GCG	AAATTG	CTGA	ATTTAAT	CCA	120
GATAAGAT	TTT	ACCAAGC	CAT	CTTGAAG	GCA	GCCCAAA	CTG	TTTATG	TTTT	GACAGAT	GAT	180
TTGCGTCA	AAA	ATCTTG	CTCA	AGTCACT	AAG	AAGGTAG	TTT	TGGATT	TACA	AGAAGCC	AAAG	240
GTGGAACG	TG	CGACTAT	CAG	TATGATT	CAA	TCTATGG	TTG	AACATCG	TTT	ATTGGGG	CGCA	300
GGTTACAT	TA	CCATTGC	AGA	ACACTAT	ATT	TCCTATC	GTT	TACAACG	TGA	CTTGGA	AAAGA	360
AGTGGTTAT	G	GAGATCAT	AT	CGCAGTT	CAT	TTACATTT	TG	AACAAAT	TCG	CTAA		414

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

AAGGAGTCAA	CCATGGAATG	TAAAAAACTA	AATATTTGGA	CAGCTTCCTC	TTTCTTCATC	60
TTTCTTACCT	ATCTTGTCTT	TCTCGTTTAT	CCTATCGTTA	CCGTGCTAAA	GCAAGCACTT	120
ATACATGAAG	GACAATTCTC	ACTAGCTAAT	TTTGTCACCT	TCTTTAGTAA	AGTCTACTAC	180
TCTGAGACAC	TAGTCAACAG	TTTCAAGGTT	TCCATTACCG	CTACTGTCAC	TTCCCTTAGTT	240
GTAGGAACCC	TATTAGCTTA	TCTCTTCTCT	ATGTATGACT	TCAAGGGGAA	GAAATTTCTA	300
CAAATATTGA	TTATCATTGC	TTCCATGTCA	GCTCCTTTTCG	TAGGAGCCTA	CTCCTGGGTT	360
CTCTTGCTGG	GACGAAAATG	GGTCATCACT	AAATTTTTGA	CAAATGCCCT	TCATCTTCCA	420
GCTATCGATA	TTTATGGATT	CAAAGGAAAT	GTACTTGTCT	TTACACTGCA	ACTATTCCCA	480
CTGGTATTTT	TATATGTTGC	TGAAACAATG	AACAGTATTG	ACAATTCTCT	ACTTGAAGCT	540
GCTGAAAGCA	TGGGGTCCCT	CGGATTTAAA	CCTATCGTAA	CGGTTGTTTT	ACCTCTCCTA	600
GTTCCAACCT	TACTAGCAGC	TCCTTGCTTG	TATTTATGA			639

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 792 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

AAAAAACCAA	CCTTTATTAT	TGTCATGATC	GGGATTTCTC	TTATTCCAGA	TCTGTACAAT	60
ATCATATTTT	TGTCATCAAT	GTGGGATCCA	TATGGGCAAT	TGTCTGACTT	ACCTGTGGCA	120
GTTGTAAATA	ATGATAAAGA	GGCTTCCTAT	AATGGTAATA	CTATGGCAAT	AGGAAAAGAC	180
ATGGTGTCCA	ATTTAAAGA	AAATAAAACC	TTGGATTTTC	ATTTTGTAGA	TGAAGAGGAA	240

GGAAAGAAGG	GATTGGAAGA	TGGCGATTAC	TATATGGTAG	TGACTTTACC	AAGTGATTTA	300
TCTGACAAAA	CAACTACATT	ATCCAATATT	CAATCGACAG	CAGCTTATCA	ATCATTGACA	360
AGTGAGCAAC	AAACTGAGAT	AAGTGATTCT	GTATCTCAAA	ATTCAACTGA	TAGTATTCAA	420
TCGGCTCAGT	CAATTGTAGC	TTTAGTACAA	GATTTACAGG	GAAGTTTAGA	AAACTTACAA	480
AATCAATCTT	CTAATCTTTC	GACTTTAAAA	AATCAAGCTA	ATCAAGTATC	ACCTATTACT	540
TCTACTTCTT	TGATAGGATT	GTCAAGTGGA	TTAACAGAGA	TACAAGGAGA	TGTTACTAGC	600
AAATTAGTTC	CTGCCAGTCA	GTGATTGCA	TCAGGTGTAA	ACGCATATAC	TACAGGTGTT	660
GATAAAGTTT	CTCAGGGCGC	AAGTCAACTA	AGTGAAAAAA	ATGCCACCTT	GACAGGTAGT	720
TTGGATAAAC	TAGTTTTCAGG	CTCAAACACC	TTGACACAAA	AATCTTCTAG	ATTGACAGCA	780
GGAGTTGGTT	AA					792

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

AGTATCGGGT	TTTACTCCAC	GAGGAAGCAA	GGACAAGAAA	ACTTCCAAGA	AGAAAAATGAC	60
AGTAGACAAAG	TAATCTTAAC	GGTAACTCAG	ATTATTGAGA	GGCTTTATCC	TATGTTTTTG	120
GACATCGAGG	GCAAGCCTCT	TGATTTTTTG	GATTTGACGG	TACTTGAAAT	CAGAGAAATG	180
ATTGAAAGCT	ATAACCGTGT	CAAAATCCAA	GAGCGGTAA			219

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

AGAGGAGCAA	CTAGTTACGG	GGATTCTCCT	TACCAATCTT	TCTCAGCCTT	CGCAGGAAAC	60
ACTCATTTTA	TCGATTTAGA	TATCTTGGTG	GAGCAAGGTT	TGTTGGAAGC	AAGTGACCTT	120
GAAGGAGTTG	ACTTTGGTAG	CGATGCGTCT	GAAGTTGACT	ATGCTAAAAT	CTACTATGCA	180
CGTCGTCCTC	TTTTAGAAAA	AGCGGTGAAA	CGTTTCTTTG	AAGTCGGAGA	TGTTAAAGAT	240
TTTGAGAAAT	TTGCTCAAGA	CAACCAATCA	TGGCTTGAGC	TCTTTGCTGA	GTATATGGCT	300
ATCAAAGAGC	ATTTTGACAA	TCTTGCTTGG	ACTGAATGGC	CAGATGCAGA	TGCTCGTGCT	360
CGTAAAGCTT	CAGCACTTGA	AAGCTATCGT	GAGCAATTGG	CAGACAAGTT	GGTTTACCAC	420
CGTGTGACTC	AATACTTCTT	CTTCCAACAA	TGGTTGAAAT	TGAAAGCTTA	CGCTAACGAC	480
AACCACATCG	AAATCGTTGG	GGACATGCCA	ATCTACGTAG	CGGAAGATTC	AAGTGATATG	540
TGGGCAAATC	CACATCTCTT	CAAAACAGAT	GTCAATGGTA	AGGCTACTTG	TATCGCAGGA	600
TGCCCCACCAG	ATGAGTTTTC	TGTAACCTGGT	CAGCTTTGGG	GTAATCCAAT	CTATGACTGG	660
GAAGCAATGG	ACAAAGACGG	CTACAAATGG	TGGATTGAAC	GCTTGCGTGA	AAGCTTCAAA	720
ATCTACGATA	TCGTTTCGTAT	CGACCACTTC	CGTGGCTTCG	AATCTTACTG	GGAAATCCCT	780
GCTGGTTCCG	ATACAGCAGC	ACCTGGTGAG	TGGGTGAAAG	GTCCAGGCTA	CAAGCTTTTT	840
GCAGCCGTTA	AGGAAGAACT	TGGTGAGCTA	AACATCATCG	CAGAAGACCT	TGGCTTCATG	900
ACAGATGAAG	TGATCGAATT	GCGTGAACGT	ACTGGCTTCC	CAGGAATGAA	GATTCTTCAA	960
TTTGCCTTCA	ACCCAGAAGA	CGAAAGCAAT	GATAGCCAC	ACTTGGCACC	TGCTAACTCA	1020
GTTATGTACA	CAGGAACATA	CGATAACAA	ACGGTTCTTG	GTTGGTACCG	TAATGAGATT	1080
GATGATGCCA	CTCGTGAGTA	CATGGCTCGT	TACACGAACC	GTAAAGAATA	CGAAACAGTG	1140
GTACACGCTA	TGCTTCGTAC	AGTATTTTCA	TCAGTTAGCT	TTATGGCAAT	TGCAACTATG	1200
CAAGATTTAC	TAGAATTGGA	TGAGGCAGCT	CGTATGAACT	TCCCATCTAC	CCTTGGTGGA	1260
AACTGGTCTT	GGCGTATGAC	TGAAGATCAA	TTGACACCAG	CTGTCGAGGA	AGGTTTGCTT	1320
GACTTGACAA	CAATTTATCG	CCGAATTAAT	GAAAATTTGG	TAGATTTAAA	GAAATAA	1377

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

AAATTAGGGT	TGGGTTATCG	AACCAATCTT	TTTCTAAATA	ATACTTTTTC	TCATGCTCAG	60
ACATATAAGC	AATCAATGAC	TGAAAATGCT	TTATGCGTTC	ATGAAGATGT	TCTATATTTT	120
CTTTCATCCA	TCCTCCTACT	CCTTAAATTT	TTCCAAATAT	ATTTTTCGCT	TGTATATTTT	180
CAACATCAAT	CTTATTGA					198

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GTTGTTCAAA	CAAGAGGAAC	AGGCCTTAAA	TTCGTAAAGG	AGGTTATCAA	TTGGAACAT	60
GAGTCGTACA	ATTCTGGGCA	TGGGAGGAAA	TTCATATTCA	ANAGAATAAT	AGAAGCCAGA	120
CTGACAAATTT	CAAATTCACC	TTTTGTTTCA	AGACGNTATC	AGATAAAACC	TGAAGCTTTT	180
TATGTTTTAT	TTAAAGNATT	ANCAGCACCT	ATTCCACTTA	ATACTGATTT	TCCAATATTC	240
GCTGCAGATG	GGAGTGATAT	CNGTATTCCT	CGAAATCCCA	TGGATACAGA	AACCTNTATC	300
CAAACCCAAA	CGGATGTTAA	ATCCTATAAT	CTCATAACAC	TAAATGCCCT	ATACGACTTG	360
ACGACTGGAG	TGTATAGAGA	TGTCTCTATT	CAAGACAAAC	ATGCACAACA	TGAGCGCTTA	420
GCTCTGATTC	AGATGATGGA	GGCTTCTCCC	TTTCGAGAAA	GCTCTTGTTA	TCATGGATAG	480

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GATGGTCAAA	CAAATGCGTC	CAGGCTCTGT	ATCGTTGACC	TTGCTGTTGA	CCAAGGTGGC	60
CTTATCGAAA	CAGCTGACCG	TGTGACAACG	CACGATGAAC	CCGTCTATGA	AAAACACGGT	120
GTCTCTCACT	ATACCGTTGC	CAATATCCCT	GGTGCGGTTG	CTCGCACTTC	AACCATCGCC	180
CTAACCAATG	TACTCTTCC	TTATATCGAA	GCTTTGGCTG	GCAAAGGATT	CGCACAAAGCA	240
ATCTCTGAAG	ATGAAGGCTT	GCGTCAAGGT	GTGACCACTT	ATCAAGGTTA	CTTGACTAGC	300
CTACCAGTTG	CTCAAGGACT	TAATCGTGAC	TACACTGATA	TCAATGATTT	AGTATAA	357

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GTATGGCAAA	CTTATCGGAG	AACTCTTCTG	AGTTCGTCCA	AACCAGAGTT	ATCACAGAAA	60
ACTAACACGG	AGGAAAACAT	TATGTTAAAA	ATGACTCTTA	ACAACTTGCA	ACTTTTCGCC	120
CACAAAAAAG	GTGGAGGTTT	TACATCAAAC	GGACGTGATT	CACAAGCAAA	ACGTCTTGGA	180
GCTAAAGCAG	CTGACGGACA	AACTGTAACA	GGTGGATCAA	TCCTTTACCG	TCAACGTGGT	240
ACACACATCT	ATCCAGGTGT	AAACGTTGGT	CGTGGTGAG	ACGATACTTT	GTTCGCTAAA	300
GTTGAAGGCG	TAGTACGCTT	TGAACGTAAA	GGACGCGATA	AAAAACAAGT	TTCTGTATAC	360
CCAATCGCAA	AATAA					375

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...2421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

AGCTATAAAA	CAAGCTATAC	AAAGGATTTG	AGACGTTTGC	TTCAAGTCTT	TTTCTTTTGT	60
CCGAAACAGA	TATATAGTTT	CAAACCTATAT	CAAACCCTAA	TTTTTTTACAA	TTATACAGAC	120
GCTTTCCTTT	CTGTTAAGAT	AGTTTCAACA	ACAAATTTTG	GAGGACACAT	CATGTCAACT	180
ACAATCGTCG	GTTTCCCTCG	TTTGGGCGAA	TTCCGTGAAT	TAAAATTTAC	AACTGAAAAA	240
TACTTTAGAA	AAGAAATCTC	AGAAGAAGAA	CTTTTAGCAG	CAGCAAAAGA	CTTGCGTGCT	300
AAACACTGGA	ACATTGTCAA	AGAAAAAGGC	ATCACTGAAA	TTCCATCAAA	TGACTTTTCT	360
CACTATGATA	ACTTCCTAGA	TGCGGCTTTC	CTTTTCAACG	TGGTGCCCTG	ATCCGTTCAA	420
AACTTGGA	TGTCTGACCT	TGAGCGCTAC	TTCGCTTTGG	GACGTGGTTA	CCAGGGAGAA	480
AAAGGGGACG	TTGCGGCCCT	CCCAATGAAG	AAATGGTTTA	ACACTAACTA	CCACTACATC	540
GTTCTTAAAT	TTGAAAAAGA	CACTCAAGTA	AAATGGCTG	GTCACAAGAT	TTTTGATGAG	600
TTCCAAGAAG	CCAAAGAAAT	TGGATTGAAC	ACTCGTCTTG	TTCTTGTAGG	TCCCTTCACT	660
TTCTTCAAT	TGTCAGACTT	TGAAGAAGGC	GTGAAAGCAG	ACGACTTCGT	AGATAGCTTA	720
GTGGCTGCTT	ACCAAGAAAGT	TTTTGCTAAA	TTGGCTGAAC	TTGGTGCGAC	TTGCATCCAA	780
TTGGATGAAG	CGGCTCTTGT	AAAAGACTTG	ACAGCTGAAG	AAAAAGCTCT	CTTCTTGAAT	840
CTTTACAACA	AACTCTTGGC	TGACAAAAAA	GGTCTTGAAG	TCTTGCTTCA	AACTTATTTT	900
GGTGATGTTT	GTGACGTATA	CGCTGACCTT	GTAAACTTGC	CAGTAGATGC	TATCGGTTTT	960
GACTTTGTTG	AAGGTAAGAA	AACTCTTGAA	CTCGTTAAAG	GTGGCTTCCC	AGCTGACAAG	1020
ACTCTCTATG	CAGGTATTGT	CAATGGTAAA	AACATCTGGC	GCAACAACCTA	TGAAAAGAGC	1080
TTGGCTGTTT	TTGAGCAAAAT	CCCAGCTGAA	AACATCGTTT	TGACAAGCTC	TTGCTCACTT	1140
CTTCATGTGC	CATTTACAAC	TGCTAATGAA	GAAATTTGAA	CAGCACTCTT	GAACCACTTT	1200
GCCTTTGCGAG	TTGAAAAAAT	GGATGAAATC	CGTGACTTGG	ATGCTATCCG	CAATGGTCAA	1260
GGTTCAGAAG	CTCTTGCAAG	CAACAAAGAA	CTCTTTGCGA	CTGAGCGTGT	TGGTGAAAAAT	1320
GCTGAACTTC	GTGCGCGTAT	CGCTGGCTTG	ACAGACACAG	ACTACACTCG	TTTGCCAGCC	1380
TTTGCAAGAA	GTGAAGCTAT	CCAAGAAGAA	GCTTTCAAAC	TTCCAGCTCT	TCCAACAACA	1440
ACGATTGGTT	CATTCCCTCA	AACAAAAGAA	GTTTCGTGCCA	AACGTTTGGC	TTACCGTAAA	1500
GGTGAATTGT	CTCAAAAAGA	GTACGATGCT	TTCTTGCTG	AAACGATTGA	CGAATGGATC	1560
AAGTGGCAAG	AAGATATTGA	CTTTGATGTC	CTTGTTACAG	GTGAATTTGA	GCGTAATGAC	1620
ATGGTTGAGT	ACTTCGGTCA	AACTTGTCA	GGATACCTCT	TCTCTAAAAA	TGGATGGGTA	1680
CAATCATACG	GTATGCGTGG	GGTAAAACCA	CCAATCATCT	GGGGTGATGT	CACTCGTCTT	1740
AACCTATCA	CTGTTAAATG	GTCTAGCTAT	GCACAAAGTC	GTACAAACAA	ACCTGTTAAA	1800
GGTATGTTGA	CTGGACCTGT	TACCATCCTT	AACTGGTCAT	TCCCACGTGA	AGACATCTCT	1860
ATCAAGGATT	CAACTCTCCA	AAATCGCCCTT	GCTATCAAGG	ATGAAGTACT	TGACCTTGAA	1920
GCTGCTGGTG	TGAAAAATCAT	CCAAATCGAC	GAGGCTGCTC	TTCTGTGAAA	ATTGCCACTC	1980
CGCCGTAGCG	ACTGGTACGA	AGACTACCTT	GACTGGGCTA	TTCTGCTT	CCGCTTGGTA	2040
CACTCAACAG	TAGCGCCAGA	CACACAAATC	CACACTCACA	TGTGTTACTC	AGAAATTTACA	2100
GATATCATCC	CAGCTATCGA	TAACATGGAT	GCAGACGTTA	TTTCTTTTGA	AGCTAGCCGT	2160
TCAAACCTTG	AAATCTTGGA	CGAACTCAAA	GCGAAAAACT	TCCAAACAGA	AGTGGGACCT	2220
GGGGTTTACG	ATATCCACTC	ACCTCGTGTA	CCAAATGAAG	GCGAAATCGA	CAACACAATC	2280
GAAGCCATCC	TTGCTAAAGT	GCCAAGCAAG	AAAGTTTGGG	TCAACCCTGA	CTGTGGTTTG	2340
AAAACACGTG	GTATCCCAGA	AACAAAAGAA	AGCTTGATCC	GCCTTGTTGA	AGCAGCTAAA	2400
GCTGCGCGTG	AGAAATTGTA	A				2421

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TATGGTAAAA	CAAAATATAAA	TAGAAAGCGT	TTTCTTGAAT	GTTTATTTAA	GAAAGTAGTT	60
GGTTTTTTAC	ACTTTGTTAG	ACATCAGGAG	GAAAAACAAA	TGAGTGAAAA	AGCTAAAAAA	120
GGGTTTAAGA	TGCCTTCATC	TTACACCGTA	TTATTGATAA	TCATTGCTAT	TATGGCAGTG	180
CTAACTTGGT	TTATCCCTGC	GGGGGCCTTT	ATAGAAGGTA	TTTACGAGAC	TCAGCCTCAA	240
AATCCACAAG	GGATTTGGGA	TGTCCTCATG	GCACCGATTC	GGGCTATGCT	AGGTACTCAT	300
CCAGAGGAAG	GTTCCGTCAT	TAAAGAAACG	AGCGCAGCGA	TTGATGTAGC	CTTCTTTCATC	360
CTTATGGTTG	GGGGTTTCCT	TGGCATTGTC	AACAAAAC TG	GTGCTCTTGA	CGTAGGGATT	420
GCCTCTATCG	TGAAGAAGTA	TAAGGGCCGC	GAAAAAATGT	TAATTTTGGT	ACTGATGCCT	480
TTGTTTGCCC	TCGGTGGTAC	AAC TTATGGT	ATGGGGGAAG	AAACAATGGC	CTTCTATCCA	540
CTCCTTGTC	CAGTTATGAT	GGCCGTTGGT	TTTGATAGCC	TGACTGGTGT	TGCAATTATT	600
TTGCTCGGTT	CTCAAAATCGG	CTGTTTGCCA	TCTACTCTGA	ATCCATTTCG	GACAGGTATT	660
GCTTCAGCGA	CTGCGGGAGT	TGGTACAGGG	GACGGTATCG	TACTTCGTCT	GATCTTCTGG	720
GTTACCTTGA	CTGCTCTTAG	TACTTGTTTT	GTTTACCGTT	ATGCGGATAA	GATTCAAAAA	780
GATCCGACTA	AGTCACTGGT	TTATAGTACT	CGCAAAGAAG	ATTTGAAACA	CTTTAACGTA	840
GAAGAATCTT	CATCTGTAGA	ATCTACACTT	AGCAGCAAAC	AAAAATCAGT	TCTCTTCTTA	900
TTTGTGTTGA	CATTCACTTT	GATGGTATTG	AGCTTCATTC	CATGGACAGA	CCTTGGCGTT	960
ACCATTTTTG	ATGACTTTAA	TGCTTGTTTG	ACTGGTCTTC	CAGTTATTGG	TAATATTGTC	1020
GGTTCATCTA	CTTCTGCACT	AGGTACTTGG	TACTTCCCAG	AAGGCGCAAT	GCTCTTTGCC	1080
TTTATGGGTA	TCCTGATTGG	TGTTATTTAT	GGTCTTAAAG	AAGATAAGAT	TATCTCTTCC	1140
TTCATGAATG	GTGCTGCTGA	CTTGCTCAGT	GTTGCCTTGA	TCGTAGCGAT	TGCTCGTGGT	1200
ATTCAAGTTA	TCATGAACGA	CGGTATGATT	ACCGATACAA	TCCTCAACTG	GGGTAAAGAA	1260
GGCTTGAGCG	GTCTATCTTC	ACAAGTCTTT	ATCGTTGTAA	CTTATATCTT	CTATCTACCT	1320
ATGTCAATCT	TGATCCCATC	TTCATCTGGT	CTTGCCAGCG	CAACTATGGG	TATCATGGCT	1380
CCACTTGAGG	AATTTGTAAA	TGTCCGTCCT	AGCTTGATTA	TCACTGCTTA	CCAATCTGCT	1440
TCAGGTGTCT	TGAAC TTGAT	TGCACCAACA	TCTGGTATTG	TGATGGGAGC	TCTTGCACTT	1500
GGACGTATCA	ACATTGGTAC	TTGGTGGAAA	TTCATGGGCA	AACTCGTAGT	CGCTATTATT	1560
GTAGTGACCA	TCGCCCTTCT	TCTCCTTGGA	ACCTTCCTTC	CATTCCCTATA	A	1611

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

AAATCCAAAA	CACAAGGCAT	GAAATTTATC	AAAAAACTCC	ATAAAATTAT	CCTCCTCAAC	60
AAACAGACTT	CCTACACGTC	ATTCTTTAGT	TCTAGCCTTT	CCAAAACAAA	CCATTTTATA	120
CTCTTCGAAA	ATCAAATTCA	AACCACGTCA	ACGTCGCCTT	GCCGTACTCA	AGTACAGCCT	180
GCGGCTAGTT	TCCTAGTTTG	CTCTTTGATT	TTCATTGAGT	ATTAG		225

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

ATTCCAAAAA	CAAAAACGTT	AGCGGAACTA	GCAGATGTGA	TTTTATGGAG	TTTCGATTTT	60
GTAAATGCTC	ATGCTCACGC	ATTTTTCATG	GATAATGTTG	AGTGGAGTCA	TGCAGATTCT	120
TACTTTCTTA	GCTTTGTTAG	TGACGATGTT	GAAGAACGTT	ACACAGAAAA	TGTCTATCTG	180
GATAGCCTAA	GTGTCAAACA	AAAATTTAAG	TTTCTTTTCG	ACTTCGGTGA	TGAATGGCGT	240
TTTGAATGCC	AAGTACTGAG	AGAAATCGAG	ACAGAGGACG	AAGAAGCTTA	TCTCGTACGT	300
TCGGTTGGAA	CGTCGCCAGA	ACAATATCCA	GATTATGATG	GTTTTGACTA	TGAAGAATGG	360
TAA						363

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1926 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ATGAAAAAAAA	CTACAATATT	ATCATTAACT	ACAGCTGCGG	TTATTTTAGC	AGCATATGTC	60
CCTAATGAAC	CAATCCTAGC	AGATACTCCT	AGTTCGGAAG	TAATCAAAGA	GACTAAAGTT	120
GGAAGTATTA	TTCAACAAAA	TAATATCAAA	TATAAGGTTT	TAACTGTAGA	AGGTAACATA	180
AGAACTGTTT	AAGTGGGTAA	TGGAGTTACT	CCTGTAGAGT	TTGAAGCTGG	TCAAGATGGA	240
AAACCATTTCA	CGATTCCCTAC	AAAAATCACA	GTAGGTGATA	AAGTATTTTAC	CGTTACTGAA	300
GTAGCTAGTC	AAGCTTTTAG	TTATTATCCA	GATGAAACAG	GTAGAATTGT	CTACTATCCT	360
AGCTCTATTA	CTATCCCATC	AAGCATAAAA	AAAATACAAA	AAAAAGGCTT	CCATGGAAGT	420
AAAGCTAAAA	CTATTATTTT	TGACAAAGGC	AGTCAGCTGG	AGAAAAATTGA	AGATAGAGCT	480
TTTGATTTTT	CTGAATTAGA	AGAGATTGAA	TTGCCTGCAT	CTCTAGAATA	TATTGGAACA	540
AGTGCATTTT	CTTTTAGTCA	AAAAATTGAAA	AAGCTAACCT	TTTCCTCAAG	TTCAAAATTA	600
GAATTAATAT	CACATGAGGC	TTTTGCTAAT	TTATCAAATT	TAGAGAAACT	AACATTACCA	660
AAATCGGTTA	AAACATTAGG	AAGTAATCTA	TTTAGACTCA	CTACTAGCTT	AAAACATGTT	720
GATGTTGAAG	AAGGAAATGA	ATCGTTTGCC	TCAGTTGATG	GTGTTTTGTT	TTCAAAAGAT	780
AAAACTCAAT	TAATTTATTA	TCCAAGTCAA	AAAAATGACG	AAAGTTATAA	AACGCCTAAG	840
GAGACAAAAG	AACTTGCATC	ATATTCGTTT	AATAAAAAAT	CTTACTTGAA	AAAACTCGAA	900
TTGAATGAAG	GTTTAGAAAA	AATCGGTACT	TTTGCAATTTG	CGGATGCGAT	TAAACTTGAA	960
GAAATTAGCT	TACCAAATAG	TTTAGAAACT	ATTGAACGTT	TAGCCTTTTA	CGGTAATTTA	1020
GAATTAAAAAG	AACTTATATT	ACCAGATAAT	GTTAAAAAAT	TTGGTAAACA	CGTTATGAAC	1080
GGTTTACCAA	AATTAAAAAAG	TTTAACAATT	GGTAATAATA	TCAACTCATT	GCCGTCCTTC	1140
TTCTTAAGTG	GCGTCTTAGA	TTTCAATAAG	GAAATTTCATA	TTAAGAATAA	AAGTACAGAG	1200
TTTTCTGTGA	AAAAAGATAC	ATTTGCAATT	CCTGAAACTG	TTAAGTTCTA	TGTAACATCA	1260
GAACATATAA	AAGATGTTCT	TAAATCAAAT	TTATCTACTA	GTAATGATAT	CATTGTTGAA	1320
AAAGTAGATA	ATATAAAACA	AGAAACTGAT	GTAGCTAAAC	CTAAAAAGAA	TTCTAATCAG	1380
GGAGTAGTTG	GTTGGGTTAA	AGACAAAGGT	TTATGGTATT	ACTTAAACGA	ATCAGGTTCA	1440
ATGGCTACTG	GTTGGGTTAA	AGACAAAGGT	TTATGGTATT	ACTTAAACGA	ATCAGGTTCA	1500
ATGGCTACTG	GTTGGGTTAA	AGACAAAGGC	TTATGGTATT	ACTTAAACGA	ATCAGGTTCA	1560
ATGGCTACTG	GTTGGGTTAA	AGACAAAGGC	TTATGGTATT	ACTTAAATGA	ATCAGGTTCA	1620
ATGGCTACTG	GTTGGGTTAA	AGACAAAGGC	TTATGGTATT	ACTTAAACGA	ATCAGGTTCA	1680
ATGGCTACTG	GTTGGGTTAA	AGACAAAGGC	TTATGGTATT	ACTTAAACGA	ATCAGGTTCA	1740
ATGGCTACTG	GTTGGGTTAA	AGACAAAGGC	TTATGGTATT	ACTTAAATGA	ATCAGGTTCA	1800
ATGGCTACTG	GTTGGTTTAC	AGTTTCTGGT	AAATGGTACT	ATACCTATAA	TTCAGGAGAT	1860
TTATTAGTAA	ACACGACTAC	ACCCGATGGC	TATCGAGTCA	ATGCTAACGG	TGAGTGGGTA	1920
GGATAG						1926

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

TGTAGAAAAA	CAGCTAAAGG	AAAGACTATG	AAACCACTAC	TTGAAACCAT	CGATACCCGC	60
TTTGGAAC TA	CCAACAAGCA	TGCCTTTTCT	CGGGGAAATA	CCCTGCCATA	CACAGGCGTG	120
CCTTTTGGGA	TGAATTATTT	TGTGCCCCAG	ACCAGTGACC	AGGACGGAGC	TTGGTTCTTC	180
GATCCGCATC	TGCCTATCTT	TCAGGGGATT	CGATTAACTC	ACCAGCCCAG	TCCTTGGATT	240
GGGGACTACT	CTTGCTCCT	TCTGACACCT	GTCACCAGTC	AACTGGGTGA	AGACAGTCTC	300
TTTCACCGCC	AGTCTTCCTA	TAATAGGGAT	AAGGCCTCTT	TCCAACCTCA	TTATCTAAAG	360
ATTTTCTCCC	TGCGCTATCA	GATTGAAACC	CAGCTCACAC	CGACTTGCTA	CGGTGCTTCT	420
ATTCGTTTGA	AGCAAAAGCA	AGGCAAAGCC	TCTCCCTCTA	TCTTCACGCA	ACAGATGAAC	480
TGA						483

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1965 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GGTAGAAAAA	CGATGAAAAT	TCAAGATTTA	TTGAGAAAAG	ATGTCATGTT	GCTGGATTTG	60
CAGGCAACTG	AAAAGACTGC	TGTCATTGAA	GAGATGATTA	AAAGCCTAAC	AGGCCACGGT	120
TATGTGACAG	ATTTTGAAAC	CTTTAAAGAA	GGCATTTTGG	CGCGTGAAGC	TTTAACTTCT	180
ACTGGTTTGG	GTGATGGAAT	CGCTATGCCT	CACAGCAAAA	ACGCTGCTGT	CAAAGAAGCG	240
ACAGTTCTCT	TTGCTAAGTC	AAACAAGGGT	GTTGACTATG	AGAGTTTGGA	TGGGCAGGCA	300
ACTGACCTCT	TCTTCATGAT	TGCAGCTCCA	GAAGGTGCCA	ATGATACTCA	CTTGGCAGCA	360
TTGACAGAAT	TGTCTCAATA	CTTGATGAAA	GACGGTTTTG	CAGACAAACT	TCGTCAAGCA	420
ACATCTGCAG	ACCAAGTTAT	CGAACTTTTT	GACCAAGCTT	CAGAAAAAAC	TGAGGAACTT	480
GTTCAAGCAC	CTGCTAATGA	CTCTGGTGAC	TTTATCGTAG	CTGTTACAGC	TTGTACAACA	540
GGTATTGCCC	ACACTTACAT	GGCCCAAGAA	GCCCTTCAAA	AAGTAGCTGC	TGAAATGGGG	600
GTTGGTATCA	AGGTCGAAAC	CAACGGTGCT	AGCGGTGTTG	GAAATCAACT	AACTGCAGAA	660
GATATCCGTA	AGGCTAAAGC	TATTATCATT	GCAGCAGACA	AGGCCGTTGA	AATGGATCGT	720
TTGATGGCA	AACCTTTGAT	CAATCGTCCA	GTTGCTGACG	GTATCCGTAA	GACAGAAGAA	780
TTGATCAACT	TGGCTATTTT	AGGAGATGCG	GAAGTCTACC	GTGCCGCTAA	TGGTGCCAAA	840
GTCGCAACAG	CCTCTAACGA	AAAACAAAGC	CTTGGTGGTG	CCTTCTACAA	ACACTTGATG	900
AGTGGTGTAT	CTCAAATGTT	ACCATTTCGT	ATCGGTGGTG	GTATCATGAT	TGCCCTTGCC	960

TTCTTGATTG	ACGGTGCTTT	GAGTGTTCCA	AATGAAAACC	TTGGCAATCT	TGGTTCTTAC	1020
CATGAGTTAG	CTTCTATGTT	CATGAAAATT	GGTGGAGCTG	CCTTTGGTTT	GATGCTTCCA	1080
GTCTTTGCGG	GTTATGTTGC	CTACTCTATT	GCTGAAAAAC	CAGGTTTGGT	AGCAGGTTTC	1140
GTGGCTGGTG	CTATTGCCAA	AGAAGGTTTT	GCCTTTGGTA	ATATTCCCTA	TGCCGCAGGT	1200
GGTGAAGCAA	CTTCAACTCT	TGCAGGTGTC	TCATCTGGTT	TCCTAGGTGC	CCTTGTTGGT	1260
GGATTTATCG	CAGGTGCCTT	GGTTCTTGCC	ATCAAGAAAT	ACGTTAAAGT	TCCTCGTTCA	1320
CTCGAAGGTG	CTAAATCAAT	CCTTCTATTG	CCACTTCTTG	GAACAATCTT	GACAGGATTT	1380
GTTATGCTAG	CTGTGAATAT	CCCAATGGCA	GCAATCAACA	CTGCTATGAA	TGACTTCCTA	1440
GGCGGTCTTG	GAGGAGGTTC	AGCTGTCTTA	CTTGGTATCG	TCCTTGGTGG	AATGATGGCT	1500
GTTGACATGG	GTGGACCACT	TAATAAAGCA	GCTTATGTCT	TTGGTACAGG	TACGCTTGCA	1560
GCAACTGTTT	CTTCAGGTGG	TTCTGTAGCC	ATGGCAGCAG	TTATGGCTGG	AGGAATGGTG	1620
CCACCACTTG	CAATCTTTGT	CGCAACTCTT	CTTTTCAAAG	ATAAATTTAC	TAAGGAAGAA	1680
CGTAACTCTG	GTTTGACAAA	CATCATCATG	GGCTTGTCT	TTATCACTGA	GGGAGCGATT	1740
CCATTTGGTG	CCGCTGACCC	AGCTCGTGCG	ATTCCAAGCT	TCATCCTTGG	TTCAGCAGTA	1800
GCAGGTGGAC	TCGTTGGTCT	TACTGGTATC	AAACTCATGG	CGCCACACGG	AGGAATCTTC	1860
GTTATCGCCC	TTACTTCAAA	TGCTCTCCTT	TACCTCGTTT	CTGTCTTGGT	AGGAGCAATC	1920
GTAAGTGGTG	TGTTTATGG	TTACCTACGC	AAACCACAAG	CATAA		1965

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

AAAAGAAAAA	CCTGGGGTCT	TGTACTCTTC	GAAAATCTCT	TCAAACCGCG	TCAACGTCGC	60
CTTGCCGTAT	GTAGGTTACT	GACTTCGTCA	GTTCTATCTA	CAACCTCAAA	GCAGTGCTTT	120
GAGCAGCCTG	CGGCTAGTTT	CCTAGTTTGC	TCTTTGATTT	TCATTGAGTA	TTGGCCTCAG	180
GTTTCCATTT	GCAATCAGAA	AGGGATTTTA	TGTCCATTAT	TCAAAAACCTT	TGGTGGTTTTT	240
TCAAGTTAG						249

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

AAAATGAAAA	CTAAGAAATT	ATTGAAAATG	GTTATTCCTG	TTTAAATGAT	AAGTGCTGTT	60
GGAACACTTT	TCGTAGAAGC	AAATCAGATA	GGTGCTTTTA	GTAATTTTGT	TATTACTACC	120
AGTTATAAGA	GAACAGGTTA	TTTGACTAAA	GAAAATGAAG	GTGCGGAATA	TATCATGAAC	180
TTAAATCCTT	GTAGAAATTT	ACATCCCATG	ACTGTTAAGC	ATCGTATAGT	AAATTCTAAT	240
GGAGAAGCTC	GTAGTGGAGA	ATCGTTAACA	ACCTGTGGTA	CTCGTTCAAC	TCATGGTAAT	300
TGGGCAACGG	TTGGCTATGT	TTATGCAGCA	GATATGGCAA	GACAAAAATTG	GTGGGATTTA	360
TCAGCTGCCA	TTTCAGGTAG	TTGGTCACCA	AATTAA			396

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

AAGGAGAAAA	CTGAAATGAT	TCAAACAGAA	ACTCGTTTGA	AAGTCGCAGA	CAACAGCGGT	60
GCTCGCGAAA	TCTTGACTAT	CAAAGTTCTT	GGTGGTTCAG	GACGTAAATT	TGCAAACATC	120
GGTGATGTTA	TCGTGGCATC	TGTAAACAA	GCTACTCCTG	GTGGTGCGGT	TAAAAAAGGT	180
GACGTTGTTA	AAGCAGTTAT	CGTTCGTACT	AAATCAGGTG	CTCGTCGTGC	TGATGGTTCA	240
TACATCAAAT	TTGACGAAAA	CGCAGCAGTT	ATCATCCGTG	AAGACAAAAC	TCCTCGCGGA	300
ACACGTATCT	TTGGCCAGT	TGCACGTGAA	TTGCGTGAAG	GTGGCTTCAT	GAAGATCGTG	360
TCACTTGCTC	CAGAAGTACT	TTAA				384

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

ATGTCTGAAA CTATCTTAGA AATCAAGGAA CTAAAAAAT CCTTCGGAGA CAATCCCATC	60
CTCCAAGGAC TTTCTCTAGA AATCAAAAAA GGGGGAAGTT GTTGTTCATCC TAGGGGCATC	120
TGGTTGTGGG AAAAGTACCC TCCTTCGTTG CCTCAACGGC TTAGAAAAGTA TTCAAGGTGG	180
AGATATTCTT CTGGATGGTC AGTCTATCGT TGA	213

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...447
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

ATTGATGAAA CAGGATTCGA TACTTATTTT TATCGAGAAT ATGGTCGCTC ATTAAAAGGT	60
CAGTTAAGAA GAGGTAAAGT ATCTGGAAGA AGATATCAGA GGATTTCTTT GGTTCAGGT	120
CTAACAAATG GTGAGTTAAT CGCTCCAATG ACTTACGAAG AGATGATGAC GAGCGACTTT	180
TTTGAAGCTT GGTTCAGAA GTTCTCTTA CCAACATTAA CCACACCATC GGTATTATT	240
ATGGATAATG CAAGATTCCA TAGAATGGGT AAGTTAGAAC TTTTATGCGA GGAGTTTGGG	300
CATAAACTTT TATCTCTTCC TCCCTACTCA CCTGAGTACA ATCCTATTGA GAAAACATGG	360
GCTCATATCA AAAAGCACCT CAAAAGGTA TTACCAAGTT GCAATACCTT TTATGAGGCT	420
CTTTTGTCCT GCTCTTGTTT CAATTGA	447

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

ATTGATGAAA	CAGGATTCTGA	TACTTATTTT	TATCGAGAAT	ATGGTCGCTC	ATTAAAAGGT	60
CAGTTAAGAA	GAGGTAAAGT	ATCTGGAAGA	AGATATCAGA	GGATTTCCTT	GGTTGCAGGT	120
CTAACAAATG	GTGAATTAAT	CGCTCCAATG	ACTTACGAAG	AGATGATGAC	GAGCGACTTT	180
TTTGAAGTAT	GGTTTCAGAA	GTTTTCTTA	CCAACATTAA	CCACACCATC	GGTTATTATA	240
GTAAAATGA						249

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...447
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

ATTGACGAAA	CAGGATTCTGA	TACTTATTTT	TATCGAGAAT	ATGGTCGCTC	ATTAAAAGAT	60
CAGTTAATAA	GAGGCAAAGT	ATCTGGAAGA	AGATATCAGA	GGATTTCCTT	GGTTGCAGGT	120
CTAACAAATG	GTGAGTTAAT	CGCTCCAATG	ACTTACGAAG	AGACGATGAC	GAGCGACTTT	180
TTTGAAGCTT	GGTTTCAGAA	ATTTCTCTTA	CCAACATTAA	ACACACCATC	GGTTATTATT	240
ATGGATAATG	CAAGATTCCA	TAGAATGGGG	AAGCTAGAAC	TCTTGTGTGA	AGAGTTTGGG	300
TATAAACTTT	TACCTCTTCC	TCCCTACTCA	CCTGAGTACA	ATCCTATTGA	GAAAACATGG	360
GCTCATATCA	AAAAGCACCT	CAAAAGGGTA	TTACCAAGTT	GCAATACCTT	TTATGAGGCT	420

CTTTTGTCTT GTTCTTGTTC CAATTGA

447

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

ATTGACGAAA CAGGATTCGA TACTTATTTT TATCGAGAAT ATGGTCGCTC ATTA AAAAGGT	60
CAGTTAAGAA GAGGCAAAGT ATCTGGAAGA AGATATCAGA GGATTTCTTT GGTTGCAGGT	120
CTAACAAATG GTGAGTTAAT CGCTCCAATA ACTTACGAAG AGATGATGAC GAGCGACTTT	180
TTTGAAGCTT GGTTTCAGAA GTTCTCTTA CCAACATTAA CCACACCATC GGTTATTATT	240
ATGGATAATG CAAGATTCCA TAGAATGGGG AAGCTAGAAC TTTTATGCGA AGAGTTTGGG	300
CATAAACTTT TACCTCTTCC TCCCTACTCA CCTGAGTACA ATCCTATTGA GAAAACATGG	360
GCCCATATCA AAAAGCACCT CAAAAAGGTA TTACCAAGTT GTTGCAATAC CTTTACGAG	420
GCTCTTTTGT CCTGCTCTTG TTTCAATTGA	450

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

TATGAAGAAA	CAAGTGGAGA	AAGCAGAGAA	TTTAATATGA	AAAAACGGGC	TATTCAAATT	60
TTACTAGCAT	TGTCCTTAAT	TTTTTACAAA	TCAACTTGGT	TTTGGAGAGT	TTTCAATCAC	120
CTCGCAAAGC	CCTATCTACC	AGCAAGTCGT	GAATTTTTTC	AGATTCTGCT	TTTGATGGAG	180
AGCGGAGTTC	TTTTCTTAGC	GGTCATCTAT	CTACTGGTTT	TTGCAGGAAA	GAAAATTTTT	240
CATTTCAAGT	GGCAGCTGAG	GTACTTCATC	TACCTTTTAC	TGGGCTACAT	CATTTTCATAT	300
ATGTCTGACT	TCCTCTTTTC	GTATTTTCATA	TCCCTGTCTT	CAAATCAGAT	TTCTCTGAAT	360
GAAACGGTAG	AAATGATGGG	GAGACAGGAG	TTCCCTTATT	TCTTGCTCAT	CGTTTGCTTC	420
ATCGCCCCTA	TTGCTGAGGA	ATTGATTTAT	CGAGGTGTGC	TTATGACAAC	CTTTTTTCAA	480
AACTCACCTT	GGTACGGAGA	TGTTTTTGCTT	TCTGCTATTA	TTTTTCGGTTA	TATTCATATC	540
AATTTTGCTT	TAACTCCTCT	TGCTTTTTTTC	ATTTATGCTA	GTGGAGGTCT	TATTTTAGCT	600
CTATTGTATC	GCATGACTAA	AAATCTCTAC	TATCCAATAC	TAGTTCATAT	TCTCATCAAT	660
ATCACTGCCT	TCTGGGATGT	TTGGTTACTC	CTATTTTCAG	GAAGTTAG		708

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1077 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1077
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GATAGAGAAA	CCGAGAGGAC	AAACATGAAA	CTAAAAAGTT	ATATTTTGGT	TGGATATATT	60
ATTTCAACCC	TCTTAACCAT	TTTGGTTGTT	TTTTGGGCTG	TTCAAAAAAT	GCTGATTGCG	120
AAAGGCGAGA	TTTACTTTTT	GCTTGGGATG	ACCATCGTTG	CCAGCCTTGT	CGGTGCTGGG	180
ATTAGTCTCT	TTCTCCTATT	GCCAGTCTTT	ACGTCGTTGG	GCAAAC TCA	GGAGCATGCC	240
AAGCGGGTAT	CGGCCAAGGA	TTTTCTTCA	AATTTGGAGG	TTCAAGGTCC	TGTAAAATTT	300
CAGCAATTAG	GGCAAAC TTT	TAATGAGATG	TCCCATGATT	TGCAGGTAAG	CTTTGATTCC	360
TTGGAAGAAA	GCGAACGAGA	AAAGGGCTTG	ATGATTGCCC	AGTTGTGCGA	TGATATTAAG	420
ACCCCTATCA	CTTCGATCCA	AGCGACGGTA	GAAGGGATTT	TGGATGGGAT	TATCAAGGAG	480
TCGGAGCAAG	CTCATTATCT	AGCAACCATT	GGACGCCAGA	CGGAGAGGCT	CAATAAACTG	540
GTTGAGGAGT	TGAATTTTTT	GACCCTAAAC	ACAGCTAGAA	ATCAGGTGGA	AACTACCAGT	600
AAAGACAGTA	TTTTTCTGGA	CAAGCTCTTA	ATTGAGTGCA	TGAGTGAATT	TCAGTTTTTG	660
ATTGAGCAGG	AGAGAAGAGA	TGTCCACTTG	CAGGTAATCC	CAGAGTCTGC	CCGGATTGAG	720
GGAGATTATG	CTAAGCTTTC	TCGTATCTTG	GTGAATCTGG	TCGATAACGC	TTTTAAATAT	780
TCTGCTCCAG	GAACCAAGCT	GGAAGTGGTG	ACTAAGCTGG	AGAAGGGCCA	GCTTTC AATC	840
AGTGTGACCG	ATGAAGGGCA	GGGCATTGCC	CCAGAGGATT	TGGAAAAATAT	TTTCAAACGC	900
CTTTATCGTG	TCGAAACTTC	GCGTAACATG	AAGACAGGTG	GTCATGGATT	AGGACTTGCG	960
ATTGCGCGTG	AATTGGCCCA	TCAATTGGGT	GGGGAAATCA	CAGTCAGCAG	CCAGTACGGT	1020
CTAGGAAGTA	CCTTTACCCT	CGTTCTCAAT	CTCTCTGGTA	GTGAAAAATA	AGCCTAA	1077

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

AATATGGAAA	CTAGTATCAG	CATGGCTGAC	TTTTATGGAA	AATACCAAAA	TGAAAATCTA	60
GAACTTATCG	ATGTCCGTGA	AGCACATGAA	TTCCAAGCAG	GACATGCACT	AGGTGCCAAA	120
AATCTTCCAT	TAAGTACCTT	AGAAGCAAGC	TACAAAGAAC	TCAAACCTGA	CCATGAATAC	180
TATGTCATTT	GTCAAGGAGG	AGTCCGCTCT	GCATCTACCT	GCCAGTTTCT	CAGCTCCCAA	240
GGCCTCACCG	TTACCAACGT	AGAAGGTGGT	ATGAATGCTT	GGCCCGGTCA	AGTAAAATAA	300

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1020 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1020
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

AGTGAGGAAA	CTAGGATGAA	AGAGATTATT	GAAAAACTAG	CAAAATTTGA	AAATTTATCA	60
GGTGTGGAAA	TGACGGATGT	CATTGAGCGT	ATCGTAACTG	GGCGTGTAAC	TGAAGCGCAG	120
ATTGCTTCTC	TCCTCTTAGC	TCTTAAGATG	AAGGGGGAAA	CACCTGAAGA	ACGCACAGCC	180
ATTGCCCCAAG	TCATGAGAGG	ACATGCCCCAG	CATATTCCAA	CTGAGATTCA	TGATGCCATG	240
GACAACTGTG	GTACAGGTGG	GGACAAAGTCT	TTCAGTTTTA	ATATTTCCAC	AACTGCAGCC	300
TTTGTCTTGG	CTGGTGCGG	TATTCACATG	GCCAAGCATG	GTAATCGCTC	GATTTCTTCT	360
AAATCTGGTT	CCGCAGATGT	CCTCGAAGCC	TTGGGAATCA	ATCTTGACCT	CAAACCAGCT	420

GAACTAGGTA	AGGTCTTTGA	TAAAACTGGA	ATCGTCTTTC	TCTTCGCTAA	AAATATGCAC	480
CCAGCTATGA	AATACATCAT	GCCAGCTCGT	TTGGAATTGG	GAATTCCAAC	GATTATGAAC	540
TTGACTGGTC	CACTGATTCA	TCCAATGGCT	TTAGAAACAC	AGCTTCTTGG	AATTAGTCGT	600
CCAGAACTCC	TAGAAAGTAC	AGCTCAGGTT	TTGAAAAATA	TGGGTCGCAA	ACGTGCCATC	660
GTGGTTGCTG	GACCAGAAGG	GTTGGATGAA	GCTGGCTTGA	ACGGAACAAC	CAAGATTGCA	720
CTTCTTGAAA	ATGGCGAAAT	CAGCTTGTCA	AGCTTTACTC	CAGAGGATTT	GGGAATGGAA	780
GGCTATGCTA	TGGAAGATAT	TCGTGGTGGG	AATGCTCAGG	AAAATGCAGA	AATTTTGCTT	840
AGCGTTCTGA	AAAACGAAGC	AAGTCCATTC	TTGGAAACGA	CAGTCTTGAA	TGCTGGTCTT	900
GGTTTCTATG	CTAATGGTAA	GATTGATAGC	ATCAAGGAAG	GAGTTGCCTT	GGCCCCGCAA	960
GTGATTGCTA	GAGGCAAGGC	CCTTGAAAAA	CTCAGACTGT	TACAGGAGTA	CCAAAAATGA	1020

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

AATTGGAGAA	CTAAGACCAT	GATTTTATTG	ATTGACAACT	ATGATTCTTT	TACCTATAAC	60
TTGGCCCAAT	ACATTGGGAA	TTTTCAGAA	GTTTCAGGTT	TGAGAAATGA	TGATTCCAAG	120
CTGTATGAAG	AAGCTGAAAA	AGCAGATGGT	CTGGTCTTTT	CTCCTGGTCC	TGGTTGGCCA	180
GTTGATGCTG	GAAAGATGGA	AGACATGATT	CGTGATTTTG	CAGGCAAGAA	GCCGATTCTA	240
GGGATTTGTT	TGGGTCACCA	AGCCATTGCA	GAAGTCTTTG	GTGGTAAGCT	AGGTTTGGCT	300
CCAAAAGTCA	TGCATGGGAA	ACAGAGCAAT	ATTAACTTTG	AAGCGCCATC	TGTTTTGTAT	360
CAAGGTATTG	AGGATGGCCG	TGCGGTCATG	CGTTATCACA	GTATTTTGAT	TGAGGAAATG	420
CCAGAAGACT	TTGAAGTGAC	AGCTCGTTTC	ACTGATGACC	AAGCCATCAT	GGGGATTCAA	480
CATAAAAACC	TACCGATTTA	TGGCTTCCAG	TACCATCCAG	AGAGCATTGG	AACGCCAGAC	540
GGCTTGTCTT	CTATTTCGAA	TTTATCGAG	AAGGTTGTAA	AGTGA		585

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2667 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

TTAAGGAGAA	CACACATGTC	TAAAGAACTT	TCATCTAAAT	ACAATCCAGC	CGAGGTTGAG	60
GCTGGTCGTT	ACCAAAAAATG	GCTTGATGCT	GATGTTTTCA	AGCCTTCAGG	CGATCAAAAG	120
GCTAAGCCTT	ATTCAATCGT	TATTCCACCA	CCAAACGTTA	CAGGTAAACT	TCACCTTGGT	180
CACGCTTGGG	ATACAACTTT	GCAAGATAAT	ATCATCCGTC	AAAAACGCAT	GCAAGGTTTT	240
GATACCTTTT	GGCTTCCTGG	GATGGACCAC	GCAGGGATTG	CCACTCAGGC	TAAGGTAGAG	300
GAGCGCTTGC	GTGGTGAGGG	CATTTCCCGC	TATGACCTTG	GTCGTGAGTC	TTTCTTGACG	360
AAAGTCTGGG	AATGGAAAAG	CGAATATGCC	ACTACTATCA	AGGAACAATG	GGGCAAGATG	420
GGGCTCTCTG	TAGACTACTC	TCGTGAGCGT	TTCACTCTTG	ACGAAGGTTT	GTCAAAAGCT	480
GTTCTGTAAG	TCTTTGTGGA	CCTTTACAAG	AAAGGCTGGA	TCTACCGTGG	TGAGTTTATC	540
ATCAACTGGG	ACCCAGCAGC	TCGCACAGCC	CTTTCTGATA	TTGAGGTGAT	TCACAAGGAT	600
GTCGAAGGTG	CCTTCTACCA	CATGAACTAC	ATGCTGGAAG	ATGGTTTACG	CGCCCTTGAA	660
GTTGCTACAA	CTCGTCCTGA	GACTATGTTT	GGGGACGTTG	CGGTTGCGGT	TAATCCAGAA	720
GACCCGCGCT	ACAAGGACTT	GATTGGTAAA	AACGTCATCC	TTCCAATCGC	TAATAAACTC	780
ATCCCAATCG	TTGGAGATGA	GCACGCAGAT	CCTGAGTTTG	GTACTGGTGT	CGTGAAAATC	840
ACACCTGCCC	ACGATCCAAA	TGACTTCTTG	GTTGGCCAAC	GTCATAACTT	GCCACAAGTC	900
AACGTCATGA	ACGACGACGG	AACATATGAAT	GAGCTTGCCCT	TTGAATTTTC	AGGCATGGAT	960
CGTTTTGAAG	CTCGTAAGGC	AGTCGTTGCT	AAGTTGGAAG	AAATCGGTGC	CCTTGTCAAA	1020
ATCGAAAAAC	GTGTCCATTC	AGTCGGTCAC	TCAGAACGGA	CAGGTGTCGT	AGTTGAGCCA	1080
CGCTTGCTTA	CTCAATGGTT	CGTCAAGATG	GACCAATTGG	CTAAGAACGC	CATTGCCAAC	1140
CAAGACACAG	AGGACAAGGT	CGAATTCTAC	CCACCTCGTT	TCAACGATAC	CTTCCTTCAA	1200
TGGATGGAAA	ATGTCCACGA	CTGGGTTATC	TCTCGTCAGC	TTTGGTGGGG	TCACCAAATC	1260
CCTGCCTGGT	ACAAATGCTGA	TGGTGAAATG	TATGTCGGCG	AAGAAGCTCC	AGAAGGTGAC	1320
GGATGGACTC	AGGACGAAGA	CGTCTTGGAT	ACTTGGTTCA	GTTCTGCCCT	CTGGCCATTT	1380
TCAACCATGG	GCTGGCCTGA	AGTCGACTCA	GAAGACTTTTA	AACGTTATTT	CCCAACTTCA	1440
ACCTTGGTAA	CAGGTTACGA	CATCATCTTC	TTCTGGGTGT	CTCGTATGAT	CTTCCAGTCA	1500
TTGGAATTCA	CAGGCCGTCA	ACCATTCCAA	AACGTCCTTA	TCCATGGTCT	AATTCGTGAT	1560
GAAGAAGGAC	GTAAGATGTC	TAAATCTCTT	GGAAATGGCA	TTGACCCAAT	GGATGTTATT	1620
GATAAATATG	GTACAGATAG	TCTTCGTTGG	TTCTTGTCAA	ACGGCTCAGC	TCCTGGTCAA	1680
GACGTTTCGT	TCTCTTACGA	GAAAATGGAT	GCTTCATGGA	ACTTTATTAA	CAAGATTTGG	1740
AACATTTCTC	GCTATATCCT	CATGAACAA	GGAGGTTTGA	CGCTGGATGT	GGCGCATGAC	1800
AATGTCACAA	AAGTTGCAAC	AGGTGAGGCT	GGTAAATGTGA	CGGACCGCTG	GATTCCTCCAC	1860
AATCTCAACG	AAACCATTGC	AAAAGTTACT	GAAAACTTTG	ATAAGTTTGA	GTTTGGTGTG	1920
GCTGGTCATA	TCCTTTACAA	CTTCATTTGG	GAAGAATTTG	CCAAC'TGGTA	TGTTGAGTTG	1980
ACCAAGGAAG	TTCTTTACAG	CGACAATGAA	GACGATAAGG	TAATTACTCG	ATCTGTTCTC	2040
CTCTATACGC	TGGATAAAAT	CCTTCGTCTC	CTTCACCCAA	TCATGCCGTT	CGTGACAGAA	2100
GAAATCTTTG	GTCAGTACGC	TGAAGGCTCT	ATCGTGACAG	CAGCATACCC	AACTGTCAAC	2160
CCAGCCTTTG	AAGACCTTGC	TGCCCACACT	GGTGTGGAAA	GTCTCAAAAA	CTTGATTTCGT	2220
GCTGTTTCGGA	ATGCGCGTGC	GGAAGTAAAT	GTAGACCAA	GCAAACCTAT	CACAATCCTT	2280
GTTAAGACTA	GCGATAGTGA	CTTGGAAGCC	TTCTTTAACA	GCAATGTCAA	CTACATCAAG	2340
CGCTTTACAA	ATCCAGAACA	TTTGGAATATC	GCATCAACCA	TCCCTGCACC	TGAACTGGCT	2400
ATGTCAAGCG	TCATCACAGG	AGCAGAAATC	TACTTGCCAC	TGGCAGACCT	TCTCAATGTC	2460
GAAGAAGAAC	TGGCTCGTCT	CGACAAGGAA	CTCGCTAAAT	GGCAAAAAGA	ACTGGATATG	2520
GTCGGTAAGA	AACTCTCTAA	CGAACGCTTC	GTAGCCAACG	CCAAACCAGA	AGTCGTCCAA	2580
AAAGAACGCG	ACAAACAAGC	TGACTACCAA	GCCAAGTATG	ATGCGACCGT	AGCACGTATT	2640
GATGAGATGA	AGAAGTTGGT	GAAATAA				2667

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...939
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GGGAGGAGAA	CAAAAATGAC	AGAGTTGGCA	AAGCAACTAT	TAGAGTTGAC	CTATATTGTG	60
ATTGGTTGTC	AATTTCTCCA	TACAGCCTAT	TGTAGTTATA	AAGATAAAAC	AAACCCAGTT	120
CGACTTGGGA	CATCTGCATT	TTGGACTCTA	TTGTCTATTA	CGTTTATAGG	TGGTTCCTAT	180
ATGCCAAATA	TGAGTATTGG	TATTATTGTA	ATCCTATTAT	CGCTGTTAAC	ATTGTTTAAG	240
CAAGTCCGTA	TCGGAACCTT	GCCATCCTTA	GATGAAATGA	AAGCCAATAT	TGAATCTAAC	300
AGGTTGAAAA	ATAAAATTTT	TATTCCAGTT	ATGCTGATGG	CAATACTTGC	GTTGGTCTTA	360
GCGCAAATGA	TTCCAGAATT	TAGCAAGATT	TCGATTAGCC	TTGCCGCCTT	GTTTGCTACA	420
ATTTCTGTTC	TTGTGATTAC	CAATAGTCAC	CCTAAGAGTC	TGTTATCAGA	AAATAATCGA	480
ATGACTCAGC	AAGTATCAAC	AAGTGGTATT	GTTCTCTCAAT	TATTAGGGGC	TTTGGGGGCT	540
ATTTTTACTG	TAGCAGGTGT	TGGTGATGTT	ATCTCTCATC	TGATTAGCGG	TATTGTTCCCT	600
TCAGATAGTC	GCTTTATAGG	AGTTTTGGCC	TATGTTCTTG	GAATGGTTCT	ATTCACAATG	660
ATTATGGGAA	ATGCTTTTGC	AGCATTCACC	GTTATTACAG	CAGGTGTTGG	AGTTCCCTTT	720
GTATTTGCTC	TGGGAGCTAA	TCCAATTGTG	GCTGGTGCTC	TTGCCATGAC	AGCAGGTTAT	780
TGTGGGACCT	TATTGACCCC	AATGGCTGCT	AATTTTAAACG	CTCTACCAGC	AGCATTGATG	840
GATATGAAAG	ATCAGAATGG	CGTTATAAAG	GCTCAAGCAG	GTGTTGCTCT	AGTAATGATT	900
GTTATTCACA	TATTCTTAAT	GTACTTTCTC	GCATTTTAG			939

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1047 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

ATCTTAGGAA	CACAAGAGGG	CAAAGATATG	AATATTACTT	ATATAGTTGG	AAATGGTTTG	60
GATTTGCAAT	ATGGTTTGAA	AACAAGATAT	AGGGATTTCT	ACGAATTCCA	AAATAAGGTT	120
TATATAAGTA	GGACAGAGAA	CGAGGAAAAA	TATTCAAATT	TCATTTATGA	GTCTCTATTT	180
TCTGATAAAG	TAAATGATTA	TGAAAATTGG	TCAGATTTTG	AATTGTCAAT	TGGTAAATTA	240
ACAAAAGATA	ACGACCTCAT	CTCCTCAAGT	ATAGAAATAA	AGGAGAAATT	TATAGATGAT	300
TTTAGTGAAG	TAGTTGATGA	TTTAAGAGAA	TATCTACGCA	TACAACAAGA	AAAAAATCTT	360
GAGAAAGGTA	ATGCAATTGA	CTTTATAAGC	ACTCTAGATA	ATATGAGGAC	CTCTCTCCCT	420
GTAATTAATC	AACCTGCTAT	CGATAAAAAA	TATAATGAAA	ATCTATATCA	ACACGATATC	480
GTGAATATAT	TAACCTTTAA	TTACACAAAT	GTAATCGATA	AATTATATAA	TGAGTCAGCA	540
AAATCATTTA	GCAATCAATT	ACGAACTAAT	AATTATAAAT	TTACATTGTC	GCCTCCAATT	600
CATGCACATG	GAAACGGTAGA	TATTTGCACA	GTTTTAGGAG	TTAGTGACGA	GACACAGATT	660
TCAAAATAGTT	TTGATGAAGA	ACAAAAAGAA	TCCTTAATAA	AAAAATTTAGT	TTTGAAGAAC	720
TATAGAGAAA	ATATGGATGT	TAAAAATAGC	GATATTATAA	AAAAATTCGA	CATCATAATT	780
CTTTATGGGG	TTTCTTTGGG	AGAGACTGAT	GGGTATATCT	GGAATCAGAT	TGCTGAACAA	840
TCAATCAGAA	GTTCTGTTCC	TGTCATAATT	TACCATTATG	TACCTCATTT	TGATGCAGGA	900
AACCCCACTA	GAGTAAACG	CTTATATAGA	AATGTAGAAG	ACAAATTCAT	ACAAAATAGT	960
GGAATTGATT	TAGAGTTAGA	GAAGAAATTA	AGAGATAACC	TTATTGTTGT	TATTGGAAAG	1020
ACTATTTTTA	ATCTGATGGA	AAGGTAA				1047

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GAAGGAGGAA	CAAACTAAT	GGCATTACTT	GAAGTAAAC	AGTTAACCAA	ACATTTTGGT	60
GGTCTAACAG	CTGTTGGAGA	TGTGACTCTT	GAATTGAACG	AAGGGGAAC	GGTTGGATTA	120
ATCGGTCCAA	ACGGAGCTGG	GAAAACCACC	CTTTTCAACC	TTTGTACCGG	TGTTTATGAA	180
CCAAGTGAGG	GAACAGTAAC	TCTAGATGGT	CACCTTTTGA	ATGGGAAATC	ACCTTATAAG	240
ATTGCCTCTT	TGGGACTTGG	ACGTACTTTC	CAAAATATCC	GTCTCTTTAA	AGATTTAACA	300
GTTTTAGACA	ATGTTTTGAT	TGCTTTTGGG	AACCATCACA	AACAGCATGT	TTTTACTAGT	360
TTCTTACGCT	TACCAGCTTT	TTACAAGAGT	GAAAAAGAAT	TAAAGGCTAA	AGCTTTGGAA	420
TTGTTGAAAA	TCTTTGATTT	AGATGGTGAT	GCAGAGACTC	TTGCTAAAAA	TCTTTCCTAC	480
GGACAACAAC	GTCGTTTGGA	AATTGTTTCGT	GCCCTTGCTA	CGGAACCTAA	AATTCTCTTC	540

TTAGATGAAC	CAGCAGCAGG	TATGAACCCA	CAGGAAACAG	CCGAATTGAC	TGAGTTAATT	600
CGTCGTATCA	AAGATGAATT	TAAGATTACA	ATCATGTTGA	TTGAACACGA	TATGAATCTG	660
GTCATGGAAG	TAACAGAACG	TATCTACGTA	CTTGAATATG	GCCGTTTAAAT	TGCTCAAGGA	720
ACTCCAGACG	AAATTAAGAC	CAATAAACGC	GTTATCGAAG	CTTATCTAGG	AGGTGAAGCC	780
TAA						783

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

AGAGGAGGAA	CTCTTATGGA	AATATCTAAA	GGAATTATTT	TTAATATTCA	ACACTTTTCA	60
ATTCATGACG	GCCCGGGTAT	TCGTACAAC	GTTTTTTTAA	AAGGATGTCC	TCTGCGCTGT	120
CCATGGTGTT	CTAATCCTGA	ATCTCAAAGA	ATGAAACCTG	AAAAAATGAA	AGATGCTCAA	180
CGAGAGAAAT	TCACCTTAGT	CGGTGAAGAA	AAGACTGTAG	AAGAAATTAT	TACAGAGGTA	240
TTAAAAGACA	AAGAATTTTA	CGAAGAATCC	GGTGGAGGTT	TAACTTTATC	AGGAGGTGAA	300
ATATTTGCTC	AGTTTGAAAT	TGCTAAAGCC	ATCTTAAAT	CAGCTAAAGA	ACATCACATA	360
CACACTGCCA	TTGAACTAC	TGCCTTTGTT	GATCATGAAA	AATTTATTGA	TTTAATTCAA	420
TATGTGGATT	TTATCTACAC	AGACCTAAAA	CATTATAAAT	CTATAAAACA	TAAAAAAGTG	480
ACTGGGGTTT	TTAATCAAAT	GATTATTAAA	AACATTCAAT	ATGCTTTTTC	TCAAAAATAAA	540
ACTATCGTTT	TAAGAAATCCC	AGTTATTCCT	AATTTTAACA	ATAGTTTAGA	GGATGCAGAA	600
AAATTCGCTA	CTCTATTTAA	CTCATTAAAT	ATCGACCAAG	TTCAACTACT	CCCTTTTCAT	660
CAATTTGGTG	AAAACAAATA	TCGTTTATTA	AATCGGAAAT	ATGAAATGGA	TGGAATCAAC	720
GCACCTCATC	CTGAAGATCT	TATTGATTAT	CAAAAGGTAT	TTCTGAACCA	CCATATTAAT	780
TGTTATTTCT	AG					792

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GCTGTTGNAA	CTANGCTGAA	AAGGACATAT	GAAGAAAAAC	TGAAAATTTT	GCTCCTTCCA	60
AAGGATCCAA	ACGATGACAA	GAATATCATC	CTTGAAATCC	GTGGAGCAGC	TGGTGGAGAC	120
GAAGCGGCAC	TTTTCGCTGG	AGATTTGCTA	ACTATGTACC	AAAAGTATGC	GGAAGCCCCAA	180
GTTTGGCGCT	TTGAAGTCAT	GGAAGCCTCT	ATGAATGGTG	TCGGTGGTTT	TAAAGAAGTG	240
GTTGCTATGG	TTTCAGGTCA	GTCTGTATAC	TCTAAGCTTA	AGTATGAATC	AGGTGCCCCAC	300
CGTGTGCAAC	GTGTTCCCTGT	GACAGAAAGC	CAAGGCCGTG	TTCATACTTC	GACAGCGACA	360
GTTCTTGTTA	TGCCAGAAAGT	TGAAGAGGTT	GAATACGACA	TTGATCCAAA	AGACCTTCGT	420
GTCGACATCT	ATCACGCCCTC	TGGTGCTGGT	GGACAGAACG	TCAATAAGGT	TGCGACTGCC	480
GTTCGTATCG	TTCACTTGCC	AACCAATATC	AAGGTTGAGA	TGCAGGAAGA	ACGTACCCAG	540
CAGAAGAACC	GCGAGAAGGC	TATGAAGATT	ATCCGTGCAC	GCGTCGCTGA	CCACTTTGCT	600
CAGATTGCTC	AGGATGAACA	AGACGCTGAG	CGTAAGTCGA	CAATCGGTAC	TGGTGACCGT	660
TCAGAACGGA	TCCGAACTTA	TAACTTCCCA	CAAAACCGTG	TCACAGACCA	CCGTATCGGC	720
TTGACCCTCC	AAAAACTAGA	TACGATTTTG	TCTGGTAAAT	TGGACGAAGT	TGTGGATGCC	780
TTGGTGCTTT	ATGACCAAAC	ACAAAACTA	GAAGAATTAA	ACAAATAA		828

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

CGAGTTTGA	CCACGTATCT	CTATGATATC	GAGTCTTGA	CCTGGTTTGA	ACTCTATCTC	60
TTTTGCAATA	CCATGCCCTT	CTTGAGCCAT	CAAGATCTGA	TTTTTTTATC	AACCTCCTTA	120
CTCGAAAAAT	CCAAAGAATT	TAAAGAGTTA	GTACACAATC	GATTGTATAT	GAAGCAAGGA	180
CTCTTAAATA	TCTTATCAGA	ACTCATGGAG	CGAAACTTT	TCTCCTACAT	CCCAATCTTC	240
GAAGCCGAGT	TGGAGAGGAT	GTTACGACCG	TATGATGTTT	TTGAAAAAGT	ATCGTGGCAA	300
TTTTTAAAGA	AGATGAGTGT	CTTTCCTTCAA	ACAAAGGGAA	GCAATCAAAA	AGAGATTGAA	360
CGCTTTATCC	AATCTCTGCA	GGTATTAGAA	AATCCACAAT	TAACATCCCT	TTTTGAATTG	420
CGTTTTTCAGC	AATATAAAGA	ACTTATAGAT	TAG			453

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...744
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

ATATCTTTGA	CTTTCTTTTG	GGAGGAAC	TTGGAATC	CTTC	TAGTAAAGAA	TTTGGGTGCC	60
CTTCCTATGA	TTTGGGTTTC	CTTTATCGTT	ACCATTCTCT	CAGCCCTTAT	CGCAACACCC		120
TTTGCTATTG	GTGCAGCAGT	TTTTATGACC	GAAGTATCAC	CAAAAGGGGC	GAAGATTTTG		180
CAACCAGCTA	TTGAACTCCT	GGTTGGGATT	CCTTCAGTAG	TGTATGGATT	TATTGGCTTG		240
CAAGTCGTCG	TTCCCTTTGT	TCGCAGTGTC	TTTGGTGGA	CTGGTTTTGG	GATTTTGTCA		300
GGGATTTCCG	TCCTCTTTGT	CATGATTTTG	CCGACCGTAA	CCTTTATGAC	AACGGATAGC		360
TTGCGTGCGG	TTCTCGTTA	TTATCGTGAA	GCCAGTTTCG	CTATGGGAGC	CACTCGCTGG		420
CAGACTATCT	GGCGTGTGAT	CTTGAAGGCG	GCCCGTTCTG	GTATTTTCAC	TGCAGTGGTC		480
TTTGGGATGG	CGCGTGCCTT	TGGTGAGGCT	TTAGCTATCC	AGATGGTTGT	CGGAAACTCA		540
GCTGTTATCC	CAACTTCCTT	GACCACACCA	GCTGCAACTT	TAACTTCTAT	ATTAACATATG		600
GGAAATGGGA	AACTGTCAT	GGGAACTGTA	AATAATAATG	TTCTCTGGTC	ACTGGCCTTG		660
GTA	CTGCTCT	TGATGAGTTT	AGTTT	TTAAC	AGTGTGATTA	AATTGATTAC	720
GGAAAGAAAA	ATTATGCGCG	CTAA					744

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

ATTAATTTGA	CTTTCCTGAT	AGAGTTGTTT	ACATCTTATT	TCAATTCAC	ATACTTTCCC	60
TTTACTCAA	TGAAATCAA	AGCGAAACT	AGGAAGCTAG	CCACAGGTTG	CTCAAAGCAC	120
TGCTTTGAGG	TTGTAGATA	GACTGACGAA	GTCAGCTCAA	AATACTGTTT	TGAGGTTGCA	180
GATAAGACTG	ACGAAGTCAG	CTCAAAATAC	TGTTTTGAGG	TTGCAGATAA	GACTGACGAA	240
GTCAGCTCAA	AATACTGTTT	TGAGGTTGCA	GATAAGACTG	ACGAAGTCAG	CTCAAAATAC	300
TGTTTTGAGG	TTGCAGATAA	GACTGACGAA	GTCAGCTCAA	AATACTGTTT	TGAGGTTGCA	360
GATAAGACTG	ACGAAGTCAG	CTCAAAATAC	TGTTTTGAAG	TTGCAGATAA	GACTGACGAA	420
GTCAGCTCAA	AATACTGTTT	TGAGGTTGCA	GATGGAAGCT	GA		462

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

ATTAATTTGA	CTTTCCTGAT	AGAGTTGTTT	ACATCTTATT	TCAAATCACT	ATATTTTAAG	60
AAGGTACTTG	CAATGACAGG	TACAGAAACA	TTTACAGTTA	TTTCAACTGA	GGACTTGGAG	120
CAAACTTCAG	GTGGTCTTGC	TGTTTGGGAA	GATGGATATA	GTAGATGGTT	ATATTATAGA	180
GAATTTGCTC	CTTATATGAG	GCAAGGGGCA	CTTAATTCTT	ATATAGATGC	TTGGAAGTAC	240
GGCTTCCGAA	CAGGGTAA					258

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGGAGCTTGA	CTGCGAGAGC	TACAACTCGA	GCAGGGACGA	AAGTCGGGCT	TAGTGATCCG	60
GTGGTTCCGT	ATGGAAGGGC	CATCGCTCAA	CGGATAAAAG	CTACCCTGGG	GATAACAGGC	120
TTATCTCCCC	CAAGAGTTCA	CATCGACGGG	GAGGTTTGGC	ACCTCGATGT	CGGCTCGTCG	180
CATCCTGGGG	CTGTAGTCGG	TCCCAAGGGT	TGGGCTGTTC	GCCCATTAAA	GCGGCACGCG	240
AGCTGGGTTC	AGAACGTCGT	GAGACAGTTC	GGTCCCTATC	CGTCGCGGGC	G TAG	294

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GGGAGCTTGA	CTGCGAGAGC	TACAACTCGA	GCAGGGACGA	AAGTCGGGCT	TAGTGATCCG	60
GTGGTTCCGT	ATGGAAGGGC	CATCGCTCAA	CGGATAAAAG	CTACCCTGGG	GATAACAGGC	120
TTATCTCCCC	CAAGAGTTCA	CATCGACGGG	GAGGTTTGGC	ACCTCGATGT	CGGCTCGTCG	180
CATCCTGGGG	CTGTAGTCGG	TCCCAAGGGT	TGGGCTGTTC	GCCCATTAAA	GCGGCACGCG	240
AGCTGGGTTC	AGAACGTCGT	GAGACAGTTC	GGTCCCTATC	CGTCGCGGGC	G TAG	294

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GGGAGCTTGA	CTGCGAGAGC	TACAACTCGA	GCAGGGACGA	AAGTCGGGCT	TAGTGATCCG	60
GTGGTTCCGT	ATGGAAGGGC	CATCGCTCAA	CGGATAAAAG	CTACCCTGGG	GATAACAGGC	120
TTATCTCCCC	CAAGAGTTCA	CATCGACGGG	GAGGTTTGGC	ACCTCGATGT	CGGCTCGTCG	180
CATCCTGGGG	CTGTAGTCGG	TCCCAAGGGT	TGGGCTGTTC	GCCCATTAAG	GCGGCACGCG	240
AGCTGGGTTC	AGAACGTCGT	GAGACAGTTC	GGTCCCTATC	CGTCGCGGGC	GTAG	294

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GGGAGCTTGA	CTGCGAGAGC	TACAACTCGA	GCAGGGACGA	AAGTCGGGCT	TAGTGATCCG	60
GTGGTTCCGT	ATGGAAGGGC	CATCGCTCAA	CGGATAAAAG	CTACCCTGGG	GATAACAGGC	120
TTATCTCCCC	CAAGAGTTCA	CATCGACGGG	GAGGTTTGGC	ACCTCGATGT	CGGCTCGTCG	180
CATCCTGGGG	CTGTAGTCGG	TCCCAAGGGT	TGGGCTGTTC	GCCCATTAAG	GCGGCACGCG	240
AGCTGGGTTC	AGAACGTCGT	GAGACAGTTC	GGTCCCTATC	CGTCGCGGGC	GTAG	294

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GCTTCATTGA	CATGTAGCCC	CTCACTTGAC	AGCATATACA	TATGCAGGGC	TAGAGAACGA	60
CCTGAAGACA	TGAGACTACT	TGGCGTATTG	GTAAGAGGTAC	CTAATGTATA	CATGAGGGCA	120
GCTGTTTCAC	CAACGATACG	GCCAATAGCT	AGTATCACTC	CAGCTAAAAT	ACCTGGCATG	180
GCAACTGGTA	GAACAATTCT	AAAAACAGTC	CGTAACTTAC	CTGCCCAAG	TCCATAA	237

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

AAAATGTTGA	CAAATAGTAT	AATAAAAACA	AAGGAGAACA	GCATGCTGAA	ATGGGAAGAC	60
TTGCCTGTGG	AAATGAAATC	AAGCGAGGTT	GAGTCTTACT	ACCAGCTTGT	CTCTAAAAGG	120
AAGGGTTCGC	TGATTTTCAA	GCGTTGCTTG	GACTGGGTTT	TGGCCTTGGT	GCTTACATGG	180
GTTCTAACTT	CTCCCATCTT	TCTCATCTTG	AGCATTTGGA	TCAAGTTGGA	TAGCAAGGGG	240
CCAGTGATTT	ACAAGCAAGA	GCGTGTGACC	CAGTACAACC	GTCGGTTCAA	GATTTGGAAG	300
TTCCGTACCA	TGGTGACGGA	TGCGGATAAA	AAAGGAAGTC	TGGTGACTTC	TGCTAACGAT	360
AGCCGTATTA	CCAAGGTTGG	AAATTTTCATC	CGACGTGTCC	GTTTGGACGA	ACTGCCTCAG	420
TTGGTCAATG	TCCTTAAAGG	TGAGATGTCC	TTTGTCGGTA	CACGACCTGA	AGTGCCACGT	480
TATACAGAGC	AGTATAGCCC	TGAAATGATG	GCAACCTTGC	TCTTGCAAGC	AGGAATTACC	540
TCTCCAGCCA	GCATCAACTA	CAAGGATGAG	GACACCATCA	TCAGTCAAAT	GACGGAGAAA	600
GGTCTGTCAG	TTGATCAGGC	CTATGTGGAG	CATGTTCTTC	CTGAAAAGAT	GCGCTATAAC	660
CTCGCCTATC	TCCGAGAGTT	TAGTTTCTTT	GGGGACATCA	AAATCATGTT	TCAAACCGTG	720
TTTGAGGTAC	TAAAATAA					738

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

ATGTTACTGA	CTTCGTCAGT	TCTATCTGCA	ACCTCAAAAC	AGTGTTTTGA	GCTGACTTCG	60
TCAGTTCTAT	CCACAACCTC	AAAACAGTGT	TTTGAGCAAC	CTGTGACTAG	CTTTCTAAGC	120
GATGCCTTGG	TTCTCATTCG	CTATAATCAA	AAAGAGAAAT	TTTCTCCTGA	AAAGCATATA	180
GAGTAG						186

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1002 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

AATAAACTGA	CTAGAAAAAA	CAAAGGAGAA	ACTATGTCTC	AACTCTATGA	TATTACCATT	60
GTGGGTGGTG	GTCTGTTCGG	GCTTTTTGCA	GCCTTTTATG	CCCACCTACG	CCAAGCCAAG	120
GTTCAAATCA	TCGACTCTCT	TCCCCAGCTA	GGTGGACAAC	CTGCTATTCT	CTACCCTGAA	180
AAGGAAATCC	TAGACGTACC	AGGCTTCCCA	AACCTGACTG	GAGAAGAGTT	GACTAACCGC	240
TTGATTGAAC	AGCTAAATGG	ATTTGATACC	CCTATTTCATC	TCAATGAAAC	GGTTCTTGAG	300
ATTGACAAAC	AAGAAGAAGA	ATTTGCCATC	ACAACTTCTA	AAGGAAGTCA	CCTGACTAAA	360
ACAGTCATCA	TCGCTATGGG	TGGCGGTGCC	TTCAAACCCAC	GTCCGCTGGA	ACTTGAAGGT	420
GTTGAGGGCT	ATGAAAATAT	CCACTACCAC	GTTTCTAACA	TTCAGCAATA	CGCTGGTAAG	480
AAAGTGACGA	TTCTTGGTGG	GGGAGACTCG	GCTGTGGATT	GGGCTTTGGC	TTTTGAAAAA	540
ATCGCACCAA	CTACCCTTGT	TCACCGCAGA	GATAATTTCC	GTGCCTTGGA	ACACAGTGTT	600
CAAGCCTTGC	AAGAATCATC	TGTAACCATC	AAGACACCAT	TCGCCCCCTAG	CCAACCTCCTT	660
GGAAATGGAA	AAACACTTGA	TAAACTTGAA	ATCACAAAAG	TCAAATCTGA	TGAAACTGAA	720

ACCATTGACC TAGACCACCT CTTTGTCAAC TATGGTTTCA AATCTTCTGT CGGTAACCTT	780
AAAACTGGG GGCTCGACCT CAACCGTCAC AAGATTATCG TCAACAGCAA ACAGGAATCC	840
AGCCAAGCAG GTATCTATGC TATCGGTGAC TGCTGCTACT ATGACGGAAA AATTGATCTG	900
ATTGCGACAG GCCTCGGAGA AGCTCCAAC TCTGTCAACA ACGCTATCAA CTACATTGAC	960
CCTGAACAAA AAGTACAACC AAAACACTCT ACTAGTTTAT AA	1002

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

AATGAACTGA CCCCAAAAGT TAGACAGAAA AAATCTAACT TTTGGGGTGT TTTTATTATG	60
AAACTAACTT ATGATGATAA AGTTCAGATC TATGAACTTA GAAAACAAGG ATATAGCTTA	120
GAGAAGCTTT CAAATAAATT TGGGATAAAC AATTCTAATC TTAGGTACAT GATTAAATTG	180
ATTGATCGTT ACGGAATAGA GTTCGGCAAA AAAGGAAAAA ATCGTTACTA TTCTCCTGAT	240
TTAAAACAAG AAATGATTTA TAAAGTCTGA	270

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

ATAGAACTGA	CGAAGTCAGC	TCAAAGCACT	GCTTTGAGGT	TGCAGATGAA	ACTGACGAAG	60
TCAGCTCAAA	ACATGTTTTT	GAGGTTGTGG	ATGAAACTGA	CGAAGTCAGC	TCAAAACATG	120
TTTTTGAGGT	TGTGGATGAA	ACTGACGAAG	TCAGCTCAAA	ACATGTTTTT	GAGGTTGTGG	180
ATGAAACTGA	CGAAGTCAGT	AACCATACAT	ACGGTAAGGC	GACGTGACGT	GGTTTGCAGA	240
GATTTTCGAA	GAGTATTAGC	CTTCCATATA	GTCTTTCAAA	GCCTGTCCTG	TTAG	294

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

ATAAGACTGA	CGAAGTCAGC	TCAAATACT	GTTTTGAGGT	TGCAGATAAG	ACTGACGAAG	60
TCAGCTCAAA	ATACTGTTTT	GAGGTTGCAG	ATAAGACTGA	CGAAGTCAGC	TCAAATACT	120
GTTTTGAGGT	TGCAGATAAG	ACTGACGAAG	TCAGCTCAAA	ATACTGTTTT	GAGGTTGCAG	180
ATAAGACTGA	CGAAGTCAGC	TCAAATACT	GTTTTGAGGT	TGCAGATAAG	ACTGACGAAG	240
TCAGCTCAAA	ATACTGTTTT	GAAGTTGCAG	ATAAGACTGA	CGAAGTCAGC	TCAAATACT	300
GTTTTGAGGT	TGCAGATGGA	AGCTGACGTA	GTTTGCAGAG	ATTTTCGAAG	AGTATTATAT	360
GAGAAAAATC	CTCTACTCTA	CTAA				384

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

TTCCTTATGA	CTAAATCATT	AATTTTGGTG	AGCCATGGTC	GCTTCTGTGA	GGAGCTTAGA	60
GGTAGCACAG	AAATGATTAT	GGGCCTACAA	GACAACATTT	ACACAGTAGC	TCTTCTTCCA	120
GAAGATGGCC	CAGAAGAATT	TACTGCTAAA	TTTGAAGCTG	TTATTGAAGG	ATTGGATGAT	180
TTCCTAGTTT	TTGCGGATCT	TCTCGGTGGG	ACACCTTGTA	ATGTGGTGAG	TCGCTTGATC	240
ATGGAAGGTC	GTGATATTGA	CCTTTACGCA	GGGATGAATC	TTCCAATGGT	GATTGAATTT	300
ATCAATGCGA	GCCTTACAGG	CGCAGATGCG	GACTACAAGA	GCCGTGCTGC	AGAAAGCATT	360
GTGAAAGTTA	ATGACCTGTT	AGCGGGCTTC	GATGATGACG	AAGATGAATA	A	411

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

ACTAATATGA	CACTAACAAC	CTTTTTATTA	CAAGCAGTAG	CAAGTTTTCT	TGCCATTATC	60
ACTTTTTTAA	TCGTACTCAA	TGTGCAACGG	TCTATGCTCT	TACCTGGAGG	GATTTTGGGC	120
ATGACTGTCT	GGCTAATCTA	TCTCTTGCTC	AAGGAACCGA	CCAATGTCAT	TGTAGCTACC	180
TTCATTGCAG	CCATTATTGG	TTCTTGTGTC	AGCCAGATTT	TAAGTATTCT	TTATAAGACA	240
CCTGCTGTGG	TCTTTATCTT	GGCCATTTTG	GCACCGCTGG	TTCCAGGTTA	TCTCTCCTAC	300
CGAACAACTG	CCTTTTTTGT	GACAGGGGAC	TATAATAAAG	CACTGGCAAG	TGGGCTCTTG	360
GTTGTCATGT	TGGCTCTGGT	AATCTCTATT	GGAATGGCTA	GCGGATCAGT	GATTCTCAGA	420
CTCTATCATT	ATATAAAAAC	ACATCGAGTA	TCGTAG			456

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

AAAGATATGA	CAGAAAGAGA	GTCTGTTTTG	CACACAATGT	CAAGGAGGAG	ACACATGTCA	60
AAAGAACAAA	AACGCCAAGC	GTTTTATACT	CAGAGCCCTG	AAGAGGTCTT	GCAGGCTGTG	120
GATGCGACCG	AGCAAGGTTT	GTCATCAAGT	GAGGCGGAAA	AGCGCCTTGC	CGAATTTGGG	180
CACAATGAAC	TCGAAGAAGG	CGAGAAACGA	TCAATCTTGG	TCAAATTCAT	CGAGCAATTT	240
AAGGATTTGA	TGATTATCAT	CCTAGTTGCG	GCAGCAATCT	TGTCAGTCGT	GACTTCTGGT	300
GGGGAAGATA	TCGCAGATGC	CATTATCATC	CTAGCTGTGG	TTATCATCAA	CGCTGCCTTT	360
GGTGTTTACC	AAGAAGGAAA	AGCTGAAGAA	GCTATTGAAG	CCCTCAAATC	CATGTCTAGT	420
CCAGTTGCCC	GCGTTCTTCG	TGATGGACAC	ATGGCAGAGA	TTGACTCTAA	AGAATTGGTA	480
CCAGGCGATA	TCGTTGCCCT	TGAAGCAGGT	GACGTGGTAC	CAGCGGACCT	ACGTTTGCTA	540
GAAGCCAACT	CTCTTAAAAT	TGAAGAAGCA	GCCTTGACGG	GTGAATCTGT	ACCAGTCGAA	600
AAAGACTTGT	CAGTCGAGCT	TGCGACAGAT	GCTGGTATTG	GTGACCGTGT	CAACATGGCC	660
TTCCAAAAC	CAAACGTAAC	CTATGGTCGT	GGGATGGGTG	TTGTTGTCAA	TACAGGTATG	720
TACACTGAAG	TTGGTCAAT	TGCTGGTATG	CTTCAAGATG	CGGATGAGAC	TGATACACCA	780
CTCAAACAAA	ACTTGAACAA	CCTTTCTAAG	GTCTTGACCT	ATGCTATCTT	GGTCATTGCC	840
CTTGTTACTT	TTGTAGTGGG	TGTCTTCATT	CAAGGGAAAA	ATCCACTTGG	TGAGTTGTTG	900
ACTTCTGTTG	CCCTTGCTGT	TGCAGCCATT	CCAGAAGGAC	TTCTTGCTAT	CGTTACCATC	960
GTTCTTTCTC	TTGGTACTCA	AGTTTTGGCC	AAACGACATT	CCATCGTTCG	TAAGTTGCCA	1020
GCAGTTGAAA	CACTTGGTTC	AACTGAAATC	ATCGCTTCTG	ATAAGACTGG	TACGCTGACT	1080
ATGAACAAGA	TGACAGTCGA	AAAAGTCTTC	TACGATGCGG	TTCTACATGA	CTCAGCTGAT	1140
GATATTGAAC	TAGGTCTTGA	AATGCCACTA	CTTCGTTTCA	TTGTCTTGGC	CAATGATACG	1200
AAAATCGATG	TGGAAGGTAA	CTTGATTGGT	GACCCAACCG	AAACAGCCTT	TATCCAATAT	1260
GCCTTGGACA	AGGGCTATGA	TGTCAAAGGT	TTCTTAGAGA	AATATCCTCG	TGTAGCTGAA	1320
TTGCCATTTG	ACTCTGACCG	TAAGCTCATG	TCAACAGTTC	ACCCATTGCC	AGATGGTCGT	1380
TTCTTGTAG	CAGTCAAGGG	TGCGCCAGAC	CAACTCTTAA	AACGTTGTCT	TCTTCGTGAT	1440
AAGGCTGGGG	ATATTGCTCC	GATTGATGAG	AAGGTTACAA	ATCTCATTCA	TACAAACAAT	1500
TCTGAAATGG	CTCATCAAGC	CTTGCGTGTC	CTTGCAAGTG	CTTATAAGAT	TATCGATAGT	1560
ATTCCAGAAA	ATCTCACTTC	TGAAGAGCTT	GAAAATGATT	TAATTTTTAC	TGGTTTGATT	1620
GGGATGATTG	ATCCTGAACG	TCCTGAAGCT	GCTGAGGCTG	TTCTGTGTGG	TAAGGAAGCT	1680
GGAATTCGTC	CAATTATGAT	TACAGGTGAC	CACCAAGACA	CCGCAGAAGC	TATTGCCAAA	1740
CGTTTGGGAA	TCATTGACGC	AAACGATACA	GAAGACCACG	TTTAACTGG	TGCTGAGCTC	1800
AACGAATTAT	CTGATGAAGA	CTTTGAAAAA	GTGTTTGGTC	AATACTCTGT	TTATGCCCGT	1860
GTGTCTCCAG	AGCACAAAGT	TCGTATCGTC	AAGGCTTGGC	AAAAACAAGG	TAAGGTCGTT	1920
GCCATGACAG	GTGACGGTGT	CAATGATGCC	CCAGCTCTGA	AAACAGCAGA	CATCGGTATC	1980
GGTATGGGAA	TCACTGGTAC	AGAGGTTTCT	AAGGGGGCTT	CTGATATGAT	TCTTGACAGT	2040
GATAACTTTG	CGACTATTAT	CGTCGCAGTG	GAAGAAGGAC	GTAAGGTCTT	CTCAAATATT	2100
CAAAAGACTA	TTCAGTACCT	ACTTTCTGCC	AATACTGCTG	AAGTATTAA	CATCTTCCTA	2160
TCAACCTTGT	TTGGTTGGGA	CGTCTTGACG	CCAGTTCATC	TTTTGTGGAT	TAACTTGGTA	2220
ACGGATACCT	TCCCAGCAAT	TGCACTAGGT	GTTGAACCTG	CGGAACCTGG	TGTCATGAAT	2280
CATAAACCAC	GTGGACGCAA	GGCAAGCTTC	TTCTCAGGTG	GTGTTTTGAG	TTCTATCATT	2340
TATCAAGGTG	TACTCCAAGC	AGCTCTTGTT	ATGAGTGTTC	ATGGCCTTGC	GATTGCTTAC	2400
CCAGTTTCATG	TGGGTGACAA	TCATGCTATT	CATGCAGATG	CCCTAACGAT	GGCCTTTGCA	2460
ACCCTTGGTT	TGATTTCAGCT	CTTCCATGCC	TACAATGTCA	AGTCTGTCTA	CCAATCCATC	2520
TTGACAGTTG	GCCCATTCAA	GTCTAAGACC	TTTAACTGGT	CCATCTTGGT	ATCCTTTATC	2580
CTTCTCATGG	CAACAATCGT	TGTAGAACCG	CTTGAAGGAA	TCTTCCACGT	AACCAAACCTA	2640
GACTTGTCAC	AATGGGGAAAT	TGTTATGGCT	GGAAGCTTCT	CAATGATTAT	CATCGTCGAA	2700

ATCGTTAAGT TTATTCAACG CAAACTCGGT TTTGACAAGA ATGCGATTTA A

2751

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

AAGTGCATGA	CTAAACGTGT	ACTCATTACA	GGAGTGAGTT	CAGGTATTGG	ATTGGCTCAG	60
GCTCGCCTCT	TTTTAGAGAA	GGGCTATCAA	GTTTATGGAG	TTGACCAAGG	TGAAAAGCCA	120
CTCTTAGAGG	GTGATTTTCA	CTTTTTACAG	AGAGATTTGA	CCTTGGACTT	GGAACCTATT	180
TTTGACTGGT	GCCCTCAGGT	GGATGTTTTG	TGTAATACTG	CCGGAGTTT	GGATGATTAC	240
AAACCACTGT	TGGAACAAAC	GGCGCAGGAC	ATTCAAGAGA	TTTTTGAAAT	CAACTACATT	300
ATTCCAGTAG	AGTTGACTCG	GTATTATTTG	ACACAAATGC	TGGAAAATAA	AAAGGGAATC	360
ATCATCAATA	TGTGTTCCAT	TGCTTCTAGC	CTAGCAGGTG	GAGGTGGTCA	CGCCTATACT	420
TCATCCAAGC	ATGCCTTGGC	TGGCTTCACC	AAGCAGTTGG	CTCTAGACTA	TGCTGAAGCT	480
GGGATTCAGG	TCTTTGGTAT	CGCTCCAGGA	GCAGTCAAGA	CAGCTATGAC	CGCTGCGGAT	540
TTTGAACCAG	GTGGTTTAGC	TGACTGGGTG	GCTAGTGAAA	CACCAATCAA	GCGCTGGATT	600
GAACCAGAGG	AAATAGCAGA	GCTTAGTCTT	TTTTTAGCAA	GTGGAAAAGC	GAGCGCCATG	660
CAAGGACAAA	TCTTGACAAT	AGATGGTGGC	TGGTCTTTGA	AGTAG		705

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GAAATAATGA	CAGAAACCTT	GATAAAAATT	GAAAATTTAC	ATAAATCTTT	TGGAAAGAAT	60
GAAGTATTGA	AGGGCATCAA	CCTCGAGATT	AAAAGAGGAG	AAGTTGTCGT	TATCATCGGT	120
CCTTCAGGGA	GTGGGAAATC	TACCTTGCTT	CGCTCTATGA	ATTTGTTGGA	GGAAGCAACC	180
AAGGGGAAGC	TTATCTTTGA	GGGAGTCGAT	ATTACGGACA	AGAAGAATGA	CCTGTTTGCC	240
ATGCGTGAGA	AGATGGGCAT	GGTTTTCCAA	CAATTTAACC	TCTTTCCTAA	TATGACTGTG	300
ATGGAAAATA	TTACCTTGTC	ACCTATCAAG	ACTAAAGGTG	AAAGCAGGGA	AGTTGCTGAG	360
AAGAGAGCCC	AAGAGCTTTT	GGAAAAAGTT	GGTTTGCCAG	ATAAGGCAGA	CGCTTATCCA	420
CAGAGTCTGT	CGGGTGGGCA	ACAACAACGG	ATTGCATCGC	GCGTGGGTTG	GCTATGGTAC	480
CAGATGTTTT	GCTCTTTGAC	GAACCAACTT	CAGCCTTGA	TCCTGAAATG	GTA	534

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

AGAGTAATGA	CATTAGTTTA	TCAATCAACG	CGTGATGCCA	ACAATACAGT	AACTGCCAGC	60
CAAGCAATTT	TGCAAGGTTT	GGCGACGGAC	GGCGGTTTGT	TTACACCGGA	TACTTATCCA	120
AAGGTAGATT	TGAACCTTGA	CAAATTGAAA	GATGCTTCTT	ACCAGGAAGT	TGCTAAGCTA	180
GTTTTGTCAG	CATTTTTAGA	TGACTTTACA	GTTGAGGAGT	TGGACTACTG	TATCAACAAT	240
GCCTACGATA	GCAAATTTGA	TACTCCAGCT	ATTGCACCAT	TAGTGAAATT	AGATGGGCAA	300
TACAATTTGG	AACTTTTCCA	TGGTTCAACG	ATTGCCTTTA	AGGATATGGC	CTTGTCATTT	360
TTGCCATACT	TTATGACGAC	TGCTGCTAAG	AAACATGGTT	TGGAGAACAA	GATTGTTATC	420
TTGACAGCGA	CATCTGGTGA	CACGGGGAAA	GCTGCTATGG	CGGGGTTTGC	GAATGTGCCT	480
GGTACTGAGA	TTATCGTCTT	TTATCCAAAG	GATGGTGTC	GCAAGATTCA	AGAGTTACAA	540
ATGACCACTC	AGACTGGCGA	CAATACTCAT	GTTATTGCTA	TTGATGGTAA	CTTTGACGAT	600
GCGCAAACAA	ATGTGAAGCA	CATGTTTAAC	GACGTGGCTC	TTCGTGAAAA	ATTGACTACC	660
AACAAGTTGC	AATTTTCATC	AGCTAACTCT	ATGAACATTG	GTCGTCTGGT	GCCACAAATT	720
GTTTATTATG	TTTATGCTTA	CGCTCAATTG	GTAAAGACTG	GTGAAATTGT	AGCTGGTGAA	780
AAGGTTAACT	TCACAGTACC	AACAGGAAAC	TTTGGAATA	TCTTGGCTGC	CTTTTATGCC	840
AAACAAATTG	GTTTGCCAGT	TGGTAAATTA	ATCTGTGCTT	CAAATGACAA	CAATGTTTTG	900
ACAGACTTCT	TTAAACACG	TGTCTATGAC	AAAAAACGTG	AGTTTAAGGT	AACAACCAGC	960
CCATCTATGG	ATATCTTGGT	ATCTTCAAAC	TTGGAGCGCT	TGATTTTCCA	TCTTTTGGGA	1020
AATAATGCTG	AAAAGACAAC	TGAACCTTATG	AATGCCCTTGA	ACACGCAAGG	ACAATATAAG	1080
TTGACAGACT	TTGATGCAGA	GATTTTGGAC	CTCTTTGCAG	CTGAATATGC	GA	1140
GAAACGGCAG	CAGAGATCAA	GCGTGTTTGT	GAGTTAGATT	CTTATATCGA	GGACCCTCAT	1200

ACAGCTGTTG	CTTCAGCAGT	TTATAAAAAA	TACCAATCGG	CCACTGGAGA	TGTAAC TAAG	1260
ACAGTGATTG	CTTCAACAGC	TAGTCCATAC	AAGTTCCCAG	TAGTTGCAGT	AGAAGCTGTA	1320
ACTGGAAAAG	CAGGTTTAAC	AGACTTTGAA	GCCTTGGCTC	AATTACATGA	AATCTCAGGC	1380
GTTGCAGTGC	CACCAGCAGT	TGATGGGCTT	GAAATAGCTC	CAATTCGTCA	CAAGACAACA	1440
GTGGCAGCTG	CTGACATGCA	AGCAGCGGTT	GAGGCTTATT	TAGGACTTTA	A	1491

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TTGGAAATGA	CAACCATCCG	ATCACTTCTT	CTTAATTTCA	TTTCTATTTT	CTATTCCATT	60
TTTATTCAAA	AAATCAAAAA	GCAAAC TAGA	AAGCTGGTCG	CTGGTGGTTC	AAAACACTGT	120
TTTGAGATTG	TCGATAGAAC	TGACAAACCC	TGTAATATAC	CTGCATATAT	ACATACGACA	180
AGGCGATACT	ACCCTAGTTT	GAAGAGATTT	TCGAAGAGTA	TTCATTTTTG	TCTTTTACTT	240
ATTATACCAT	ATTACATAAA	AAAAACGAAC	ATTCTTATCC	TAAAAAATGC	TCATTTTTCT	300
TAA						303

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

AAATTTGTGA	CCAGTTTTTA	TCCTATCTAC	GCTATGGTTA	AGGAAGTATC	TGGTGACTTG	60
AATGATGTTT	GGATGATTCA	GTCAAGTAGT	GGTATTCAC	CTTTTGAACC	TTCGGCAAAT	120
GATATCGCAG	CCATCTATGA	TGCAGATGTC	TTTGTTTACC	ATTCTCATAC	ACTCGAATCT	180
TGGGCAGGAA	GTCTGGATCC	AAATCTAAAA	AAATCCAAAG	TGAAGGTCTT	AGAGGCTTCT	240
GAGGGAATGA	CCTTGGAAAC	TGTCCCTGGA	CTAGAGGATG	TGGAAGCAGG	GGATGGAGTT	300
GATGAAAAAA	CGCTCTATGA	CCCTCACACA	TGGCTAGATC	CTGAAAAAGC	TGGAGAAGAT	360
ACCCAAATTA	TCGCTGATAA	ACTTTCAGAG	GTGGATAGTG	AGCATAAAGA	GACTTATCAA	420
AAAAATGCGC	AAGCCTTTAT	CAAAAAAGCT	CAGGAATTGA	CTAAGAAATT	CCAACCAAAA	480
TTTGAAAAAG	CGACTCAGAA	AACATNTGTA	ACACAACATA	CAGCCTTTTC	TTATCTAGCG	540
AAGAGATTTG	GGCTTAATCA	ACTTGGTATT	GCAGGCATCT	CTCCTGAACA	AGAACCAAGT	600
CCACGACAAT	TAACAGAAAT	TCAGGAATTT	GTTAAAACCT	ATAAGGTTAA	AACGATTTTT	660
ACAGAAAAGT	ATGCTTCTTC	AAAAGTAGCT	GAAACTCTTG	TCAAATCAAC	AGGTGTGGGT	720
CTTAAACTCT	TGAATCCTTT	AGAGGCAGAC	CCACAAAATG	ACAAGACCTA	TTAGAAAAT	780
CTGGAAGAAA	ATATGAGTGT	TCTAGCAGAA	GAATTAAAGT	GA		822

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

CTCGAATCGA	CTAATAAAGA	AAAATTGGTA	GATGATTTAT	TGGCATTCCT	AGCACCAATT	60
ACCCATCCAG	AGCGACTTGG	CAAGCCAAAT	TCTCAAATTG	AGTATACTGA	AGACGAAGTT	120
CGTATTGCTC	AATTAGCTGA	TAAGTATACA	ACGTCAGATG	GTTACATTTT	TGATGAACAT	180
GATATAATCA	GTGATGAAGG	AGATGCATAT	GTAACGCCTC	ATATGGGCCA	TAGTCACTGG	240
ATTGGAAGAA	ACAGCCTTTC	TGATAAGGAA	AAAGTTGCAG	CTCAAGCCTA	TACTAAAGAA	300
AAAGGTATCC	TACCTCCATC	TCCAGACGCA	GATGTTAAAG	CAAATCCAAC	TGGAGATAGT	360
GCAGCAGCTA	TTTACAATCG	TGTGAAAGGG	GAAAAACGAA	TTCCACTCGT	TCGACTTCCA	420
TATATGGTTG	AGCATAACAG	TGAGGTTAAA	AACGGTAATT	TGATTATTCC	TCATAAGGAT	480
CATTACCATA	ATATTAAATT	TGCTTGGTTT	GATGATCACA	CATACAAAGC	TCCAAATGGC	540
TATACCTTGG	AAGATTTGTT	TGCGACGATT	AAGTACTACG	TAGAACACCC	TGACGAACGT	600
CCACATTCTA	ATGATGGATG	GGGCAATGCC	AGTGAGCATG	TGTTAGGCAA	GAAAGACCAC	660
AGTGAAGATC	CAAATAAGAA	CTTCAGAGCG	GATGAAGAGC	CAGTAGAGGA	AACACCTGCT	720
GAGCCAGAAG	TCCCTCAAGT	AGAGACTGAA	AAAGTAGAAG	CCCAACTCAA	AGAAGCAGAA	780
GTTTTGCTTG	CGAAAGTAAC	GGATTCTAGT	CTGAAAGCCA	ATGCAACAGA	AACTCTAGCT	840
GGTTTACGAA	ATAATTTGAC	TCTTCAAATT	ATGGATAACA	ATAGTATCAT	GGCAGAAGCA	900
GAAAAATTAC	TTGCGTTGTT	AAAAGGAAGT	AATCCTTCAT	CTGTAAGTAA	GGAAAAAATA	960
AAC						963

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...747
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

CTGCAGTCGA	CTCAAGTCGA	TGCCCATGGT	TATATGGGAC	GTGGCTGGGA	CTGGGCCGAC	60
ATGCTGGGCT	TCACCGTAGC	TGGTTACGGT	GTTGTTTCCA	TGGATGTGCG	GGGCCAGTCA	120
GGTTACTCAC	AAGACGGCTT	GC GTTCTCCT	TTAGGAAAATA	CCGTGAAGGG	GCATATTATC	180
CGTGGTGCTA	TGGAAGGTCG	GGACCACCTC	TTTTATAAAG	ATGTTTATCT	GGATATTTAC	240
CAGTTGGTCG	AAATTGTTGC	TAGTCTGTCT	CAGGTTGATG	AGAAGCGTCT	TTCTAGCTAT	300
GGTGCCTCAC	AAGGAGGGGC	TCTAGCTCTA	GTTGCAGCAG	CGCTCAATCC	TCGAATTCAG	360
AAAACAGTTG	CCATTTATCC	CTTCTTGTCA	GACTTCAGAC	GGGTGATTGA	GATTGGTAAT	420
ACTAGCGAGG	CTTACGACGA	ACTTTTCCGT	TATTTCAAGT	TTCACGACCC	CTTCCATGAA	480
ACAGAGGAGG	AAATCATGGC	GACCCTTGCC	TATATCGATG	TCAAAAATCT	TGCCCATCGT	540
ATCCAAGGTG	AGGTTAAGAT	GATTACGGGC	TTGGACGACG	ATGTTTGCTA	TCCCATTACC	600
CAGTTTGCGA	TTTATAATCG	TCTGACCTGC	GATAAAACCT	ATCGCATCAT	GCCTGAGTAT	660
GCTCACGAAG	CCATGAATGT	ATTTGTCAAT	GACCAAGTCT	ACAACTGGCT	CTGTGGAAGT	720
GAGATTCCTT	TTAAATATCT	AAAATAA				747

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

AAAAACACGA	CTTCACCCTT	TTTGGTAAAT	ACCGTATCGT	GCTTGGTAGT	GTTTTGCTAC	60
TTTACAGTTT	TGTCCGTTTA	TTTGTATAAG	AAAAACCTTG	AAGGGGTAAC	TCTTCAAGGT	120
TTTATACTCT	TAGAAAATCT	CTTCAAACCG	CGTCAGCTTT	ATCTGCAACC	TCAAAACAGT	180
GTTTTGAGCA	GCCTGCGGCT	AGCTTCCTAG				210

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

ATCGCAACGA	CCTGGTATAT	CTATTTACCG	CCCCTTAACC	TGACCAGCTG	GGAATTTCTC	60
TTCTTCCTCT	GTGGGCATTT	GTTAGTTGTG	GCAATCTTAT	TTGGCTTTGG	CAAGGGGATA	120
AACCTTGTC	AAACGGTTCA	TGTGCGCCAC	GGTAAGGCGG	AAGCTGCCTT	AAATCTTGAG	180
GGTTTCAAAA	TCAATCGGTT	AGGGAAAAAT	CTGTTAGCTT	CGATTGGAGG	AATTCTTCTC	240
TTGGCAGCTT	TGGTTTCCTT	GGTAACCTCC	AGCATGTTTC	AGGCTAAAAA	TTATGCCAAT	300
GTAATCACGG	TTACGGAAAA	AGACTTTACT	GAATTTCCCTA	GGAGTGACAC	CAGTAAGGTT	360
CCTATCCTAG	ATAGAAGTAC	TGCTGAAAAA	ATTGGAGACC	GCTACTTGGG	TTCCCTAACC	420
GATAAGGTGT	CGCAATACGT	AGCGGCAGAT	ACCTATACCC	AATTGACAAT	TGATGGGAAA	480
CCTTATCGGG	TCACACCACT	AGAATATGCA	GACCCTATCA	AATGGTTTAA	CAATCAAGCC	540
AAGGGAATCG	GTGAATATAT	CAAGGTGGAC	ATGGTAACCTG	GAAATGCGGA	TTTGGTGGAC	600
TTGAAGACAC	CAATCAAGTA	TTCAGACTCG	GAGTATTTTA	ACCGTGATGT	CAAACGTCAC	660
CTGCGCTTGA	AGTACCCGAC	CAAAAATCTTT	AAAACTCCAT	CTTTTGAGGT	GGACGATGAG	720
GGCAATCCTT	TCTATGTAGC	AACGGTTTAC	CAAAAAGCAAT	TTGGACTTGC	TGTTCCCTCGT	780
CCTGCTTCAG	TCATTATCTT	GGATGCTACA	AATGGAGAAA	CCAAGGAATA	CAGCTTATCA	840
GATGTTCCAG	AATGGGTGGA	CAGGATCTAT	CCAGCAGAGG	AAACCATTGA	GCAAATCAAC	900
TACAACGGCA	AGTACAAGGA	CGGTTTCTTG	AATGCCATGA	TTTCCAAGAA	AAACGTGACC	960
CAGACTACCA	AGGGCTATAA	TTACTTGTCT	ATCGGTAATG	ACATCTATCT	CTACACAGGT	1020
GTGACGTCGG	CTAATGCGGA	TGAGAGTAAT	CTTGTTTCA	TCCTTGAAAA	TATGCGAACA	1080
GGAGAAATCA	CTAAGTATAG	CTTGGCTTCT	GCGACAGAAG	AATCAGCCCC	TGAATCAGCA	1140
GAAGGTGCTG	TTCAGGAGAA	ATCCTACAAA	GCAACCTTCC	CAATCCTCAT	CAACCTCAAT	1200
GACAAGCCTC	TCTACATCAT	GGGCTTGAAG	GACAATGCTG	GCTTGGTCAA	AGAGTACGCC	1260
CTGGTAGACG	CAGTCGAGTA	CCAAAATGTT	ATCGTTGCTA	CTACAGTGGA	AGAGATGCTC	1320
AGCAAGTATG	CCAATAAAAA	CGACCTTGAA	ATTGACAATG	CAACGACAGA	AAGCATCAAT	1380
GGAGTAGTAG	CAGACCTCAA	ATCAGCTGTT	ATCAAGGGAG	ACACTGTCTA	CTTCTTTAAA	1440

GTTGATGGCA AGATATACAA GGTCAAGGCT TCAGTATCCG ATGACTATCC TTACCTTGAA	1500
AATGGTAAAA CCTTCGAAGG TCAAGTAGGA AAAGACAAAT ATCTCAAGAC CTTTAAGCTA	1560
CGGTAA	1566

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GACATGACGA CAAATCGTAA GGACGAGCAT ATCCTCTATG CCCTTGAGCA GAAAAGTTCC	60
TATAATAGCT TTGATGAGGT GGAGCTGATT CATTCTTCCT TGCCTCTTTA CAATCTGGAT	120
GAAATCGATC TTTCGACAGA GTTTGCTGGT CGAAAGTGGG ACTTTCCTTT TTATATTAAT	180
GCCATGACTG GTGGAAGTAA TAAGGGAAGA GAAATCAATC AAAAGCTGGC TCAGGTGGCG	240
GAATCCTGTG GTATTTTATT TGTAACGGGT TCTTATAGCG CAGCCCTCAA AAATCCAACG	300
GATGATTCTT TTTCTGTCAA GTCTAGTCAT CCCAATCTCC TCCTTGGAAC CAATATTGGA	360
TTGGACAAGC CTGTCGAGTT AGGACTTCAG ACTGTAGAAG AGATGAATCC TGTTCTATTG	420
CAAGTGCAATG TCAATGTCAT GCAGGAATTA CTCATGCCCG AGGGAGAAAG GAAGTTTAGA	480
AGCTGGCAAT CGCATTTAGC AGATTATATC AAGCAAATTC CCGTTCCTAT TGTCCTCAAG	540
GAAGTGGGCT TTGGAATGGA TGCCAAGACA ATCGAAAGAG CCTATGAATT CGGTGTTTCGT	600
ACAGTGGACC TATCGGGTCG TGGTGGCACC AGCTTTGCCT ATATCGAAAA CCGTCGTAGT	660
GGCCAGCGTG ATTACCTCAA TCAATGGGGT CAGTCTACCA TGCAGGCCCT TCTCAATGCC	720
CAAGAATGGA AAGATAAGGT CGAACTCTTG GTTAGTGGAG GGGTTCGGAA TCCGCTGGAT	780
ATGATTAAGT GCTTGGTTTT TGGTGCTAAG GCTGTGGGAT TGTCACGAAC CGTTCTGGAA	840
TTGGTTGAAA CCTACACAGT TGAAGAAGTG ATTGGCATTG TCCAAGGCTG GAAAGCAGAT	900
CTACGCTTGA TTATGTGTTT CCTTAACTGT GCCACCATAG CAGATCTACA AAAAGTAGAC	960
TATCTTCTTT ATGGAAATTT AAAAGAAGCA AAGGATCAGA TGAAAAAGGC GTAA	1014

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GCCTTTGCGA	CCAAGCCAAA	ACAGTTCATC	TTTATGGCAA	AAAAAGAACT	CTTTACCAAC	60
CGTATCTTTG	GTTGGTGGAT	TCGTATGTGT	GGCGCCTTTC	CCATCGACCG	TGAAAATCCC	120
AGCGCCTCAG	CCATCAAATA	TCCTATCAAC	GTTCTCAAAA	AAAGTGACCG	CTCTCTCATC	180
ATGTTTCCAA	GTGGTAGCCG	CCACTCAAAC	GATGTCAAGG	GGGGCGCAGC	ACTGATTGCC	240
AAAATGGCCA	AGGTCCGTAT	CATGCCGGTT	ACCTACACCG	GTCCCATGAC	TTTGAAGGGC	300
TTGATTAGCC	GTGAACGTGT	CGATATGAAC	TTTGGAATC	CAATCGATAT	CTCAGATATC	360
AAGAAAATGA	ATGATGAAGG	CATTGAAACA	GTCGCCAATC	GTATTCAAAC	AGAATTCCAA	420
CGTCTGGACG	AAGAAACGAA	ACAATGGCAC	AATGATAAAA	AACCAAATCC	ACTCTGGTGG	480
TTTATCCGCA	TCCCTGCCCT	CATCCTTGCT	ATTATCCTCG	CTATCCTAAC	CATCATCTTT	540
AGCTTTATCG	CAAGCTTCAT	CTGGAACCCA	GATAAGAAAA	GGGAGAAATT	GCATAGAAGA	600
GAATGA						606

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

AAAACCTCAGA	CTGTTACAGG	AGTACCAAAA	ATGAGTCAGG	AATTTTTTAGC	ACGAATCTTA	60
GAGCAGAAGG	CGCGTGAGGT	GGAGCAGATG	AAGCTGGAGC	AAATCCAGCC	TCTGCGCCAG	120
ACCTATCGCT	TGGCAGAATT	TTTGAAGAAAT	CATCAGGACT	GCTTGCAGGT	AATCGCTGAG	180
GTCAAGAAAG	CTAGCCCTAG	TTTGGGAGAT	ATCAATCTCG	ATGTGGATAT	TGTGCAACAG	240
GCCAGACTT	ATGAAGAAAA	CGGAGCAGTG	ATGATTTCGG	TGTTGACAGA	TGAGGTTTTTC	300
TTTAAAGGGC	ATTTGGATTA	TCTACGGGAA	ATTTCCAGTC	AGGTAGAGAT	TCCGACGCTC	360
AACAAAGACT	TTATCATAGA	TGAAAAGCAA	ATCATCCGCG	CTCGCAATGC	AGGTGCGACA	420
GTTATCTTGC	TTATTGTGGC	AGCCTTGTCC	GAAGAACGCC	TCAAGGAACT	GTATGACTAC	480
GCGACAGAGC	TTGGTCTGGA	AGTCTTAGTG	GAGACTCACA	ATCTAGCTGA	ACTAGAGGTA	540
GCCACAGAC	TTGGTGCTGA	GATTATCGGG	GTCAACAACC	GCAACTTGAC	TACCTTTGAG	600
GTGCACTTGC	AGACCAGTGT	AGATTTAGCC	CCTTACTTTG	AGGAAGGTCTG	CTATTACATT	660

TCTGAATCTG	CCATTTTCAC	AGGGCAGGAT	GCGGAACGAC	TAGCCCCATA	CTTTAACGGA	720
ATTTTGGTAG	GGACAGCTCT	TATGCAGGCA	GAAAATGTGG	CCCAGAGAAT	CAAGGAGTTG	780
CAGATTGACA	AAGGTTAA					798

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

AGAAATAAGA	CAATAATCAG	GAGACAACTA	AACATGTTAT	CACTACAAGA	ATTTGTACAA	60
AATCGTTACA	ATAAAACCAT	TGCAGAAATGT	AGCAATGAAG	AGCTTTACCT	TGCTCTTCTT	120
AACTACAGCA	AGCTTGCAAG	CAGCCAAAAA	CCAGTCAACA	CTGGTAAGAA	AAAAGTTTAC	180
TACATCTCAG	CTGAGTTCTT	GATTGGTAAA	CTCTTGTCAA	ACAACTTGAT	TAACCTTGGT	240
CTTTACGACG	ATGTTAAAAA	AGAACTTGCA	GCTGCAGGTA	AAGACTTGAT	CGAAGTTGAA	300
GAAGTTGAAT	TGGAACCATC	TCTTGGTAAAT	GGTGGTTTGG	GACGTTTGGC	TGCCTGCTTT	360
ATCGACTCAA	TTGCTACTCT	TGGTTTGAAT	GGTGACGGTG	TTGGTCTTAA	CTACCACTTT	420
GGTCTTTTCC	AACAAGTTCT	TAAAAACAAC	CAACAAGAAA	CAATTCCAAA	TGCATGGTTG	480
ACAGAGCAAA	ACTGGTTGGT	TCGCTCAAGC	CGTAGCTACC	AAGTACCATT	TGCAGACTTT	540
ACTTTGACAT	CAACTCTTTA	CGATATTGAT	GTTACTGGTT	ATGAAACAGC	GACTAAAAAC	600
CGCTTGCGTT	TGTTTGACTT	GGATTCAAGT	GATTCTTCTA	TTATTAAAGA	TGGTATCAAC	660
TTTGACAAGA	CAGATATCGC	TCGCAACTTA	ACTCTCTTCC	TTTACCCAGA	TGATAGTGAC	720
CGTCAAGGTG	AATTGCTCCG	TATCTTCCAA	CAATACTTCA	TGGTTTCAAA	CGGTGCGCAA	780
TTGATCATCG	ACGAAGCAAT	CGAAAAAGGA	AGCAACTTGC	ATGACCTTGC	TGACTACGCA	840
GTTGTCCAAA	TCAACGATAT	TCACCCATCA	ATGGTGATTG	CTGAATTGAT	TCGTCCTTTG	900
ACTGCACGTG	GTATCGATCT	TGACGAAGCA	ATCTCAATTG	TTCGTAGCAT	GACTGCCTAC	960
ACTAACCACA	CAATCCTTGC	TGAAGCGCTT	GAAAAATGGC	CTCTTGAATT	CTTGCAAGAA	1020
GTGGTTCCCTC	ACTTGGTACC	AATCATCGAA	GAATTGGACC	GTCGTGTGAA	GGCAGAGTAC	1080
AAAGATCCAG	CTGTTCAAAT	CATCGATGAG	AGCGGACGTG	TTCACATGGC	TCACATGGAT	1140
ATCCACTACG	GATACAGTGT	TAACGGGGTT	GCAGCACTCC	ATACTGAAAT	CTTGAAAAAT	1200
TCTGAGTTGA	AAGCCTTCTA	CGACCTTTAC	CCAGAAAAGT	TCAACAACAA	AACAAACGGT	1260
ATCACTTTCC	GTCGTTGGCT	TATGCATGCT	AACCCAAGAT	TGTCTCACTA	CTTGGATGAG	1320
ATTCTTGGAG	ATGGTTGGCA	CCATGAAGCA	GATGAGCTTG	AAAAACTGTT	GTCTTATGAA	1380
GACAAAGCAG	CTGTCAAAGA	AAAATTGGAA	AGCATCAAGG	CTCACAACAA	ACGTAAATTG	1440
GCTCGTCACT	TGAAAGAACA	CCAAGGTGTG	GAAATCAATC	CAAATTCTAT	CTTTGATATC	1500
CAAATCAAAC	GTCTTCACGA	GTACAAACGC	CAACAAATGA	ACGCTTTGTA	CGTGATCCAC	1560
AAATACCTTG	ACATCAAAGC	TGGTAACATC	CCTGCTCGTC	CAATCACAAT	CTTCTTTGGT	1620
GGTAAAGCAG	CTCCAGCCTA	CACAATCGCT	CAAGATATCA	TTCACTTGAT	CTTTTGCATG	1680
TCAGAAGTTA	TTGCTAACGA	TCCAGCAGTA	GCTCCACACT	TGCAAGTAGT	TATGGTTGAA	1740
AACTACAACG	TTACTGCAGC	AAGCTTCCTT	ATCCCAGCAT	GTGATATCTC	AGAACAAATC	1800

TCACCTTGCTT	CTAAAGAAGC	TTCAGGTACT	GGTAACATGA	AATTCATGTT	GAACGGAGCT	1860
TTGACACTTG	GTACTATGGA	CGGAGCTAAC	GTGGAAATCG	CTGAGTTGGT	TGGTGACGAA	1920
AACATCTACA	TCTTTGGTGA	AGATTTCAGAA	ACTGTTATCG	ACCTTTACGC	AAAAGCAGCA	1980
TATAAATCAA	GCGAATTCTA	CGCTCGTGAA	GCTATCAAAC	CATTGGTTGA	CTTCATTGTT	2040
AGCGATGCAG	TTCTTGCAAG	TGGAAACAAA	GAGCGCTTGG	AACGTCTTTA	CAATGAATTG	2100
ATCAACAAAG	ACTGGTTCAT	GACTCTTCTT	GACTTGGAAG	ACTACATCAA	AGTCAAAGAG	2160
CAAATGCTTG	CTGACTACGA	AGACCGTGAC	GCATGGTTGG	ATAAAGTCAT	CGTTAACATT	2220
TCTAAAGCAG	GATTCTTCTC	ATCTGACCGT	ACAATCGCTC	AGTATAACGA	AGACATCTGG	2280
CACCTGAACT	AA					2292

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

AAGGATAAGA	CAAAGATGGG	AAAATATGAT	TTTACAAGCC	TGCCCCAACCG	TTTAGGGCAC	60
CATACCTATA	AATGGAAAGA	AACAGAAACG	GATAGTGAAG	TTCTACCAGC	TTGGATAGCG	120
GATATGGACT	TTGTGGTCTT	GCCTGAAATC	CGCCAAGCCG	TGCAAACCTTA	CGCAGACCAA	180
CTGGTTTATG	GTTATACCTA	TGCCAGTGAA	GACTTAATTA	AGGAAGTTCA	AAAGTGGGAA	240
GCTACACAAAT	ACGGTTACAA	CTTTGACAAA	GAGGCTCTTG	TCTTTATCGA	GGGTGTGGTA	300
CCAGCCATCT	CAACAGCTAT	TCAAACCTTT	ACAAAAGAAG	GCGAGGCGGT	TTTAATTTAAC	360
ACGCCTGTCT	ACCCACCCTT	TGCTCGCAGT	GTCAAGTTGA	ATAATCGTAG	ATTGATTACT	420
AATTCCTTAG	TGGAAAAGGA	TGGTCTGTTT	GAGATTGACT	TTGACCAACT	TGAAAAGGAT	480
TTGGTGGGAA	AGGAGGTTAA	ACTCTATATT	CTTTGCAACC	CTCACAAATCC	TGGTGGACGT	540
GTTTGGGAAA	AAGAAGTGTT	GGAGAAGATT	GGCCAACTCT	GCCAAAAACA	CGGTGTTTTG	600
TTAGTTTTCGG	ATGAGATTCA	CCAAGATTTG	ACCCTCTTTG	GTCAACAAACA	CCAGTCTTTC	660
AATACCATCA	ATCCTGCCCT	CAAAAATTTT	GCTATCGTCT	TGAGCAGTGC	CACTAAAACA	720
TTTAATATTG	CTGGAACAAA	AAATTCCTAT	GCAGTCATTG	AAAATCCTAA	GTTGAGACTA	780
GCTTTCCAGA	AACGCCTGTT	GGCCAATAAT	CAGCATGAAA	TTTCAGGCTT	GGGTATTATTG	840
GCGACAGAAG	CTGCCTATCG	ATACGGTAAA	GATTGGCTAG	AGGAACTCAA	GCAAGTCTTT	900
GAAGACCACA	TCAATTATGT	GGTGGATCTA	TTTGGAAAAG	AGACTAAAAT	CAAGGTCATG	960
AAACCGCAAG	GTACCTACTT	GATTTGGCTT	GACTTTTCAG	CTTATGACCT	GACTGATGAA	1020
ACATTGCAAG	AGTTGTTGAG	AAATGAAGCC	AAGGTTATCC	TCAACCGTGG	TTTGGATTTT	1080
GGAGAGGAAG	GAAGTCTCCA	TGCCCCGATC	AATATAGCTA	TGCCCCAATC	TCTGTTGCAA	1140
GAAGTCTGTC	AGCGGATTGT	GGCTACTTTT	GCCAAACGTT	AA		1182

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...288
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

AATTTAAAGA	CAGACCTTTA	TTTGGTTTGG	GTTACACCTTT	TCCGGGAGGC	CAGAAAGGAA	60
GCTAGAGTAA	TTCAATTGGC	CTTGGATTAC	CATCTGGAAA	AAATCTTTGT	CCAAGCCATG	120
CAGGAATTTT	CAGGAAAATA	CCATGGGAAA	TCAAAAGGTG	TCAGCTCTTA	TCTTCATTCC	180
TTCTGGAGCT	CAGCCATTGT	CTCTGTCCTT	CTAAAATGGA	TCAAGGATGG	CATGAAGGTA	240
CCAGCTGAAA	AGATTGCAGA	TTTAGGTTTA	CCATTTTTTA	AAAAATAG		288

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1041
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

TTGAGAAAGA	CTAGTAAAAT	GATTAATCAA	ATTTATCAAC	TAACTAAACC	TAAGTTTATC	60
AATGTCAAAT	ATCAGGAAGA	GGCTATTGAC	CAAGAGAATC	ATATCCTTAT	CCGTCCCAAC	120
TACATGGCTG	TCTGTCATGC	GGATCAGCGT	TACTACCAGG	GAAAACGTGA	TCCAAGATT	180
TTGAATAAAA	AGCTTCCAAT	GGCAATGATT	CACGAGTCAT	GTGGAATCGT	CATTCTGAC	240
CCGAGCGGAA	CCTACGAGGT	TGGTCAAAAA	GTGTCATGA	TTCCCAATCA	GTCTCCTATG	300
CAGAGTGATG	AAGAATTCTA	TGAAAACCTAC	ATGACAGGGA	CCCATTTCTT	GTCTAGTGGA	360
TTTGATGGCT	TTATGAGAGA	GTTTGTCTT	CTCCCTAAAG	ATCGTGTGGT	GGCTTATGAT	420
GCTATTGAAG	ATACGGTTGC	AGCCATTACA	GAGTTTGTCA	GTGTGGGCAT	GCACGCTATG	480

AATCGTCTAT	TGACTCTTGC	TCATAGCAAG	CGGGAGCGGA	TCCCCGTTAT	TGGAGATGGA	540
AGTTTAGCTT	TTGTGGTTGC	CAATATTATC	AACTATACTT	TGCCAGAAGC	AGAGATTGTG	600
GTTATTGGTC	GTCATTGGGA	AAAGTTGGAA	CTCTTCTCAT	TTGCCAAAGA	ATGCTATATT	660
ACGGATAATA	TTCTGAAGA	GTTGGCCTTT	GACCATGCTT	TTGAATGTTG	TGGTGGTGAT	720
GGTACTGGAC	CAGCTATTAA	TGACTTGATT	CGCTACATTC	GTCCCTCAGG	AACAATTCTC	780
ATGATGGGAG	TTAGCGAATA	TAAAGTCAAT	CTCAATACTC	GCGATGCCTT	AGAAAAGGGC	840
TTGCTCTTGG	TTGGGTCATC	TCGTTCTGGT	CGCATTGATT	TTGAAAATGC	TATCCAAATG	900
ATGAAAGTCA	AGAAATTTGC	CAATCGTCTT	AAAAATATCC	TTTATCTAGA	AGAACCTGTA	960
AGAGAAATTA	AAGATATTCA	CCGTGTCTTT	GCAACCGATT	TAAACACAGC	CTTTAAAACA	1020
GTGTTTAAGT	GGGAAGTATA	A				1041

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

AAAGTGAAGA	CAATGAAAAA	AGTTGCCATT	ATTGGAGCAG	GAATTGTGGG	AGCAACAGCT	60
GCCTACTACC	TCTCGAGAGA	AAGTGACCTA	GAGGTGACCG	TTTTTGACCA	TGAGCAAGGT	120
CAAGCCACCA	AGGCCGCAGC	AGGAATTATC	AGTCCTTGGT	TTTCCAAACG	CCGTAATAAA	180
GCCTGGTACA	AGATGGCGCG	CTTGGGGGCT	GATTTTTATG	TGGATTTATT	AGCTGATTTA	240
GAGAAATCAG	GACAAAAAAT	CGACTTTTAC	CAGCGTTCGG	GAGTCTTTCT	CTTGAAAAAG	300
GATGAATCCA	AGTTGGAAGA	ACTTTATCAA	CTGGCCCTCC	AGCGCAGAGA	AGAATCTCCC	360
TTGATAGGGG	AATTAGCCAT	TCTGGACCAA	GCTTCAGCTA	ATGAATTATT	CCCTGGTTTG	420
CAGGGATTTG	ACCGCTGCT	CTATGCTTCT	GGTGGAGCGA	GAGTAGATGG	CCAACCTCTG	480
GTAACCTCGT	TGCTAGAAGC	CAGTCATGTC	AAGCTGGTCA	AAGAAAAAGT	GACTCTGACA	540
CTCTTATCAT	CAGGCTACCA	GATTGGCGAA	GAGGTGTTTG	ATCAGGTTAT	TTTGGCAACG	600
GGAGCTTGGT	TGGGGGACAT	GTTAGAGCCT	TTAGGTTATG	AAGTGGATGT	CCGTCCTCAA	660
AAAGGACAAC	TACGAGATTA	TCAGCTTGCC	CAAGACATGG	AAGCTTACCC	TGTTGTCATG	720
CCAGAAGGGG	AGTGGGATTT	GATTCCCTTT	GCAGGTGGGA	AATTATCCTT	GGGCGCTACC	780
CATGAAAATG	ACATGGGATT	TGATTTGACG	GTAGATGAAC	CCTTGCTCCA	ACAAATGGAG	840
GAGGCGGCCT	TGCCTCATTA	CCCAGTTTTA	GCTAGAGCGA	CTTCAAGGGC	TGAGCGTGTG	900
GGAATCCGTG	CCTATACCAG	TGATTTCTCT	CCCTTCTTTG	GGCAGGTGCC	AGAATTGGCA	960
GGTGTCTATG	CAGGCAGTGG	ACTAGGTTCA	TCAGGCCTCA	CAACTGGTCC	TATCATTTGGT	1020
TACCATCTAG	CCCAACTGAT	CCAAGACAAG	GAGTTGACCT	TGGACCTCT	AAATTACCCA	1080
ATTGAAAAC	ATGTCAAACG	AGTAAAAAGC	GAATAA			1116

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

AGGACGAAGA CCTCTTGGTT CCGCTTGATT ATTCAAAAAT TGAAGGAATC GAAAATATCG	60
GACCAGAGTT TCTCAACCAG TCCTTTGACC CAGGTAATAA ATTCTCCATC CCTTACTTCT	120
GGGGCGACTC ACTTTGTGGA GAACTTTTCA GACACGGAAC AACTCAATAA AAAGGTTAAG	180
ATTATTCCTT TGGAAAGTCGT GCTCCGCAAC TATACTGCTG GTTCCTTTTC AAAACGTTTT	240
GGTGTGGATG AGGGAATCGC CTTGGAGACT CCGATTGTCG AATTTTACTA CAAAAATGAT	300
GATTTGGATG ATCCATTTAT CAATGATGAG CATGTGAAAT TCCTACAGAT TGCGGGTGAC	360
CAGCAGATTG CCTACTTGAA GGAAGAAACG CGTCGTATCA ATGAACTATT GAAAGTCTGG	420
TTTACTGAGA TTGGGCTTAA ATTGATTGAC TTTAAGCTAG AGTTCGGTTT TGACAAGGAT	480
GGCAAGATTA TCTTGGCAGA CGAATTTTCA CCAGATAACT GCCGCTTGTG GGACGCTGAT	540
GGCAACCACA TGGATAAGGA TGTTTTCCGT AGAGGATTGG GAGAACTAAC CGACGTTTAT	600
GAGATTGTTT GGGAAAAGTT GCAGGAATTG AAATAA	636

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1671 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GGACGGAAGA CTGCTTCCTC CCTTTTATCA GAAAAGGAGA AACAGATGAC ACTTGATAAA	60
GGAAAAGTAG TCTATCAAAT CTATCCAAAA TCTTACAAAG ACACCACTGA AAACGGTATT	120

GGGGATTTCC	GTGGGATTAT	CGAAAAAATT	CCCTATTTAG	CCAAACTAGG	TGTGGATATG	180
GTCTGGCTCA	ATCCATTCTA	TCCAAGCCCT	CAACGGGATA	ATGGTTACGA	TATTTTCAGAT	240
TATATGGCAG	TGGATCCTCT	TTTTGGTGAT	ATGGCTGATT	TTGAGGAAAT	GGTGTGTGTC	300
GGTAAAGAGC	ACAAGATTGA	CTTTATGCTG	GACATGGTAC	TTAATCATTG	TTCGACAGAG	360
CATGAATGGT	TTCAGAAAAGC	CCTAGCTGGT	GATAAGTATT	ATCAAGACTT	TTTCTTCATC	420
CAAGACCAAC	CAACAGATTG	GCAGTCTAAG	TTTGGTGGTT	CTGCATGGGC	GCCTTTTCGGG	480
GATACTGGGA	AATACTATCT	TCACCTATTT	GATGAGACCC	AGGCTGACCT	TAACTGGCGC	540
AATCCCAATG	TCCGTAAGGA	GCTTTTCAAG	GTTGTTAATT	TCTGGCGCGA	CAAGGGTGTC	600
AAAGGTTTTC	GATTTGATGT	GATCAATTTG	ATCGGTAAGG	ACGAGGTTTC	AGTGGACTGT	660
CCTGAAAAATG	AAGGGAAGCC	AGCTTATACA	GACAAAACCCA	TCGTTTCATAA	CTATTTGCGT	720
ATGATGAACC	AAGCCACTTT	TGGATCTGAC	GATAGCTTTA	TGACAGTTGG	GGAAATGTCT	780
TCTACCACCA	TGGAAAACTG	TGTCCTCTAT	TCGTCGCCCTG	ATCGTCAGGA	ATTATCCATG	840
ACCTTTAATT	TTCATCACCT	CAAGGTGGAC	TATAAGGATG	GACAAAAGTG	GACCTTGGCT	900
CCCTTTGATT	TTGAAGAGTT	GAAGAGTCTT	TACCATAGTT	GGGGTAAGGA	AATGAGTGAT	960
AAAGACGGTT	GGAGTGCCCT	CTTTTGGAAC	AATCACGATC	AACCACGTGC	CTTGAACCGT	1020
TTTGTGCGATA	TTCAAAACTT	CCGCAAGGAA	GGAGCCACTA	TGCTAGCAGC	CAGCATTCAC	1080
CTGTCACGTG	GGACACCTTA	TATCTACATG	GGTGAGGAAA	TCGGGATGAT	TGACCCAGAC	1140
TATGATTCTA	TGGCTGATTA	TGTGGATGTC	GAATCGCTTA	ATGCCTATCA	GATGCTCTTA	1200
GAAGAAGGAA	AGAGTCAGCA	AGAAGCCCTT	CAGATTATTC	AAGCTAAGTC	GCGTGATAAT	1260
TCACGCATT	CCATGCAGTG	GGATGCTTCG	GAAAAATGCAG	GATTTTCAAC	AGGCACTCCT	1320
TGGTTGAAAAG	CTGGTAAATC	CTATAAATAC	ATCAATGTAG	AAAAATGAAAT	CCAGGGTCCG	1380
ATTTTACCT	TCTATCAAGA	CTTGATTCGA	CTGCGTAAGG	AAATGCCAAT	CATTTTCAGAA	1440
GGAAGTTACA	AACCAGCCTT	TGAAGATAGC	AAACAAGTCT	ACGCTTTTGA	ACGCCAGTTT	1500
GAGGATCAAA	AGTTACTAGT	GCTCAATAAC	TTTTATGCTA	AAGAAGTGGA	AATCGACTTG	1560
CCAGCAGTCT	ACCAAAATGG	ACAGATTTTG	ATATCAAAC	ATGAAGATGC	AGAAGTGTCT	1620
GAGAAAATTC	TACTCAAACC	CTATCAAACA	CTGGCTATTT	ATGTAAATTA	A	1671

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

AGAAATGAGA	CTTTAAAAAT	GGCAGTTAAA	ATCCGTTTGA	CTCGTATGGG	TTCTAAGAAA	60
AAACCTTTCT	ACCGTATCAA	CGTAGCAGAT	TCACGTTTAC	CACGTGACGG	ACGTTTCATC	120
GAAACAGTTG	GAACCTTACAA	CCCACTTGTT	GCTGAAAACC	AAGTAACTTT	GAAAGAAGAC	180
CGCGTTCTTG	CATGGTTGGC	TAATGGAGCT	CAACCTTCAG	ACACAGTACG	TAACATCCTT	240
TCAAAAAGAAG	GCGTATTGAA	AAAATTCAC	GATTCTAAAT	TTTCAAAAATA	A	291

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

CAAAAGGAGA CTTGTATGAA TACTTATTGT AATATAAATG AAACAATGCT GAGTGAGGTT	60
TATGGAGGTA ATTCCGGAGG AGCAGCTGTA GTTGCTGCTT TAGGTTGTGC AGCGGGTGGA	120
GTGAAATATG GGAGACTTCT AGGACCATGG GGCCTGCAA TAGGAGGAAT TGGAGGAGCA	180
GTGGTTTGTG GATATTTAGC CTATACCGCT ACATCATAA	219

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

AGAAAGGAGA CAGCTATGCA ATCTACAGAA AAAAAACCAT TAACAGCCTT TACTGTTATT	60
TCAACAATCA TTTTGCTCTT GTTGACTGTG CTGTTTCATCT TTCCATTCTA CTGGATTTTG	120
ACAGGGGCAT TCAAATCACA ACCTGATACA ATTGTTATTC CTCCTCAGTG GTTCCCTAAA	180
ATGCCAACCA TGGAAAACTT CCAACAACCTC ATGGTGCAAG ACCCTGCCTT GCAATGGATG	240
TGGAAGCTCAG TATTTATCTC ATTGGTAACC ATGTTCTTAG TTTGTGCAAC CTCATCTCTA	300
GCAGGTTATG TATTGGCTAA AAAACGTTTC TATGGTCAAC GCATTCTATT TGCTATCTTT	360
ATCGCTGCTA TGGCGCTTCC AAAACAAGTT GTCCTTGTAAC CATTGGTACG TATCGTCAAC	420

TTCATGGGAA	TCCACGATAC	TCTCTGGGCA	GTTATCTTGC	CTTTGATTGG	ATGGCCATTC	480
GGTGTCTTCC	TCATGAAACA	ATTTAGTGAA	AATATTCCTA	CAGAGTTGCT	TGAATCAGCT	540
AAAATCGACG	GTTGTGGTGA	GATTTCGTACC	TTCTGGAGTG	TAGCCTTCCC	GATTGTGAAA	600
CCAGGGTTTG	CAGCCCTTGC	AATCTTTACC	TTCATCAATA	CTTGGAATGA	CTACTTCATG	660
CAATTGGTAA	TGTTGACTTC	ACGTAACAAT	TTGACCATCT	CACCTGGGGT	TGCGACCATG	720
CAGGCTGAAA	TGGCAACCAA	CTATGGTTTG	ATTATGGCAG	GAGCTGCCCT	TGCTGCTGTT	780
CCAATCGTCA	CAGTCTTCCT	TGTCTTCCAA	AAATCCTTCA	CACAGGGTAT	TACTATGGGA	840
GCGGTCAAAG	GATAA					855

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

TCTCCTTGGA	CTACAAGACT	TTCAAAACCT	TTGCCATCAA	GACCTACTGT	ATCCATACCG	60
ATGTGGATGA	GCAATTCAAC	TCCCTCGTCA	GAGACAATGC	CGATGGCATG	CTTGGTAGGG	120
AAAAGAACCG	TACTGTTC	ATTAACTGGA	GAGGTCAACT	CACCTTGGCT	TGGTTCAATG	180
ACCAGACCTT	GCCCCATGAC	ACCTGATGCA	AAAACAGGAT	CCGTCGCTTG	A	231

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

CAAAAATGGA	CAAAAGAGCT	AATGGTTACT	TGGATTTTGT	GGGCACTTAT	ACTAGCAATG	60
TTGGCGTGGA	TGGGCTTTAA	CTATCTTCGT	ATTCGCCGTG	CGGCTAAAAT	TGTGGACAAT	120
GAGGAGTTTG	AAGCCTTGAT	TCGTACGGGT	CAATTGATTG	ATTTGCGCGA	CCCAGCAGAA	180
TTCCACAGAA	AACATATCCT	TGGTGCACGC	AATATTCCTT	CAAGTCAGTT	GAAAAC TAGT	240
CTTGCAGCCC	TTCGTAAAGA	TAAACCTGTC	CTTCTCTACG	AAAACCAACG	TGCGCAACGA	300
GTTACAAATG	CAGCTCTTTA	CTTGAAAAAA	CAAGGTTTTT	CTGAGATTTA	TATCCTTTCT	360
TATGGCTTGG	ATTCTTGGA	AGGGAAAAGT	AAGACTAGCT	AA		402

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

ATGGAATGGA	CAACTGAGCG	TCGTTACAGA	CTTTATCAAG	AATGGACGCA	AGAAGAAATT	60
CAACATATAA	ATGAAAATAT	GGCACAACT	CCATGGCATA	CTCATTANCA	TGTTGAAGCA	120
AAAACAGGAC	TTCTCAACGA	CCCAAATGGC	TTTTCTTACT	TCGATGGCAA	TTGGATCCTC	180
TTTAACCAGA	TTTTTCCTTT	TGGTGCANCC	CACGGTTTAN	ATTCTTGGGC	CCACCTAAAA	240
ATTAATGATT	GGGTTCACTT	ANAAAAACCT	GAAATCAAGT	TTTGGCAAAA	TCCTCATTNA	300
ATNTTCAGGG	TCCCAACCTC	GGTTCGTCCA	TCCAATTTGG	GCAAAAATTA	TTCTTTTTTT	360
TTCCGGAGAT	TTTCCCAAT	AAAAAATGGA	TCGTCCCCCT	AA		402

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```
AGTTCTCGGA  CTTCAGCCCT  TTTTAAAGGA  GTAGAAATGA  AATTAACAAT  CCATGAAATT      60
GCCCAAGTTG  TTGGAGCCAA  AAATGATATC  AGTATCTTTG  AGGACACCCA  GTTAGAAAAA     120
GCTGAGTTTG  ATAGTCGTTT  GATTGGAAct  GGAGATTTAT  TTGTGCCACT  TAAAGGTGCG     180
CGTGATGGCC  ATGACTTTAT  TAAAACAGCC  TTTGAAAATG  GTGCAGCAGT  AACCTTGTCT     240
GAGAAAGAGG  TCTCAAATCA  TCCTTACATT  CTAGTAGATG  ATGTTTTGAC  AGCCTTTCAA     300
TCCCTAGCAT  CCTACTATCT  TGAAAAACG  ACTGTTGATG  TCTTTGCTGT  TACAGGTTCA     360
AATGGCAAGA  CAACGACTAA  GGATATGTTG  GCGCATTTAC  TGTCAACAAG  ATACAAGACC     420
TACAAAACAC  AAGGCAATTA  CAATAATGAG  ATTGGCCTTC  CTTACACAGT  TCTCCACATG     480
CCTGAAGGAA  CAGAAAAGTT  GGTCTTGGAG  ATGGGGCAGG  ACCACTTGGG  AGATATTCAT     540
CTCTTGCTCG  AATTGGCTCG  TCCAAAAACA  GCCATCGTGA  CCTTGGTTGG  AGAAGCTCAT     600
TTGGCCTTTT  TCAAAGATCG  TTCTGAGATT  GCTAAAGGAA  AAATGCAAAT  TGCAGACGGA     660
ATGGCTTCAG  GTTCCTTGCT  TTTAGCGCCG  GCTGACCCTA  TCGTAGAGGA  CTATTTGCCA     720
ACTGATAAAA  AGGTGGTCCG  TTTTGGGCAA  GGGGCAGAGT  TGGAAATCAC  AGACTTGGTT     780
GAGCGCAAAG  ATAGCTAAC  CTTCAAGGCC  AATTTCTTAG  AGCAAGCCCT  TGATTTGCCA     840
GTAAC TGGA  AGTACAATGC  TACCAATGCT  ATGATTGCAT  CCTATGTTGC  CCTACAAGAA     900
GGAGTTTCAG  AGGAGCAAAT  TCATCAGGCC  TTCCAAGGTC  TTGAATTGAC  GCGTAATCGT     960
ACTGAGTGGA  AGAAAGCAGC  CAATGGAGCA  GATATCCTGT  CAGACGTATA  TAATGCCAAT    1020
CCAACTGCTA  TGAAGCTGAT  TTTAGAGACT  TTCTCTGCCA  TTCCAGCCAA  TGAAGGTGGC    1080
AAGAAAAATTG  CAGTGTGGC  GGATATGAAG  GAGCTTGGTG  ACCAGTCTAT  TCAACTCCAT    1140
AACCAGATGA  TTTTGAGCCT  TTCTCCAGAT  GTGCTTGATA  CCGTTATTTT  CTATGGAGAA    1200
GACATTGCTG  AATTAGCCCA  ATTGGCCAGT  CAAATGTTCC  CAATAGGCCA  CGTTTACTAC    1260
TTCAAGAAAA  CAGAAGACCA  AGACCAATTT  GAAGACCTAG  TCAAGCAGGT  CAAGGAAAGC    1320
CTCAGTGCCA  ATGATCAAAT  CTTGCTCAAG  GGCTCTAACT  CTATGAACCT  AGCCATGTTG    1380
GTAGAAAGTT  TAGAAAATGA  AACCAAGTGA                                     1410
```

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```
ATACGACGGA  CACTTTCGCG  AACATGCTTG  GCCTTGACGG  GAGCGTCTGC  TTCCACCTCA      60
```

CCCAAGCGTT	CTCGCAACTT	ACTATTTTCC	AAGCGAAGAG	CTGTATTTTC	TTCTACCAAG	120
CTCTTGAGAT	TTTTCTTGAT	GGCTTCCACA	TCGGCTAAGG	TTACCAATAA	TTGTTGGGAA	180
AAATCATCCA	GCGCGTCAAA	TAATTCTTTT	GTGTCCATAA	AACAAGCCCC	TTTCCTGTCT	240
TTATCATTCA	TTTTTGAGTT	TATATTTCTT	TCAAGACCAG	ATATTCCATG	GCATTTTGAA	300
AGCTGA						306

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

CACACTGGGA	CACATTTCAA	AAACAGTTGG	TTTTTGAATG	TCCCAAACAT	GGCTAAAATA	60
GGTCTTGGA	ATATTCCTCG	TGAAACTCCT	CTTAAGACTG	TAGCAGCTGA	AAGCAATCCA	120
ACTGGATATG	CAACAAAATT	AGAGGAAGTA	TCTCTTGGTA	AGGATACTAT	GA CTGGACAC	180
TGGGAAATCA	TGGGACTCAA	CATTACTGAG	CCTTTCGATA	CTTTCTGGAA	CGGATTCCCA	240
GAAGAAATCC	TGACAAAAAT	CGAAGAAATC	TCAGGACGCA	AGGTTATTCG	TGAAGCCAAC	300
AAACCTTATT	CAGGAACGGC	TGTTATCGAT	GATTTTGGAC	CACGTCAGAT	GGAAACTGGA	360
GAGTTGATTA	TCTATACTTC	AGCTGACCCT	GTTTTGCAGA	TTGCTGCCCA	CGAAGACATT	420
ATTCCTTTGG	ATGAATTGTA	CCGTATCTGT	GAATACGCTC	GTTTCGATTAC	CCTTGAGCGT	480
CCTGCCCTTC	TTGGTCGCAT	CATTGCTCGC	CCTTATGTAG	GTGAACCAGG	TAACCTTCACT	540
CGTACGGCAA	ACCGTCGTGA	CTTGGCTGTA	TCTCCATTTT	CCCCAACTGT	TTTGGATAAA	600
TTGAATGAGG	CTGGTATCGA	TACTTATGCT	GTGGGTAAAA	TCAACGATAT	CTTTAACGGT	660
GCTGGTATCA	ACCATGACAT	GGGTCACAAC	AAGTCAAATA	GTCATGGAAT	TGATACACTA	720
TTGAAGACTA	TGGGACTTGC	TGAGTTTGAA	AAAGGATTCT	CATTACAAAA	CCTAGTTGAC	780
TTTGATGCCC	TTTACGGCCA	TCGTCTTAAT	GCTCACGGTT	ACCGTGATTG	CTTGCA TGAG	840
TTTGATGAAC	GCTTACCTGA	AATTATCGCA	GCTATGAGAG	AGAATGACCT	TCTCTTGATT	900
ACTGCGGACC	ATGGAAATGA	CCCAACGTAT	GCAGGAACGG	ATCACACTCG	GGAATATATT	960
CCATTGTTGG	CCTATAGCCC	TGCCTTTAAA	GGAAATGGTC	TCATTCCAGT	AGGACATTTT	1020
GCGGATATTT	CAGCGACTGT	TGCCGATAAC	TTTGGTGTGG	AAACTGCTAT	GATTGGGGAA	1080
AGTTTCTTAG	ATAAATTGGT	ATAA				1104

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...867
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAATTTTATT	TTCCAAGACT	GGCTCGTCGT	TTGCTTGTA	ATGATGATTA	TGATGTTGAA	60
GTTTCTTTTA	CCATTATGAA	TCCACCACTG	TTGTTCTCTA	AAAGAAGAGA	AGTCAAGAAG	120
ATATCTTGGA	TTCATGGAAG	TATTGAAGAA	CTTCTTAAGG	ATAGCTCTAA	AAGAGAATCA	180
CATAGAAGCC	AGTTGGATGC	TGCGAATACA	ATTGTAGGGA	TTTCAAAAAA	GACCAGCAAT	240
TCTATCAAGG	AAGTTTATCC	AGATTATGCT	TCTAAATTAC	AGACAATCTA	CAATGGATAT	300
GATTTTCAGA	CTATTCTAGA	AAAATCTCAA	GAGAAGATCG	ATATCGAGAT	TGCTCCTCAA	360
AGTATCTGTA	CTATCGGACG	GATTGAGGAA	AATAAGGGTT	CTGACCGTGT	AGTGGAAGTG	420
ATACGATTAT	TACACCAAGA	GGGAAAAAAC	TATCATCTCT	ATTTTATCGG	GGCTGGTGAT	480
ATGGAAGAGG	AACTGAAAAA	ACGAGTCAAA	GAGTATGGGA	TTGAGGACTA	TGTACATTC	540
CTTGTTTATC	AAAAAAATCC	TTATCAGTAT	TTATCTCAGA	CGAAAAGTTCT	CTTGCTATG	600
TCTAAACAAG	AAGGTTTTCC	TGGAGTGTAT	GTGGAGGCCT	TGAGTCTGGG	ACTCCCTTTT	660
ATCTCTACGG	ACGTTGGAGG	GGCTGAGGAA	TTATCCCAAG	AAGGACGATT	TGGACAAATC	720
ATTGAGAGCA	ATCAAGAGGC	AGCTCAGGCG	ATTACTAATT	ACATGACTTC	TGCCTCAAAC	780
TTTGATGTCG	ATGAGGCTAG	CCAATTCATT	CAACAATTTA	CAATTACAAA	ACAAATCGAA	840
CAAGTAGAAA	AACTATTAGA	GGAGTAG				867

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GATAAATTTG	CTAAGTTGTA	TGCCCCTTTT	ATGAAAAAAG	ATAAAGAGGT	TTATGATAAA	60
GTTTGTGAAT	ATCTTAGTCC	TCATTTGAAT	AAAGATATGG	AGGTGCTTGA	ACTTGCTTGT	120
TGGTTTCGTG	TCATAACAGT	TATAGAGGCA	AATAGTTATG	TAAATATAAG	GAGTTCAGA	180

CTTCTACCAA	AGTTTAAAC	TCAAAAATA	AATAGTTGGT	GTGCTGCTTA	CAATATCCAT	240
TTTAATAATG	GATATTGTAA	GCAGCATACC	AATGAATTTA	AAGATTCTTT	AAAGAGTCTT	300
ATTTTGTGA						309

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GGGAAATTTG	CTAAGATAAA	TAAAAAGAAA	GGAGCTCTTA	TGGCCAATAT	TTTTGACTAT	60
CTGAAAGATG	TCGCATATGA	TTCTTATTAC	GACCTTCCCT	TGAATGAGTT	AGACATTCTA	120
ACCTTAATAG	AAATCACCTA	CCTCTCCTTT	GATAATCTGG	TCTCCACACT	TCCTCAACGT	180
CTTTTAGATC	TAGCACCTCA	GGTTCCAAGA	GATCCCACCA	TGCTTACTAG	CAAAAATCGC	240
CTTCAATTAT	TAGATGAATT	GGCTCAACAC	AAGCGCTTCA	AAAATTGCAA	ACTCTCCCAT	300
TTTATCAACG	ACATCGACCC	TGAAGTCAA	AAGCAATTTG	CGGCTATGAC	TTATCGTGTC	360
AGCCTCGATA	CCTATCTGAT	TGTCTTTCGT	GGGACAGATG	ACAGTATCAT	TGGCTGGAAG	420
GAAGATTTCC	ACCTGACCTA	TATGAAGGAA	ATTCTTGCTC	AAAAGCACGC	CCTTCGCTAT	480
TTAAAGAACT	TTTTTGCCCA	TCATCCTAAG	CAAAAAGGTTA	TTCTAGCTGG	GCATTCCAAG	540
GGAGGAAATC	TCGCTATCTA	TGCTGCTAGC	CAAAATTGAGC	AAAGTTTGCA	AAATCAGATC	600
ACAGCAGTTT	ATACATTTGA	TGCACCTGGT	CTCCATCAAG	AATTGACACA	GACTGCGGGT	660
TATCAAAGGA	TAATGGATAG	AAGCAAGATA	TTCATTCCAC	AAGGTTCCAT	TATCGGTATG	720
ATGCTGGAAA	TTCTTGCTCA	CCAAATCATC	GTTTCAAGTA	CTGCCCTGGG	TGGCATCGCC	780
CAGCAGGATA	CCTTTAGTTG	GCAGATTGAG	GATAAGCACT	TCGTCCAAC	GGATAAGACC	840
AACAGTGATA	GCCAGCAAGT	AGACACAACC	TTTAAAGAAT	GGGTGGCCAC	AGTCCCTGAC	900
GAAGAAGTTC	AGCTCTACTT	CGACCTCTTC	TTTGGCCTTA	TTCTTGAGGC	TGGTATTAGC	960
TCTATCAATG	ACTTGGCTTC	CTTAAAGGCG	CTTGAATACA	TTCATCATCT	CTTTGTCCAA	1020
GCTCAATCCC	TCACTCCAGA	AGAAAAGAGAA	ACCTTGGGTC	GCCTTACCCA	GTTATTGATT	1080
GATACTCGTT	ACCAGGCATG	GAAAAATAGA	TAA			1113

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

ATGAATATTG	CAAAAATAGT	CAGAGAAGCG	CGTGAGCAGA	GTCGCTTGAC	AACCTTGGAC	60
TTTGCGACAG	GCATTTTGA	TGAATTTATC	CAATTACATG	GTGACCGTTC	TTTTCGTGAT	120
GATGGTGCAG	TTGTTGGTGG	TATTGGTTGG	CTTGGAGACC	AAGCTGTAAC	AGTGGTTGGT	180
ATCCAAAAAG	GCAAGAGTTT	GCAAGACAAC	CTCAAACGGA	ATTTTGGCCA	ACCACATCCA	240
GAAGGCTACC	GAAAGGCACT	GCGGTTGATG	AAACAGGCTG	AGAAATTTGG	CCGTCCAGTT	300
GTGACCTTTA	TCAATACAGC	AGGTGCTTAT	CCTGGTGTCTG	GAGCGGAAGA	ACGTGGTCAA	360
GGGAAGCTA	TTGCTCGCAA	TCTCATGGAA	ATGAGTGACC	TGAAAGTTCC	TATTATCGCC	420
ATTATTATCG	GTGAAGGTGG	TTCAGGCGGG	GCTCTGGCTC	TAGCTGTCGC	GGACCGTGTC	480
TGGATGCTGG	AAAAATCTAT	CTATGCCATT	CTCAGTCCAG	AAGGCTTTGC	TTCCATTTTA	540
TGGAAGGACG	GTACTCGCGC	CATGGAAGCA	GCAGAACTGA	TGAAAATCAC	TTCGCATGAA	600
CTGTTAGAAA	TGGACGTGGT	GGATAAGGTG	ATTTCTGAAG	TAGGACTTTC	TAGTAAAGAA	660
CTGATTAAGA	GTGTCAAAAA	AGAACTCCAA	ACGGAGCTGG	CTAGACTTTC	ACAAAAACCG	720
CTAGAAGAGT	TGCTGGAAGA	ACGCTATCAA	CGATTTAGAA	AATACTAA		768

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 612 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

TACGATATTG	CAGAAAGTCA	TTTCTATGCT	TCAGCTAATA	ATGTAATCCG	TGATGACGCT	60
TCGTCCTTCC	ACACCTTCTA	TTTTGATCCT	GAGACAGGTC	AACCCTTTAA	AGGTGTAACG	120
AGACAAGGGT	ATAGTGATGA	TTCATGCTGG	GCACGTGGTC	AATCATGGGG	AGTCTATGGT	180
ATTCCTTTGA	CTTATCGTCA	CTTAAAAGAC	GAGTCCTGCT	TTGACTTGTT	TAAGGGTGTG	240
ACCAATTTTT	TCTTGAATCG	TCTGCCAAAA	GATCATGTGT	CCTATTGGGA	TTTGATTTTT	300
AATGATGGTA	GTGATCAATC	ACGAGATTCT	TCAGCAACAG	CTATCGCCGT	CTGTGGGATT	360
CATGAAATGC	TAAAACATCT	CCCAGAGGTG	GATGCTGACA	AAGATATTTA	TAAACATGCT	420

ATGCATGCCA TGCTTCGTTT CTTGATCGAA CATTATGCAA ATGATCAATT TACCCCTGGT	480
GGGACAAAGTC TCCTCCACGG TGTGTACTCA TGGCATTGAG GTAAAGGAGT GGATGAAGGC	540
AATATCTGGG GTGACTACTA TTACCTAGAA GCCCTTATCC GTTTCTACAA AGACTGGAAC	600
CTATATTGGT AG	612

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

CCTGCCATTG CATCTACTAC ACTTCCATCC TTCGAGTATT GCTCCCGATA TCTAGCTAAG	60
TTCCCATCTA CTCCATCTAG TAAGTTCCAT AAAAAAATA GAAACCATGC CAGCAATAAT	120
AGAATGAAAT TAGTTGTAAA TGTCATTGTC AGAAATCCAA GAATCAAAGG GGCTATAGAT	180
AAATAA	186

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1074 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1074
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

AAGCTAATTG	CCGCATTCTA	CAATATGTAC	AAGAAGAGGT	CGGTTGCAAG	GTCTTGCTTG	60
CCCAGAAGGG	CATATTCCCT	CTACAAAAC	TATCCCTTGA	TTAGCCAGTA	TCTATCAGGT	120
ACGACAGCTA	GTGGACTCTA	TGAGGCCAAA	TTGGCAAGGG	AAGAATTTCC	TGGTGAAGTC	180
CATGTATTTG	CGCCTGCTTT	CAAGGATGCA	GACTTGGAGG	AATTGCTAGA	GATAATGGAC	240
CATATCGTCT	TTAACTCAGA	GAGACAGTTG	CGTAAACACG	GTCCGCGTTG	TCGAGAGGCT	300
GGTGTCAAGT	TTGGTTTGCG	CCTCAACCC	CAGTGTTCAA	CTCAAGGAGA	TCACGCGCTC	360
TATGACCCTT	GTGCACCAGG	TTCTCGCTTT	GGAGTTACTA	TAGACAAGAT	TCCGAGTGAT	420
TTGCTAGATT	TGGTTGACGG	ACTTCATTTT	CATACCCTTT	GCGAGCAGGG	AGCAGATGAT	480
TTACAAACAA	CTTTGAAAGC	AGTAGAAGAA	CAGTTTGGTC	CCTACTTACA	TGAGGTAAAA	540
TGGCTCAATA	TGGGTGGTGG	TCATCATATT	ACAAGAGAAG	GTTACGATGT	GGATTTGCTG	600
ATTTTCAGAAA	TCAAGCGTAT	CCGAAAAACT	TACAATCTTG	AAATCTATAT	CGAGCCTGGT	660
GAAGCCATTG	CGCTTAATGC	GGGTTATTTA	GCAACTGAGG	TATTAGATAT	TGTAGAAAAC	720
GGTATGGA	TCTTGGTTTT	AGACGCCCTC	GCGACCTGCC	ATATGCCCTGA	TGTACTTGAG	780
ATGCCCTATC	GTCCATCTTT	GAGAAATGGC	TTTGAGGCAC	AGGAAAAAGC	CCATACCTAC	840
AGACTTTCTT	CTAATACCTG	TCTGACGGGC	GATGTGATTG	GTGATTATAG	TTTTGAAAAT	900
CCAGTCCAAA	TCGGAGACAG	ACTTTATTTT	CAAGACATGG	CCATTTATTC	TTTTGTCAAA	960
AATAATACCT	TTAATGGTAT	TGGATTGCCA	AGCCTCTATC	TCATGGACGA	ACAGGGAGAC	1020
TGTAGCTTAC	TCAAAGCTTT	TGGCTATCAA	GACTTTAAAG	GGAGATTATC	ATGA	1074

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

ATGAGAATTG	CAGATTATAG	CGTGACCAAG	GCAGTGTTGG	AGCGTCACGG	TTTTACCTTT	60
AAAAAGTCCT	TTGGGCAAAA	TTTCTTGACG	GATACCAATA	TCCTTCAAAA	AATTGTGGAT	120
ACGGCTGAAA	TTGATGATCA	GGTCAATGTC	ATCGAAATCG	GGCCAGGTAT	TGGTGCCTTG	180
ACAGAATTTT	TGGCTGAGCG	TGCAGCCCAA	GTCATGGCTT	TTGAGATTGA	CCACCGTTTG	240
GTGCCAATTT	TGGCAGATAC	CCTGCGTGAT	TTTGATAATG	TGACTGTAGT	TAACGAAGAT	300
ATTCTCAAGG	TTGATTTGGC	GCAACATATC	CAAAATTTTA	AAAATCCTAA	CCTGCCAATC	360
AAGGTAGTGG	CTAATTTGCC	TTACTACATC	ACGACGCCTA	TTCTCATGCA	CTTGATTGAG	420
AGTGGCATTG	CTTTTAGTGA	GTTTGTGGTC	ATGATGCAGA	AAGAAGTAGC	GGACCGCATT	480
TCAGCCCAGC	CTAACACCAA	GGCTTACGGT	AGCTTGTCTA	TCGCCGTGCA	GTATTACATG	540
ACAGCCAAGG	TTGCCTTTAT	CGTGCCCTCGT	ACGGTCTTTG	TGCCAGCGCC	AAATGTGGAT	600
TCAGCCATCT	TGAAAAATGGT	GCGCCGTCCA	GAGCCAGCTG	TAGCAGTGGA	AGATGAGAAC	660
TTCTTCTTTA	AGGTTTCCAA	GGCTAGTTTT	ACCCATCGCC	GTAAGACCTT	GTGGAATAAC	720
TTGACAGGTT	ACTTTGGCAA	GA CTGAGGAA	GTCAAGGACA	AGCTGACCAA	GGCTTTGGAC	780
CAGGCAGACT	TGTCGCCAAG	TGTGCGTGGG	GAAGCTCTCA	GCTTGGCAGA	ATTTGCCGGT	840
CTAGCAGACG	CACTTAAAGG	GCAAGGACTC	TAA			873

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

CCTATGATTG	CAGAATTTAT	CGATGGATTG	CAAAAATTCC	ATTTCCCTACA	AAATGCCTTG	60
ATAACAGCTA	TTGTCGTCGG	GATTGTAGCT	GGAGCCGTGG	GATGTTTCAT	TATTCTACGC	120
GGGATGTCAC	TCATGGGAGA	TGCCATTTCA	CATGCTGTCT	TACCAGGTGT	AGCCCTCTCC	180
TTCATCTTGG	GCCTTGACTT	CTTTATCGGA	GCCATTGTCT	TTGGATTGCT	AGCTGCCATC	240
ATCATTACCT	ACATCAAAGG	AAACTCGATT	ATCAAAAGCG	ATACCGCCAT	CGGCATTACC	300
TTTTCTTCTT	TCTTAGCCCT	CGGTATCATC	TTGAATGGTG	TCTCTAAAAG	TTCAACTGAA	360
CTTTTCCATA	TCCTTTTTTG	GTATATCCTG	GCCGTCCAAG	ATACGGATAT	GTTTATTACT	420
ATGGGTGTGG	GGGCAGCCAT	CCTCTTGTTA	ATCTGGATTT	TCTTCAAGCA	ACTCTTGATA	480
ACTTCCTTTG	ATGAACTCTT	GGCTAAAGCC	ATGGGAATGC	CTGTCAATTT	CTATCACTAC	540
CTTCTCATGG	TACTCCTGAC	TCTCGTGTCT	GTGACAGCCA	TGCAAAGTGT	CGGAACTATC	600
CTGATTGTAG	CCATGCTGAT	TACCCCAGCT	GCAACTGCTT	ATCTGTATGC	TAATAGTCTG	660
AAAAGCATGA	TTTTCCCTTC	CTCAACCTTC	GGAGCTACTG	CTTCAGTTTT	GGGACTCTTT	720
ATTGGCTATA	GTTTAAATGT	TGCGGCAGGT	TCTAGTATCG	TGCTTACAGC	TGCTAGTTTC	780
TTTCTCATT	GCTTCTTTAT	CGCTCCCAA	CAACGATATT	TGAAACTGAA	AAATAAACAT	840
TTGTTAAAA	AA					852

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

CCGATGATTG	CCAAGGAGTT	TGAGACTTTC	TTGTTGGGGC	AGGAGGAAAC	TTTTTTGACC	60
CCTGCTAAAA	ATCTAGCTGT	GTTGATTGAT	ACCCACAATG	CGGATCATGC	GACCCCTCTTG	120
CTTAGTCAGA	TGACCTATAC	CCGTGTTCCC	GTTGTGACAG	ATGAAAAACA	GTTTGTGGG	180
ACGATTGGAC	TCAGAGATAT	TATGGCTTAT	CAGATGGAGC	ATGACTTGAG	CCAAGAAATC	240
ATGGCGGATA	CGGATATCGT	TCATATGACA	AAAACGGACG	TAGCGGTTGT	TTCGCCTGAT	300
TTCACCATTA	CGGAGGTCTT	GCACAAGCTA	GTAGATGAGT	CCTTCTTACC	GGTTGTGGAT	360
ACAGAGGGTA	TTTTCCAAGG	GATTATTACG	CGCAAGTCCA	TCCTCAAGGC	CGTTAATGCC	420
CTCTTGCATG	ATTTTAGTAA	GGAATATGAG	ATTTCGATGCC	AATGA		465

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

AATAATGTTG	CAATCGGCGT	GACCTTCTCT	GGTGAAGCCA	GCCAAATGTT	AGAAAAAAT	60
GAAAACTAC	GTTATGTGGT	ACCGACAGAG	GCCAGCAATC	TTTGGTGTGA	CAATATGGTC	120
ATTCCCAAAA	CAGTTAAAAA	CCAAAACTCA	GCCTATGCCT	TTATCAACTT	TATGTTGAAA	180
CCTGAAAAATG	CTCTCCAAAA	TGCGGAGTAT	GTCGGCTACT	CAACACCAAA	CCTACCAGCG	240
AAGGAATTGC	TCCCAGAGGA	AACAAAGGAA	GATAAGGCCT	TCTATCCCGA	TGTTGAAACC	300
ATGAAACACC	TAGAAGTTTA	TGAGAAATTT	GACCATAAAT	GGACAGGGAA	ATATAGCGAC	360
CTCTTCCTAC	AGTTTAAAAAT	GTATCGGAAG	TAG			393

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

TCACAGGTTG	CTCAAAACAC	TGTTTTGAGG	TTGTGGATAG	AACTGACGAA	GTCAGCTCAA	60
AACACTGTTT	TGAGGTTGCA	GATAGAACTG	ACGAAGTCAG	TAACATCTAT	ACGGCAAGGT	120
GAAGCTGACC	ATGGTTTGAA	AAGATTTTCG	AAGAGTATCA	TTTCATCTCA	CTCTAAATCT	180
TACCAACATA	AAACGCATAG	TATCAAAGTT	TTCATCACCT	GA		222

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

CCGCAGGTTG	CTCAAAGCAC	TGCTTTGAGG	TTGCAGATAG	AACTGACGAA	GTCAGCTCAA	60
AACACTGTTT	TGAGGTTGCA	GATAGAACTG	ACGAAGTCAG	TAACATATAT	AGCGGCCAAG	120
GCGACGTTGA	CGCGGTTTGA	AGAGATTTTT	GAAGAGTATG	AAACGAAAAG	GAGGTTGGTC	180
ATTGTACCAG	CCTCCTTTTG	A				201

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

TTGGGGGTTG	CCCCCTGTGA	GATAGGGAAG	TCGCTTAGCT	CTAGGGAGTT	TAGCTCAGCT	60
GGGAGAGCAT	CTGCCTTACA	AGCAGAGGGT	CAGCGGTTTCG	ATCCCGTTAA	CTCCCAAAGG	120
TCCCGTAGTG	TAGCGGTTAT	CACGTCGCCC	TGTCACGGCG	AAGATCGCGG	GTTCGATTCC	180
CGTCGGGACC	GTTTAAGGTA	A				201

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

TTGGGGGTTG	CCCCCTGTGA	GATAGGGAAG	TCGCTTAGCT	CTAGGGAGTT	TAGCTCAGCT	60
GGGAGAGCAT	CTGCCTTACA	AGCAGAGGGT	CAGCGGTTTCG	ATCCCGTTAA	CTCCCAAAGG	120
TCCCGTAGTG	TAGCGGTTAT	CACGTCGCCC	TGTCACGGCG	AAGATCGCGG	GTTCGATTCC	180
CGTCGGGACC	GTTTAAGGTA	A				201

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

TTGGGGGTTG	CCCCCTGTGA	GATAGGGAAG	TCGCTTAGCT	CTAGGGAGTT	TAGCTCAGCT	60
GGGAGAGCAT	CTGCCTTACA	AGCAGAGGGT	CAGCGGTTTCG	ATCCCGTTAA	CTCCCATTTT	120
AGCGGGTGTA	GTTTAGTGGT	AAAACCTACAG	CCTTCCAAGC	TGTTGTCGCG	AGTTCGATTC	180
TCGTCACCCG	CTTTGAACTT	TGTTCTTTGT	ACCAAGTTTT	TGACTTGGGC	GCGTAGCTCA	240
GGTGGTTAG						249

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2928 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

ATGTCTTATT	TCAGAAATCG	GGATATAGAT	ATAGAGAGGA	TCAGTATGAA	TCGGAGTGTT	60
CAAGAACGTA	AGTGTCGTTA	TAGCATTAGG	AAACTATCGG	TAGGAGCGGT	TTCTATGATT	120
GTAGGAGCAG	TGGTATTTGG	AACGTCTCCT	GTTTTAGCTC	AAGAAGGGGC	AAGTGAGCAA	180
CCTCTGGCAA	ATGAAACTCA	ACTTTCGGGG	GAGAGCTCAA	CCCTAACTGA	TACAGAAAAG	240
AGCCAGCCTT	CTTCAGAGAC	TGAACCTTCT	GGCAATAAGC	AAGAACAAGA	AAGGAAAGAT	300
AAGCAAGAAG	AAAAAATTTT	AAGAGATTAC	TATGCACGAG	ATTTGGAAAA	TGTCGAAACA	360
GTGATAGAAA	AAGAAGATGT	TGAAACCAAT	GCTTCAAATG	GTCAGAGAGT	TGATTTATCA	420
AGTGAAGTAG	ATAAACTAAA	GAAACTTGAA	AACGCAACAG	TTACATGGA	GTTTAAGCCA	480
GATGCCAAGG	CCCCAGCATT	CTATAATCTC	TTTTCTGTGT	CAAGTGCTAC	TAAAAAAGAT	540
GAGTACTTCA	CTATGGCAGT	TTACAATAAT	ACTGCTACTC	TAGAGGGGCG	TGGTTCGGAT	600
GGGAAACAGT	TTTACGGTAA	TTACAACGAT	GCACCTTAA	AAGTTAAACC	AGGTCAGTGG	660
AATTCTGTGA	CTTTCACAGT	TGAAAAACCG	ACACCAGAAC	TACCTAAAGG	CCGAGTGC GC	720
CTCTACGTAA	ACGGGGTATT	ATCTCGAACA	AGTCTGAAAT	CTGGCAATTT	CATTAAAGAT	780
ATGCCAGATG	TAACGCATGT	ACAAATCGGA	GCAACCAAGC	GTGCCAACAA	TACGTTTTGG	840
GGGTCAAATC	TACAGATTCG	GAATCTCACT	GTGTATAATC	GTGCTTTAAC	ACCAGAAGAG	900
GTACAAAAAC	GTAGTCAACT	TTTTAAACGC	TCAGATTTAG	AAAAAAAAC	ACCTGAAGGA	960
GCGGTTTTAA	CAGAGAAAAAC	GGACATATTC	GAAAGCGGGC	GTAACGGTAA	ACCAAATAAA	1020
GATGGAATCA	AGAGTTATCG	TATTCCAGCA	CTTCTCAAGA	CAGATAAAGG	AACTTTGATC	1080

GCAGGTGCAG	ATGAACGCCG	TCTCCATTCG	AGTGACTGGG	GTGATATCGG	TATGGTCATC	1140
AGACGTAGTG	AAGATAATGG	TAAAACTTGG	GGTGACCGAG	TAACCATTTAC	CAACTTACGT	1200
GACAAATCCAA	AAGCTTCTGA	CCCATCGATC	GGTTCACCAG	TGAATATCGA	TATGGTGTTC	1260
GTTCAAGATC	CTGAAACCAA	ACGAATCTTT	TCTATCTATG	ACATGTTCCC	AGAAGGGAAG	1320
GGAATCTTTG	GAATGTCCTC	ACAAAAAGAA	GAAGCCTACA	AAAAAATCGA	TGGAAAAACC	1380
TATCAAATCC	TCTATCGTGA	AGGAGAAAAG	GGAGCTTATA	CCATTTCGAGA	AAATGGTACT	1440
GTCCTATACAC	CAGATGGTAA	GGCGACAGAC	TATCGCGTTG	TTGTAGATCC	TGTTAAACCA	1500
GCCTATAGCG	ACAAGGGTGA	TCTATACAAG	GGTGACCAAT	TACTAGGCAA	TATCTACTTC	1560
ACAACAAACA	AAACTTCTCC	ATTTAGAAAT	GCCAAGGATA	GCTATCTATG	GATGTCCTAC	1620
AGTGATGACG	ACGGGAAGAC	ATGGTCAGCG	CCTCAAGATA	TTACTCCGAT	GGTCAAAGCC	1680
GATTGGATGA	AATTCTTGGG	TGTAGGTCCT	GGAACAGGAA	TTGTACTTCG	GAATGGGCCCT	1740
CACAAGGGAC	GGATTTTGAT	ACCGGTTTAT	ACGACTAATA	ATGTATCTCA	CTTAGATGGC	1800
TCGCAATCTT	CTCGTGTCAT	CTATTCAGAT	GATCATGGAA	AAACTTGGCA	TGCTGGAGAA	1860
GCGGTCAACG	ATAACCGTCA	GGTAGACGGT	CAAAAGATCC	ACTCTTCTAC	GATGAACAAT	1920
AAACGTGCGC	AAAATACAGA	ATCAACGGTG	GTACAACTAA	ACAATGGAGA	TGTTAAACTC	1980
TTTATGCGTG	GTTTGACTGG	AGATCTTCAG	GTTGCTACAA	GTAAAGACGG	AGGAGTGACT	2040
TGGGAGAAGG	ATATCAAACG	TTATCCACAG	GTTAAAGATG	TCTATGTTCA	AATGTCCTGCT	2100
ATCCATACGA	TGCACGAAGG	AAAAGAATAC	ATCATCCTCA	GTAATGCAGG	TGGACCGAAA	2160
CGTGAANAATG	GGATGGTCCA	CTTGGCACGT	GTCAAGAAAA	ATGGTGAGTT	GACTTGGCTC	2220
AAACACAATC	CAATTCAAAA	AGGAGAGTTT	GCCTATAAAT	CGCTCCAAGA	ATTAGGAAAT	2280
GGGGAGTATG	GCATCTTGTA	TGAACATACT	GAAAAAGGAC	AAAATGCCTA	TACCCCTATCA	2340
TTTAGAAAAAT	TTAATTGGGA	ATTTTTGAGC	AAAAATCTGA	TTTCTCCTAC	CGAAGCGAAA	2400
GTGAAGCGAA	CTAGAGAGAT	GGGCAAAGGA	GTTATTGGCT	TGGAGTTCCA	CTCAGAAGTA	2460
TTGGTCAACA	AGGCTCCAAC	CCTTCAATTG	GCAAATGGTA	AAACAGCGAC	TTTCCTAACC	2520
CAGTATGATA	GCAAGACCTT	GTTGTTTGCA	GTAGATAAGG	AAGATATCGG	ACAGGAAATT	2580
ATTGGTATAG	CTAAAGGAAG	CATCGAAAAGT	ATGCATAATC	TTCTGTAAA	TCTAGCAGGT	2640
GCCAGAGTTC	CTGGCGGAGT	AAATGGTAGC	AAAGCAGCGG	TGCATGAAGT	TCCAGAATTT	2700
ACAGGGGGAG	TTAATGGTAC	AGAGCCAGCT	GTTTCATGAAA	TCGCAGAGTA	TAAGGGATCT	2760
GATTCGCTTG	TAACTCTTAC	TACAAAAGAA	GATTATACTT	ACAAAGCTCC	TCTTGCTCAG	2820
CAGGCACTTC	CTGAAACAGG	AAACAAGGAG	AGTGACCTCC	TAGCTTCACT	AGGACTAACA	2880
GCTTTCTTCC	TTGGTCTGTT	TACGCTAGGG	AAAAAGAGAG	AACAATAA		2928

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1968 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1968
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

AGACTATCTG	CTACAGCAGG	TCTTGTTTTA	TTAGCAGCAG	GTGTACTTGC	AGCATGCAGT	60
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TCTTCAAAAT	CATCTGATTC	ATCAGCCCCCT	AAAGCTTATG	GCTATGTTTA	TACAGCAGAC	120
CCAGAAACCT	TGGACTACCT	GATTTCAAGT	AAAAATAGTA	CAACAGTAGT	GACTTCAAAT	180
GGGATTGATG	GTTTATTAC	TAACGATAAT	TACGGTAATC	TTGCTCCTGC	AGTTGCAGAG	240
GATTGGGAAG	TCTCTAAGGA	TGGTTTGACC	TACACTTATA	AGATTTCGTAA	AGGGGTTAAA	300
TGGTTTACCT	CTGATGGAGA	AGAATATGCA	GAGGTGACGG	CTAAAGATTT	CGTGAACGGT	360
TTAAAACACG	CAGCAGATAA	AAAATCAGAA	GCTATGTATT	TAGCTGAAAA	TTTCGGTTAAA	420
GGCTTGGCAG	ATTATCTATC	AGGAACTTCA	ACAGATTTTT	CAACAGTTGG	TGTCAAGGCG	480
GTTGATGATT	ATACGTTACA	ATACACTTTG	AACCAGCCTG	AACCGTTCTG	GAACCTCTAAG	540
TTGACCTATT	CTATTTTCTG	GCCTCTGAAT	GAAGAATTTCG	AAACATCAAA	AGGAAGCGAT	600
TTTGCTAAAC	CAACAGATCC	GACATCCTTG	CTTTATAATG	GTCCATTCTT	GTTGAAAGGG	660
TTGACTGCAA	AATCTTCTGT	AGAGTTTGTA	AAAAATGAGC	AATATTGGGA	TAAAGAAAAT	720
GTCCACCTAG	ATACTATCAA	TCTAGCTTAC	TATGATGGAT	CAGATCAGGA	GTCGCTAGAG	780
CGTAACTTCA	CTAGTGGAGC	TTATAGTTAT	GCCCCGTCTT	ACCCTACCAG	CTCCAACAT	840
TCTAAGGTTG	CAGAAGAATA	CAAGGACAAT	ATCTATTACA	CACAATCAGG	CTCTGGGATT	900
GCTGGTCTGG	GTGTGAATAT	TGATCGCCAA	AGTTACAAC	ATACTTCTAA	AACTACAGAT	960
TCAGAGAAAAG	TAGCTACTAA	GAAGGCATTG	CTTAACAAAG	ATTTCCGTCA	AGCCTTGAAT	1020
TTTGCTCTTG	ATCGCTCAGC	TTACTCAGCT	CAAAATCAATG	GTAAAGATGG	AGCAGCTTTA	1080
GCAGTTCGTA	ATTTATTTGT	AAAACCAGAC	TTTGTTTTCAG	CTGGTGAGAA	GACCTTTGGT	1140
GATTTAGTCG	CTGCTCAACT	TCCTGCTTAT	GGTGATGAGT	GGAAAGGTGT	GAATTTAGCT	1200
GATGGGCAGG	ATGGTTTATT	CAATGCTGAC	AAGGCCAAGG	CAGAGTTTGC	GAAAGCTAAG	1260
AAAGCTTTAG	AAGCAGACGG	CGTTCAGTTT	CCTATTTCATC	TGGACGTTCC	AGTAGACCAA	1320
GCATCAAAAA	ACTACATATC	TCGTATTGAG	TCCTTTAAAC	AATCTGTAGA	AACAGTTCTT	1380
GGTGTGAAA	ATGTCGTTGT	TGATATTCAA	CAAAATGACAA	GTGATGAATT	CCTTAATATT	1440
ACTTACTATG	CTGCCAATGC	TTCATCTGAG	GATTGGGATG	TATCAGGAGG	AGTTTCATGG	1500
GGTCCAGACT	ATCAAGACCC	ATCTACTTAC	CTGGATATTT	TAAAAACAAC	TAGCAGTGAA	1560
ACTACAAAAA	CATATTTAGG	ATTTGATAAT	CCAAATAGCC	CTTCAGTAGT	TCAAGTTGGT	1620
TTGAAAGAAT	ACGATAAAAT	AGTTGATGAA	GCTGCCAGAG	AGACAAGCGA	CTTGAATGTC	1680
CGTTATGAAA	AATATGCAGC	GGCTCAAGCA	TGGTTGACAG	ATAGTTCACT	CTTTATTCCT	1740
GCTATGGCTT	CTTCTGGTGC	AGCACCAGTG	CTTTCACGAA	TTGTTCCATT	TACTGGAGCT	1800
TCTGCGCAAA	CAGGCTCTAA	GGGGTCAGAT	GTTTACTTCA	AATATTTGAA	ATTACAAGAT	1860
AAAGTGGTGA	CTAAGGAAGA	GTATGAAAAA	GCTCGTGAAA	AATGGTTGAA	AGAAAAAGCT	1920
GAATCAAATG	AGAAAGCTCA	AAAAGAATTG	GCAAGTCATG	TGAAGTAA		1968

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...807
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

ATGACTTATT	TACCCGTTGC	TTTGACCATT	GCAGGGACTG	ACCCTAGTGG	TGGTGCTGGC	60
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ATTATGGCAG	ATTTAAAGTC	ATTCCAAGCG	AGAGATGTCT	ATGGAATGGC	TGTTGTAACC	120
AGTCTTGTCG	CTCAAAATAC	CAGAGGTGTT	CAGCTAATCG	AGCACGTTTC	TCCTCAAATG	180
TTGAAAGCCC	AATTGGAGAG	TGCTTTTCT	GATATTCCAC	CTCAGGCTGT	AAAAACTGGA	240
ATGTTGGCTA	CTACTGAAAT	CATGGAAATC	ATCCAACCCT	ATCTTAAAAA	ACTGGATTGT	300
CCCTATGTCC	TTGATCCTGT	TATGGTTGCT	ACAAGTGGAG	ATGCCTTGAT	TGACTCAAAT	360
GCTAGAGACT	ATCTCAAAAC	AAACTTACTA	CCTCTAGCAA	CTATTATTAC	GCCAAATCTT	420
CCTGAAGCAG	AAGAGATTGT	TGGTTTTTCA	ATCCATGACC	CCGAAGACAT	GCAGCGTGCT	480
GGTCGCCTGA	TTTTAAAAAG	ATTTGGTCCT	CAGTCTGTGG	TTATCAAAGG	CGGACATCTC	540
AAAGGCGGAC	ATCTCAAAGG	TGGTGCTAAA	GATTTCCCTCT	TTACCAAGAA	TGAACAATTT	600
GTCTGGGAAA	GCCCACGAAT	TCAAACCTGT	CACACCCATG	GTACTGGATG	TACCTTTGCT	660
GCAGTGATTA	CTGCTGAACT	AGCCAAGGGC	AAGAGTCTTT	ACCAGGCAGT	TGATAAGGCC	720
AAGGCCTTTA	TCACAAAAGC	TATTCAAGAT	GCCCCTCAAC	TCGGTCATGG	TTCTGGTCCA	780
GTCAACCATA	CAACTTTTAA	AGATTAA				807

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...927
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

AGACGACCTG	CAACTGGCCA	TGGCCATGCA	GGACCTGCAC	CTCCACGGCG	CCGAGCTGGG	60
GCAATCGCAC	CTGCAGGCGC	GCCGCATGGC	TTTCGGCTGC	GCTGGCGACC	TGGATGCGCC	120
CCTGCACGGC	ATCTAGCAGG	CGCGCGAGAT	CGGCCAGCGG	CAGTGGCCGG	CTCCCGCTCG	180
ATGCCAGCAG	GCGTGCCAGC	AGGCGGTCGC	CGGGGGTTTG	CATGGCAGGC	AATGGCACAG	240
GCGCTTGGTC	GTCGGGGGGC	AGTGCGGATG	GATCGGTTTC	TCCGGGTTGC	CGACGCTCCT	300
CTCCGCGGCC	TTCGCCGCCC	GCTGTCGGCG	CGGGCGGCGA	GACCTGGACA	CTGGCCTGCG	360
CCGTGGACGC	GACCTCGGCT	GCGGTTTTTC	CCGGGAAGCC	GGGGCCGGGC	TGTGGCCGCT	420
CATGCGTCCG	ACCTGCGATT	TGCGGGTGGG	AGGACACCGG	CACCAGCGGC	GGTTCGTCTGA	480
CCGGAGGCGC	CGAAACGCTG	GCCGGCTCCC	GGGCTTGCGT	GGACGCCGCG	ACGCGCGCGG	540
AAACCGCCGG	CGCTTGCCGT	GCTACCGATC	CGGACGGCAA	CACTGTTGGC	GTTGGCGTTG	600
GCGTTGGCGT	TGGCGTTGGC	GTTGGCGTTG	GCGTTGGCGT	TGCTTCCGCG	GCAACTGGCA	660
CGGGGGCTTG	CCNATTGGTC	GGCGGCCGGT	CGGCGGCAGG	CGCCGCGGGC	TGGTCGGCGA	720
GAGGCGTCGA	GGTCGGCGCG	TCGCTGTTTC	CGGCGGGCTC	TTCGGCCTCT	GTCGTTTCGT	780
CGCCCTTGTC	GAACGGTGGC	CTGGGCGCCG	GCGGTGCGTG	CGCGGGCAGG	GCCTGTTCTGA	840
AGGCGATCTG	CTGCGCGCGC	AGCGGCGGAA	GGGGGGCAGG	GGTGTCTGGAC	GACACGAGCG	900
GAGCCGTATC	CACGGCGTTC	AGCTTGA				927

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

ACTATTACTG	CGGGCCAAAT	CGGTAAGTAC	CAACTTGAAG	AAATAAAGAC	AATCGTCAAA	60
AGAAATTCTA	ATACAATATC	TTTCTTAACC	GAAACATCCA	GTTTTTTAGA	TAGAATTAGT	120
TCTGCTATTA	CGCTACGTAA	AGCTAGCAAA	ACAACTATCG	ATACAACAGT	CAGCTCTAAA	180
CTATTTAATA	ATAGAGTAGT	TATTTAG				207

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 909 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GAACTAACTG	CTGATTGCGC	CCTTTTTATG	GTAAAAACAA	TGACCATTGC	AACGATTGAT	60
ATCGGAGGGA	CTGGGATTAA	GTTTGCCAGT	CTGACTCCTG	ATGGGAAAAT	ACTGTATAAG	120
ACAAGTATTT	CAACGCCTGA	AAACTTGGAG	GATTTACTAG	CGTGGCTAGA	TCAACGCTTG	180
TCAGAACAGG	ATTACAGTGG	GATTGCTATG	AGCGTTCCAG	GTGCGGTCAA	TCAAGAGACA	240
GGTGTGATTG	ATGGCTTCAG	TGCGGTGCC	TACATCCATG	GCTTTTCTTG	GTATGAGGCG	300
CTTAGCTCTT	ATCAGCTACC	TGTCCATTTA	GAAAATGATG	CCAACTGCGT	TGGACTCAGT	360
GAACTACTAG	CTCATCCAGA	TCTTGAAAAT	GCAGCCTGTG	TCGTGATTGG	GACAGGGATT	420
GGCGGAGCCA	TGATTATCAA	TGGTAGACTT	CATCGAGGTC	GCCACGGTCT	GGGTGGAGAA	480
TTTGGCTACA	TGACAACCCT	TGCCCCTGCT	GAAAAACTTA	ATAACTGGTC	GCAACTAGCA	540

TCAACTGGGA	ATATGGTACG	ATACGTGATT	GAAAAATCTG	GTCATACTGA	TTGGGACGGT	600
CGCAAGATTT	ACCAAGAGGC	CGCAGCTGGT	AATGCTCTTT	GTCAAGAAGC	CATTGAGCGC	660
ATGAACCGCA	ATCTGGCGCA	AGGCTTGCTC	AATATCCAGT	ATCTCATCGA	TCCAGATGTC	720
ATCAGTCTGG	GTGGCTCTAT	CAGTCAAAAT	CCAGATTTTA	TCCAAGATGT	CAAGAAGGCT	780
GTTGATAACT	TTGTCGATAC	CTACGAAGAA	TACACGGTCG	CACCAGTTAT	CCAGACCTGC	840
ACCTATCACG	CAGATGCCAA	TCTCTACGGT	GCCCTTGTC	ACTGGCTACA	GGAGGAAAAG	900
CAATGGTAA						909

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

CGAACAAC	CTG	CACGGATGGC	AGCGTTCATA	CCAGGTGCGT	CTCCGCCACT	AGTCAAGACA	60
GCAATACG	TT	TCATATTGGT	TTATGCTCCT	TTTTCTTTTA	ACATTCTTCT	TGATTATATC	120
ACATTTGAT	T	TTAAATTTCT	TCTATTTTCC	GTATTTT	TTAG	CGATAAATCG	180
GATTTCA	TT	CAATTTCTCCT	CTAA				204

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GGCAAGACTG	CGCGTCACCA	TACCATGTTT	GAAATGTTGG	GGAAC TTCTC	TATCGGGGAT	60
TACTTCCGTG	ACGAAGCTAT	CACTTGGGCT	TATGAGCTTT	TGACAAGCCC	TGAATGGTTT	120
GATTTCCCTG	CTGAAAAACT	TTACATGACC	TACTATCCAG	ACGATAAAGA	TTCTTACAAC	180
CGCTGGATTG	AAGTGGGAGT	GGATCCAAGT	CAC TTGATT	CAATTGAGGA	CAACTTCTGG	240
GAAATCGGTG	CGGGACCTTC	TGGACCAGAT	ACAGAAATCT	TCTTTGACCG	TGGGGAAGCC	300
TTTGACCCAG	AAAATATCGG	TCTTCGCCTG	CTTGCAGAAG	ATATTGAAAA	CGACCGTTAT	360
ATTGAAATCT	GGAACATCGT	TTTGTACACA	TTTAACGCAG	ACCCTGCTGT	TCCTCGTAGC	420
GAATACAAGG	AATTGCCACA	TAAGAACATT	GATACGGGCG	CTGGT TTGGA	GCGT TTGGTG	480
GCCGTTATCC	AAGGGGCTAA	GACCAACTTT	GAAACGGACC	TCTTCATGCC	GATTATCCGT	540
GAAGTCGAGA	AATTGTCTGG	TAAGGTTTAT	GACCAAGATG	GCGACAACAT	GAGCTTCAAG	600
GTTATCGCAG	ACCACATTCG	TTCTCTTTCA	TTTGTCTATCG	GTGATGGTGC	CCTTCCAGGA	660
AATGAAGGTC	GTGGTTATGT	TCTTCGTCGT	CTTCTCCGTC	GTGCTTCTAT	GCATGGTCAA	720
AAATTGGGTA	TCAACGAGCC	TTTCC TTTAC	AAACTCGTTC	CAACTGTTGG	AAAAATCATG	780
GAAAGCTACT	ACCCAGAAGT	GCTTGAGAAA	CGTGACTTTA	TTGAGAAAAAT	CGTTAAGAGC	840
GAAGAAGAAT	CA TTTGCCCG	TACCC TTTAC	TCAGGTCAAC	ACTTTGCCCA	AGGAATTGTG	900
GCAGACTTGA	AAGAAAAAGG	TCAATCTGTC	ATTGCTGGTC	AAGATGTCTT	TAAACTCTAT	960
GATACATACG	GATTCCAGT	TGAATTGACT	GAAGAAATTG	CTGAAGAAGC	TGGTATGACT	1020
GTAGACCGTG	AAGGTTTTGA	AGCAGCCATG	AAAGAACAGC	AAGAACGCGC	GCGTGCGTCA	1080
GCTGTCAAGG	GTGGCTCAAT	GGGTATGCAA	AATGAAATC	TTCAAAACAT	CACTGTAGAA	1140
AGTGCTTTCA	ACTACAATGC	TAGCCAATTG	TCTTCTAAAT	TGGTAGCTAT	CGTTGCTGAC	1200
AATGCAGAA	TAGGAGCTGT	TTCAGAAGGA	ACTGCCTCTC	TTATCTTTGC	GGAAACGTCA	1260
TTTTATGCTG	AAATGGGTGG	ACAGGTAGCT	GACTACGGAC	AAATCTTGA	TGAGTCAGGT	1320
AAGGTTGTGG	CTACTGTGAC	CAATGTTTCA	AAAGCCCCAA	ATGGTCAAGC	CCTTCATACA	1380
GTTGAAGTCC	TTGCACCGCT	TGCCTTGAAC	CAAGAATATA	CCTTGGCAAT	TGATAGCAAT	1440
CGCCGTCACC	GTGTCATGAA	AAACCACACT	GCGACTCAT	TGCTTCACGC	TGCCCTTCAC	1500
AATATCCTTG	GAAACCACGC	AACACAGGCA	GGATCTCTTA	ACGAAGTTGA	ATTCTTTCGC	1560
TTTGACTTTA	CCCACTTCCA	AGCAGTAACT	GCTGAGGAAC	TTCGTGCGAT	TGAACAGCAA	1620
GTTAACGAGA	AAATTTGGGA	AGCACTTGAA	GTGAAGACAG	TTGAAACGGA	TATTGACACT	1680
GCTAAAGAAA	TGGGAGCGAT	GGCCCTCTTT	GGTGAGAAAT	ACGGCAAGGA	AGTTCGTGTC	1740
GTGACTATCG	GTGACTACTC	TATTGAACTT	TGTGGTGGTA	CTCATGTTGG	CAACACTTCT	1800
GAGATTGGTC	TCTTCAAAAT	TGTCAAAGAA	GAAGGAATCG	GTTTCAAGAAC	TCGCCGTATC	1860
TTGGCAGTGA	CTGGTAAGGA	AGCCTTTGAA	GCCTATCGTG	AACAAGAGGA	TGCTCTTAAA	1920
GCTGTGCGAG	CAACCTTGAA	AGCACCTCAA	GTCAAGGAAG	TACCTCACAA	GGTAGAAGGA	1980
CTTCAAGAAC	AACTTCGTCA	ACTTCAAAAA	GAAAATGCTG	AGTTGAAAGA	AAAAGCCGCA	2040
GCTGCAGCCG	CAGGTGATAT	CTTCAAAGAT	GTTAAGGAAG	TCAACGGTCA	TCGTTACATT	2100
GCTAGTCAAG	TGTCTGTATC	CGATGCCGGT	GCCCTTCGTA	CTTTTGCAGA	TAAC TGGA	2160
CAAAAAGACT	ACTCTGATCT	TCTTGTCTTA	GTTGCCGCTA	TCGGTGACAA	AGTCAATGTC	2220
CTTGTAGCAA	GCAAGACAAA	AGACCTTCAT	GCAGGAAACC	TTGTCAAAGA	ATTAGACCA	2280
ATCATCGATG	GACGTGGTGG	TGGTAAACCA	GACATGGCCA	TGGCAGGAGG	AAGCAACCAA	2340
GCTAAGATCC	AAGAATTGTT	GGATGCAGTA	GCAGGTAAAT	TGTAA		2385

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

TATAATTATT	TTATGATTAT	TACTATTTCCT	ATAAAAAACC	AAAAAGATAT	TGGCACACCA	60
TCTGATTGAG	TCGTTGTTCT	CGGCTATTTT	GATGGCATA	ATAAGGGGCA	TCAAGAATTA	120
TTTCGTGTTG	CCAACAAGGC	TGCGAGAAAG	GATTTATTAC	CTATCGTCGT	TATGACCTTT	180
AATGAATCTC	CAAAGATCGC	TTTAGAGCCT	TATCATCCAG	ATTTGTTTTT	GCATATTTTG	240
AACCCTGCTG	AACGTGAAAG	AAAATTAAAG	CGCGAAGGTG	TAGAAGAATT	ATATCTCCTT	300
GATTTTAGTA	GTCAATTTCG	TAGTCTCACT	GCACAAGAAT	TCTTTGCAAC	TTATATCAAG	360
GCTATGAATG	CCAAAATTAT	TGTTGCAGGT	TTTGATTATA	CATTTGGTTC	TGACAAAAAA	420
ACAGCAGAAG	ATTTAAAGGA	TTACTTTTGAT	GGAGAAGTTA	TCATTGTTCC	ACCTGTAGAA	480
GATGAGAAAAG	GAAAGATTAG	TTCAACTCGT	ATCCGTCAAG	CTATTTTAGA	TGGAAATGTG	540
AAAGAAGCAG	GAAAACTTTT	GGGGGCACCG	CTTCCATCAA	GAGGTATGGT	GGTTCATGGT	600
AATGCTCGTG	GTCGTACAAT	TGGTTATCCG	ACAGCGAATT	TAGTGCTTTT	AGACCGTACT	660
TATATGCCAG	CAGATGGCGT	TTATGTCGTT	GATGTTGAGA	TTCAAAGACA	GAAGTATCGT	720
GCTATGGCTA	GTGTCGGGAA	AAATGTGACC	TTTGATGGAG	AAGAAGCACG	TTTTGAAGTC	780
AATATTTTGT	ATTTTAATCA	AGATATTTAT	GGGGAACCG	TCATGGTTTA	TTGGCTTGAT	840
CGCATTCGTG	ATATGACCAA	ATTTGACTCA	GTTGACCAAT	TAGTGGATCA	GTTAAAGGCT	900
GATGAAGAAG	TAACTCGGAA	TTGGTCTTAA				930

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 603 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GTCAATTATT	TGAATAAAAT	GGAAAGGAAT	ATCAATATGA	AAAAATGGCA	AACATGTGTT	60
CTTGGAGCAG	GTTTCGTCCT	TTGTTTGACG	GCTTGTTTCAG	GCAAGTCCGT	GACTAGTGAA	120
CACCAAACGA	AAGATGAAAT	GAAGACGGAG	CAGACAGCTA	GTAAAACAAG	CGCAGCTAAA	180
GGGAAAGAGG	TGGCTGATTT	TGAATTGATG	GGAGTAGATG	GCAAGACCTA	CCGTTTATCT	240
GATTACAAGG	GCAAGAAAAGT	CTATCTCAAA	TTCTGGGCTT	CTTGGTGTTT	CATCTGTCTG	300
GCTAGTCTTC	CAGATACGGA	TGAGATTGCT	AAAGAAGCTG	GTGATGACTA	TGTGGTCTTG	360
ACAGTAGTGT	CACCAGGACA	TAAGGGAGAG	CAATCTGAAG	CGGACTTTAA	GAATTGGTAT	420
AAGGGATTGG	ATTATAAAAA	TCTCCCAGTC	CTAGTTGACC	CATCAGGCAA	ACTTTTGGAA	480

ACTTATGGTG TCCGTTCTTA CCCAACCCAA GCCTTTATAG ACAAAGAAGG CAAGCTGGTC	540
AAAACACATC CAGGATTCAT GGAAAAAGAT GCAATTTTGC AAACCTTGAA GGAATTAGCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

AACTTTTATG CGAAGAGTTT GGGCATAAAC TTTTACCTCT TCCTCCCTAC TCACCTGAGT	60
ACAATCCTAT TGAGAAAACA TGGGCCCATATA TCAAAAAGCA CCTCAAAAAG GTATTACCAA	120
GTTGTTGCAA TACCTTTTAC GAGGCTCTTT TGTCTGCTC TTGTTTCAAT TGAATATAGC	180
AGATTGAAAT AA	192

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

AACTTTTATG CGAGGAGTTT GGGCATAAAC TTTTATCTCT TCCTCCCTAC TCACCTGAGT	60
ACAATCCTAT TGAGAAAACA TGGGCTCATA TCAAAAAGCA CCTCAAAAAG GTATTACCAA	120

GTTGCAATAC CTTTTATGAG GCTCTTTTGT CCTGCTCTTG TTTCAATTGA CTATAGTTCA	180
CGGATACAGT TGGGAAAGAA GCTATTAAAT ATTTGGAGAG TCCTTTTGGG ATGA	234

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

ATGATTTATG CAGGAATTCT TGCCGGTGGA ACTGGCACAC GCATGGGAAT CAGTAACTTG	60
CCAAAACAAT TTTTAGAGCT AGGTGATCGA CCTATTTTGA TTCATACAAT TGAAAAATTT	120
GTCTTGGAAC CAAGTATTGA AAAAATTGTA GTTGGGGTTC ATGGAGACTG GGTTTTACAT	180
GCAGAAGATC TTGTAGATAA ATATCTTCCT CTTCATAAGG AACGTATTAT CATTACAAAG	240
GGTGGTGCTG ACCGCAATAC AAGTATTGAG AACATCATTG AAGCCATTGA TGCTTATCGC	300
CCGCTTACTC CAGAGGATAT CGTTGTTACC CACGATTCTG TTCGTCCATT TATTACGCTT	360
CGCATGATTC AAGACAGTAT CAACTTGCT CAAAATCATG ACGCAGTGA TACAGTAGTA	420
GAAGCAGTGG ATACTATCGT TGAAAGTACC AATGGTCAAT TCATTACAGG TATTCCAAAT	480
CGTGCTCACC TCTATCAGGG ACAACACCT CAAACATTCC GTTGCAAGGA CTTCATGGAC	540
CTTTATGGAT CTCTTTCTGA TGAAGAGAAG GAAATCTTGA CAGATGCATG TAAAATCTTT	600
GTGATCAAAAG GAAAAGATGT AGCCTTGGCC AAAGGCGAAT ACTCAAAATCT GAAGATTACA	660
ACCGTAACAG ATTTGAAGAT TGCAAAAAGT ATGATTGAGA AAGACTAG	708

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAAATGCATG	CAAAAATGCG	AAATAAAACA	CAAATACACC	TAGGCATAAT	TTTTGTAATC	60
TGCCTAGGTC	TTCTTATTAC	AATATTTTTG	TCATTAAAGC	TTGGAACAAA	AGAAATTAAT	120
ATCAGAGATT	TTTTCAGCAGC	TTTTGGAATG	GGCAATACAA	ATGATGATTT	TATTAAATCA	180
ATTATATATA	AAAGAATACC	TAGAACTATT	TTTGCAATTT	TAGCAGGTTC	TAGTCTTGCC	240
ATAAGCGGTG	TATTGATGCA	ATCAGTTACT	AGAAAACCCAA	TAGCTGATCC	AGGTATACTC	300
GGTATAAACA	CAGGAGCAAG	TCTTAGTGTA	GTAATTGGTC	TTTCTTTTTT	AGGAATTTCA	360
TCAAGCATAA	GCCATATAAG	TTTTGCAATC	ATTGGTGGCT	TAGTAAGTGT	AATTTTTGTA	420
TACGCGATTG	CTGTAAGCGG	AAAAGCAGGC	CTTACCCCTA	TAAAACTAGC	CTTATCAGGA	480
ACTTGTGTTA	GTATGGCTTT	AAGCAGTTTT	GTAAGTTTTT	TAATTTTACC	GAATAATAAC	540
GTCTTAGACA	AATTTAGATT	TTGGCAAATA	GGTAGCCTTG	GAGCAGCTAC	ATTATCTTCT	600
ATATCTACAC	TACTACCTTT	TATAATTTTA	GGTCACTTGA	TAGCTATATT	TATTTTCATCA	660
GATTTAAACG	CTTTAGCTAT	GGGTGATGAA	ATGGCTGTTG	GTCTTGGAGT	TAATGTTAAT	720
AGGATAAGAT	CACTTGCAAT	AATTGCAAGT	GTGCTTTTAT	GTTCAAGTAT	TACTGCAATT	780
GGTGGACCTA	TTGGCTTCGT	AGGTCTTATA	GTTCCCTCACT	TTTGTGGCTT	ATTTATAAGC	840
AAAGATATAC	GCACAATGAC	CATTTCTTCA	TCTTTTATAG	GTGCAGAGCT	CTTGCTTATA	900
TGTGATATAA	TCGGCCGTAT	GTTAGGTAAA	CCAGGTGAAA	TTGAAGTAGG	GATAATTACT	960
GCAATAATCG	GGGGTCCAGT	ACTTATTTAT	GTAAGTATGA	AAAATAGAGG	GGTTAATAAC	1020
TAA						1023

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

TCGCATGATG	CTCAAAACAC	CGTTTTGAGG	TGGCAGATAG	AACTGACGAA	GTCAGCTCAA	60
AACACCGTTT	TGAGGTGGCA	GATAGAACTG	ACGAAGTCAG	CTCAAAACAC	CGTTTTGAGG	120
TGGCAGATAG	AACTGACGAA	GTCAGCTCAA	AACACCGTTT	TGAGGTGGCA	GATAGAACTG	180
ACGAAGTCAG	CTCAAAACAC	CGTTTTGAGG	TGGCAGATAG	AACTGACGAA	GTCAGCTCAA	240
AACACCGTTT	TGAGGTGGCA	GATAGAACTG	ACGAAGTCAG	CTCAAAACAC	CGTTTTGAGG	300
TGGCAGATAG	AACTGACGAA	GTCAGCTCAA	AACACCGTTT	TGAGGTGGCA	GATAGAACTG	360
ACGAAGTCAG	CTCAAAACAC	CGTTTTGAGG	TGGCAGATAG	AACTGACGAA	GTCAGCTCAA	420
AACACCGTTT	TGAGGTGGCA	GATAGAACTG	ACGAAGTCAG	CTCAAAACAC	CGTTTTGAGG	480
TGGCAGATAG	AACTGACGAA	GTCAGTAACA	TATATACGGC	AAGGCGAAGC	TGACGTGGTT	540

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

CCGCTCGATG CAGGACAACG ATTTAGATAT GGAGTTTCCA TTATCCCAGA CGACTACGAC	60
CCAATCGCTT ATGTCGTCAG CAAGTCCATG GAGCCAAAGA TAAGAAACAG CGACTACCTA	120
TTTATCAAGA ATACCCACACA GATTGACTAT AATACCATCG GCATCTTCCA AGTAGACGGC	180
GCTAACTATG TCAAGAAACT CCGCCAAGGC TACCTTAAAA AAACCTCAATC CCAAATACCC	240
CGACATCCAC CTAGACGAAA GCAACCATAT TCGTACCATC GGGAAAGTTG TCAGGCTATA	300
TAG	303

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

AAATACTGTG CGTTCGTACC TTTATGGTGT TTCGATTTGT GCNTGGAGAA TTACGCACTC	60
GAAATGGAAG ATTTATTCTGA ATACATAGGA TATTTATTAG ACAATTTTAG ACGTAATACT	120

GTCAATTTGC	GA	CTACATGG	AGTAAATAAC	TATCTGCCTT	TTATTGGTCA	TGATGATTTG	180
AAATTAAAA	TTGTCAAAAGT	ACATCAAAAA	CCGTTTTTAG	AAGATGTCAT	TAGCCATGCT		240
GATTACCTTT	TTCTTAAACG	TAGTTTGAAA	AAAGATGGTA	TTTTAAAAAG	GCATTTTGTC		300
GTTTGGTTTT	TAGGTGCAAC	TGGGGCTCGT	GTAAGTGAAC	TTATTAAACT	AAAAGTAGAG		360
CATGTAGAAA	TCGGTTATTT	TGACATTTAC	TCAAAAAGTG	GTAAAATTCG	TAGACTGTAC		420
ATTCCTAAAA	AATTAAGAAA	TAGTTGTCTT	AGTTGGTTAG	AATCAGAAAA	TCGCCGAAGT		480
GGTTATTTAT	TTTTGAATAA	ATTTAACGAA	CCAATTACAG	CAAGAGGAGT	TGCTCAACAG		540
TTAAAAAATT	ATGCTGATAA	ATACAAAAATG	AATCCTAAAG	TAATTTACCC	TCATTCTTTT		600
AGGCATTTAT	TTGCTAAGAA	TTTTTTTAGCG	AAGTATAATG	ATATTGCCTT	GCTTGCAGAT		660
TTGATGGGAC	ACGAAAAGTAT	AGAAACTACT	CGAATTTATC	TAAGGAAAAC	AGCTACTGAA		720
CAACAAAATA	TTGTAGATAA	AATTGTTAAT	TGGTAA				756

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

AAGATCTATT	TGACGAGGAC	TTCTCAATG	ACTAGTCCAC	TATTAGAATC	TAGACGCCAA	60
CTCCGTAAAT	GCGCTTTTCA	AGCTCTCATG	AGCCTTGAGT	TCGGTACGGA	TGTCGAAACT	120
GCTTGTCGTT	TCGCCTATAC	TCATGATCGT	GAATATACGG	ATGTACAACT	TCCAGCCTTT	180
TTGATAGACC	TCGTTTCTGG	TGTTCAAGCT	AAAAAGGAAG	AACTAGATAA	GCAAATCACT	240
CAGCATTTAA	AAGCAGGTTG	GACCATTGAA	CGCTTAACGC	TCGTGGAGAG	AAACCTCCTT	300
CGCTTGGGAG	TCTTTGAAAT	CACTTCATTT	GACACTCCTC	AGCTGGTTGC	TGTTAATGAA	360
GCTATCGAGC	TTGCAAAGGA	CTTCTCCGAT	CAAAAATCTG	CCCGTTTTAT	CAATGGACTG	420
CTCAGCCAGT	TTGTAACAGA	AGAACAATAA				450

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

ATGATATTCG	CTACGAGTCA	GGTGAATCCA	TTGACCAACT	CTTCCGTCAG	GAATTTAAGG	60
CCTAAGCAAA	GGAGATTATT	TATGTTTTGG	AATTTAGTTC	ACTACGAATT	TAAAAATGTT	120
AACAAGTGGT	ATTTAGCCCT	CTACGCAGCC	GTGCTAGTCC	TTTCTGCCCT	CATCGGAATA	180
CAGACACAAG	GCTTTAAAAA	TCTACCTTAC	CAAGAAAGTC	AGGCTACTAT	GCTACTTTTT	240
CTAGCTACAG	TCTTTGGTGG	CTTGATGCTT	ACACTTGCGA	TTTCAACCAT	TTTCTTGATT	300
ATTAAACGCT	TCAAAGGTAG	TGTCTACGAC	CGACAAGGCT	ATCTGACTTT	GACCTTGCCA	360
GTTTCTGAAC	ACCATATCAT	CACAGCCAAA	CTAATCGGTG	CCTTTATCTG	GTCATTGATT	420
AGCACCGCTG	TATTGGCTCT	AAGTGCTGTT	ATTATTCTGG	CTTTAACAGC	TCCAGAATGG	480
ATTCTCTTTT	CTTATGTGAT	TACATTTGTA	GAAACACATC	TCCCTCAGAT	CTTTCTTACA	540
GGTATATCCT	TCCTACTAAA	TACCATTTC	GGAATCCTCT	GCATCTACCT	GGCTATTTCC	600
ATTGGACAGC	TTTTCAATGA	ATACCGTACA	GCACTCGCTG	TTGCAGCCTA	CATTGGTATC	660
CAAATCGTCA	TTGGATTTAT	TGAACTTTTC	TTCAATCTTA	GTTCTAATTT	CTATGTCAAT	720
TCACTGGTAG	GACTCAATGA	CCATTTCTAT	ATGGGAGCAG	GTATAGCCAT	TGTTAAAGAA	780
CTCATATTCA	TAGCTATCTT	TTATCTCGGA	ACCTACTACA	TCTTGAGAAA	TAAGGTTAAT	840
TTGCTTTTAA						849

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GATTGCCTCG	CAACGACATT	GCTGGACAAC	CTCTGCTATT	TTAGAATCAA	TTTCCTGAAG	60
GTGATAGCCG	ATATTTCTCCA	AGGTGAAAAT	CAGCTCCTCA	AACAAGTTCT	CCATGGTAAA	120
TTGATGATTG	GGATTTTGAA	AGAGAATGCC	AACCTTCTGG	ACACGTGCGA	TGATAGAAAG	180
CTGACTGACC	TCGCTCCCAT	CTATCAGGAC	TTGACCACTA	TAGGGAAGAG	AACTGACTTG	240
GGCAATGACT	TGAAAAAGGC	TGGATTTTCC	TGA			273

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...378
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

AAATCAATCG	CCCTAAAAAA	ACAATTAGCG	AATCATTTCTG	GTAAAAAGAA	ATTTACACGCT	60
ATGAAGGCTC	AAGCGATTGT	CACAAGTCAA	GGGAGAATTG	TTTCTTTGGA	TATCACTGTG	120
AACTATTGTC	ATGATATGAA	GTTGTTCAAA	ATGAGTTGCA	GAAATATCGG	ACAAGCTGGT	180
AAAATCTTGG	CTGACAGTGG	TTATCAAGGG	CTCATGAAGA	TATATCCTCA	AGCACAAACT	240
CCACGTAAAT	CCAGCAAAC	CAAGCCGCTA	ACAGCTGAAG	ATAAGGCTTA	TAACCATGCG	300
CTATCTAAGG	AGAGAAGCAA	GGTTGAGAAC	ATCTTTGCCA	AAGTAAAAAC	GTTTAAAATG	360
TTTTCACAAA	CCTATTGA					378

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

AAATCAATCG	CCCTAAAAAA	ACAATTAGCG	AATGATTTTG	GTAAAAAGAA	ATTTACACGCT	60
ATGAAGGCTC	AAGCGATTGT	CACAAGTCAA	GGGAGAATTG	TTTCTTTGGA	TATCGCTGTG	120
AACTATTGTC	ATGATATGAA	GTTGTTCAAA	ATGAGTCGCA	GAAATATCGG	ACAAGCTGGT	180
AAAATCTTGG	CTGACAGTGG	TTATCAAGGG	CCCATGAAGA	TATATCCTCA	AGCACAAACT	240
CCACGTAAAT	CCAGCAAAC	CAAGCCGCTA	ACAGTTGAAG	ATAAAGCCTG	TAACCATGCG	300

CTATCTAAGG AGAGAAGCAA GGTGAGAAT ATTTTGGCCA AAGTAAAAAC GTTTAAAATG	360
TTTTCACAA CCTATCGAAA TCATCGTAAA CGCTTCGGAT TACGAATGAA TTTGATTGCT	420
GGCATTATCA ATCATGAACT AGGATTCTAG	450

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

AAATCAATCG CCCTAAAAAA AGAATTAGCG AATTATTCTG GTAAAAAGAA ATGCTACGCT	60
ATGAAGGCTC AAGCGATTGT CACAAGTCAA GGGAGAATTG TTTCTTTGGA TATCACTGTG	120
AACTATTGTC ATGATATGAA GTTGTTCAAA ATGAGTCGCA GAAATATCGG ACAAGCTGGT	180
AAAATCTTGG CTGACAGTGG TTATCAAGGG CTCATGAAGA TATATCCTCA AGCACAACT	240
CCACGTAAAT CCAGCAAAT CAAGCCGCTA ACAGTTGAAG ATAAAAACCTA TAACCATGCG	300
CTATCTAAGG AGAGAAGCAA GGTGAGAAC ATCTTTGCCA AAGTAGAAC GTTTAAAATG	360
TTTTCACAA CCTATCGAAA TCATCGTAAA CGATTTCGGAT TACGAATGAA TTTGATTGCT	420
GGTATTATCA ATCATGAACT AGGATTCTAG	450

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

ATTATGGTTCG	CAAAACTAAC	TGATGTCGCC	AAACTTGCAG	GCGTCAGTCC	TACTACCGTT	60
TCTCGGGTTA	TCAATAAAAA	AGGGTATCTA	TCTGAGAAAA	CCATCCAAAA	AGTCAATGAA	120
GCCATGCGAG	AATTGGGCTA	TAAACCCAAC	AACCTGGCTC	GTAGTCTGCA	AGGAAAATCA	180
GCTAAGTTAA	TCGGCTTGAT	TTTCCCCAAT	ATTTCCAATG	TTTTCTATGC	AGAATTGATT	240
GATAAATTGG	AACACCAACT	CTTCAAAAAAT	GGTTACAAGA	CCATCATCTG	CAACAGTGAA	300
CATGATTCTG	AGAAGGAACG	TGAATACATC	GAAATGTTGG	AAGCCAATCA	GGTGGACGGC	360
ATCATTTCTG	GTAGTCACAA	CCTAGGAATC	GAAGACTACA	ATCGTGTGAC	AGCGCCGATT	420
ATTTCCCTTG	ACCGAAACCT	ATCGCCAGAC	ATCCCTGTGC	TCTCCTCTGA	CAACTATGCT	480
GGTGGGGTTC	TTGCTGCCCA	AACCTTGGTC	AAGACAGGTG	CCCAGTCTAT	CATCATGATT	540
ACAGGGAATG	ACAATTCCAA	TTCCGCCAAC	GGACTGCGCC	ACGCTGGTTT	TGCATCCGTA	600
CTCCCAAAAG	CTCCTATTAT	CAATGTTTCC	AGTGACTTTT	CTCCCGTCAG	AAAAGAAATG	660
GAAATCAAGA	ATATCTTGAC	CCGGGAAAAA	CCAGATGCCA	TTTTTGCTTC	GGATGATTTG	720
ACAGCTATTG	TGGTCATTAA	AATCGCTCAA	GAATTGGGCA	TTTCTGTCCC	AAAAGAGCTC	780
AAGGTCATCG	GCTATGATGG	GACCTACTTT	ATCGAAAATT	ACTACCCTCA	ATTGGCTACT	840
ATCAAGCAAC	CTTTGGAAGA	GATTGCTTGT	CTCACTATTG	ATCTTCTCTT	GCAAAAGATT	900
GAAGGCAAGG	AAGTCGCCAC	AACTGTTTAC	TTCTTACCAG	TTACGCTATT	ACCAGGAAAA	960
AGTATTTTAA						969

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GTCGCGGTCG	CCATACCACT	CGAGCTGTTA	GTTTTTTACAA	TCTCAACGGG	GGTAAAATCG	60
CAGATACACC	AGGATTTTCA	TCCTTGGACT	ATGAAGTATC	AAGGGCTGAA	GACCTCAATC	120
AGGCTTTCCC	AGAGATTGCT	ACTGTTAGCC	GAGATTGTAA	GTTCCGTACT	TGTACCCATA	180
CCCATGAGCC	GTCTTGTGCC	GTCAAACCAG	CTGTTGAAGA	GGGTGTTATT	GCAACCTTCC	240
GTTTTGACAA	TTACCTGCAA	TTCTTAGTGT	AAATTGAAAA	TCGTAGAGAA	ACCTATAAAA	300
AAGTCAGCAA	AAAAATTTCA	AAATAAGGAG	AAACCTATGT	CTCAATACAA	GATTGCTCCG	360
TCAATTCTGG	CAGCAGATTA	TGCCAATTTT	GAACGTGAAA	TCAAACGTCT	AGAAGCAACT	420
GGGGCAGAAAT	ATGCCCATAT	CGATATCATG	GACAGTCATT	TTGTACCGCA	AATCAGTTTTT	480
GGTGCAGGTG	TGGTCGAGAG	CCTTCGTCCT	CATAGTAAGA	TGGTTTTTCGA	TTGCCACTTG	540
ATGGTGTCAA	ACCTTGAGCA	TCATCTGGAA	GATTTTTGCGC	GTGCAGGTGC	AGACATCATC	600
AGTATCCATG	TAGAAGCAAC	ACCTCATATT	CATGGCGCCC	TCCAAAAAAT	TCGTTCACTC	660
GGAGTTAAGC	CTTCAGTCGT	TATCAATCCT	GGCACACCAG	TTGAAGCCAT	CAAGCACGTC	720
CTTCATCTAG	TTGACCAAGT	TTTAGTCATG	ACGGTTAATC	CAGGTTTTTG	TGGGCAAGCC	780

TTTCTGCCAG AAACCATGGA TAAGGTTTCGT GAGTTGGTTG CTCTTCGTGA GGAAAAAGGT	840
TTGAACTTTG AAATCGAAGT GGATGGTGGG ATTGATGACC AAACCTATTGC TCAAGCCAAA	900
GAAGCTGGTG CGACTGTTTT TGTAGCAGGT TCCTATGTCT TTAAGGGAGA AGTCAATGAG	960
CGAGTACAAA CTCTCAGAAA ACAACTGGAC TAG	993

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

ACCAACTATT TTGGGAGGAA GAAGATGAAA AATAGATTTT ATTATTATCA ATTACTAGAC	60
GAAAGAGAAG AACAACTGTT CAATAAAGCG GGCTCTGAAA GTTTCCTATAT CTGCATCGCT	120
TTGTCGCTCC TATCTTATAT CATTTAGTA TTAGCACCAA GCCTTTTAA TTCTAATATG	180
CTGCTAATCG TTATCATCAT AGGGACATT TACTTTTCA ATCGTGCCCG TTATCTGGGA	240
GTGACCTACT ATAGTCGTT TCATTTTACG ATTTTGGGTT GTTTTTTCCT AACCTTGGCT	300
ATTACGGCTC TTTTGATGTT GCAGAATTAT CAATCAACA TAGAAATTA TCAGCACAAT	360
CCTTTGAATT TTAAATACCT GTCTGCTTGG GTCATTACTT ATGTCATTTA CCTTCCGTGG	420
GCTTTATTG GCAATCTTGG TCTTAAGAGC TATGGCGAAT GGGCTCAGAA AAAATTTGAA	480
CAAGATATGG ATGAATTGGA GAGTGGAGAA TAG	513

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TTTATCCCCG	CCACCCTTTT	TCATTTTATA	CTCTTCGAAA	ATCTCTTCAA	ACCNCACGGT	60
CAGCTGTTAT	CTTCCACACC	TACAATAGTG	TGTGCTGTTG	AGACAACCTG	TGGGGCTAGA	120
CTTCCGCTGT	GTTTGACACT	TGTGATGTTT	CTATTGACTA	TTAGCGATTG	TCACTGTAAA	180
TAA						183

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GGTGGCACCG	CGTTACCAAC	GCCCTCACAC	GGAAGTATAT	TCTGTGTGTG	GGCTTTTTTC	60
TATCCGTCGT	TTGCTTTATC	TTTTATTAGG	GCCTTAAGTC	GCTTTGATGA	ACTTGAGTTC	120
TATCTACAGC	TCTTGCTTCC	TACTAAAAGT	AAACAAAAAG	GCTGGACTAA	TACGAAAAAA	180
GCTAGTAATA	CTCAATGA					198

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

AAATCTTACG	CCAAGGCGCA	ATTAAACGAG	AAGATATTCT	TGCTCGGTTG	CCAGAGATTT	60
CTTTTGAGGA	GGCTTGAAAT	GCTAAGAGAT	TTGCAAGAAA	CAGATGTGAA	AGCGATATGT	120
GACATCAACC	AAGAGACTTT	GGGTTATACT	TTTAGTCCAG	AGGAAACGGC	TAGCCAACTA	180
GCTAGACTGT	CTCAGGATTC	CCATCATTTC	CTACTTGGCT	ATGAGGATGC	AGCTAATCAT	240
GTCTTACTTG	GATATGTCCA	CGCTGAAGTT	TACGAATCAC	TCTATTCCAA	AGCAGGATTT	300
AATATCTTAG	CTTTAGCAGT	TTCACCTCAA	GCGCAAGGTC	AAGGTATCGG	TAAAAGTTTA	360
CTACAAGGGT	TGGAACAAGA	AGCCAAAAGA	TGTGGTTATG	GGTTTATCCG	CTTAAATTCT	420
GCCAATCATC	GTCTGGGTGC	TCATGCATTT	TATGAAAAAG	TTGGCTATAC	TTGTGATAAA	480
ATGCAGAAAC	GGTTTATTCG	CATCTTT				507

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GAAAACTACG	CCAACCAAGT	CGCAGCAAAC	CGCTTCGTGA	TTTTATTGAA	GACTAAGAGT	60
GAGGAAAATA	TGGCTTATAC	AGAAGAGCAA	ATTGAAAACA	TCAAAACACG	GATTTTAAACA	120
GCCTTGGAAG	AAGTCATCGA	CCCTGAGTTG	GGAATCGATA	TTGTCAATCT	TGGTTTGATC	180
TATGAGATTC	GTTTGTACGG	TGACACAGGG	CAAACAGAGA	TTGACATGAC	TTTGACAACT	240
ATGGGTTGTC	CCTTAGCAGA	CCTTTTGACA	GACCAGATTT	ATGATGCTAT	GATAGAGGTT	300
CCAGAAAGTAA	CGGATACTGA	GGTTAAATTA	GTCTGGTATC	CAGCATGGAC	AGTTGAAAAA	360
ATGAGTCGGT	ATGCCCGCAT	TGCCATAGGC	ATTAAGTAA			399

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

ATGAAAAACG	CTCTTGTTTT	TCACCAAAAT	ACTTTTCCAT	TATTCCTCCT	TGAAATAAAA	60
TTTATATATG	TTACAAAGAC	CTTTATTATA	TTAGTGTATT	ATCTATTATC	TATAGAAAAG	120
GCAGTATACC	TTAATTATAC	TCTTAATTTA	CAAAAAAGTC	TTAAAATTGA	GATGCGCTTT	180
CATACTTTGT	TTTATATTAT	TTGGGGGTAC	AATAACACCT	ACCATGAAAT	TTACACGGTA	240
GGTGTACTC	ATATCACTAA	TCGTTCTAAA	AATGGTTTGA	GGCAGTTGAG	GAGAATTCCT	300
TCTATCCAGC	TTCTTGTC	TGATGAGCGA	TAG			333

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1005 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

ATACCTTGCG	CCACCGTGTC	ATTGCCATTG	AAAATGGCCG	TGTCGTTTCGT	GACGAATCAA	60
AAGGAGAGTA	TGGATACGAT	GATTAGTAGA	TTTTTTTCGCC	ATTTATTTGA	AGCCTTAAAA	120
AGTTTGAAAC	GAAATGGTTG	GATGACAGTA	GCTGCTGTCA	GTTCAGTCAT	GATTACTTTG	180
ACCTTGGTGG	CAATATTTGC	ATCTGTTATT	TTCAATACAG	CGAAACTAGC	TACAGATATT	240
GAAAAATAATG	TCCGTGTAGT	AGTTTATATC	CGAAAGGATG	TGGAAGATAA	TAGTCAGACA	300
ATTGAAAAAG	AAGGTCAAAC	TGTTACAAAT	AATGACTACC	ACAAGGTATA	TGATTCCTTG	360
AAGAACATGT	CTACGGTTAA	AAGTGTTACC	TTTTCAAGTA	AAGAAGAACA	ATATGAAAAA	420
TTAACCGAGA	TAATGGGAGA	TAACTGGAAA	ATCTTTGAAG	GAGATGCCAA	TCCTCTCTAT	480
GATGCCTATA	TTGTAGAGGC	AAACACTCCA	AATGATGTAA	AACTATAGC	CGAAGATGCT	540
AAAAAAATTG	AAGGTGTCTC	TGAGGTTCAA	GATGGCGGTG	CCAATACAGA	AAGACTCTTC	600
AAGTTAGCTT	CATTTATCCG	TGTTTGGGGA	CTAGGGATTG	CTGCTTTGTT	AATTTTTTATC	660
GCAGTTTTCT	TGATTTCAA	TACCATTTCGT	ATTACCATTA	TTTCCCGCAG	TCGCGAAATT	720
CAAATCATGC	GCTTGGTCCG	AGCTAAAAAC	AGTTATATCC	GTGGACCGTT	CTTGTTAGAA	780
GGAGCCTTTA	TCGGTTTATT	GGGAGCTATC	GCACCATCTG	TTTTGGTCTT	TATTGTTTAT	840
CAAATTGTTT	ACCAATCTGT	CAACAAATCG	TTGGTAGGGC	AAAATCTATC	CATGATTAGT	900
CCAGATTTAT	TTAGTCCGTT	GATGATTGCC	CTACTATTTG	TGATTGGGGT	TTTCATTGGT	960

TCATTGGGAT CAGGAATATC CATGCGCCGA TTCTTGAAGA TTTAG

1005

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

TCCCGTTGCG	CCGCCTGGCG	CTCGGTGTGT	TCCTGCGCCG	CGGCGCGAAC	CCGTAGCAAT	60
TGGCGGCCCT	GGGCGCGCTC	GGCCCGGTCC	AGGCGCAGGC	GTCGGACGCG	CAACAGCAGC	120
GCCAGGCTCA	TGCGCAGAGG	CTCCGCAACT	GCGCGCAGGC	CTGTGCGTAA	TCGCTGGTTT	180
CGTGGGTACC	CTGGCGCAGC	CACTGGCGGA	TCGCCGCGAT	CTTCTCGATG	GCCTGGTCGG	240
CTTCGCTGTC	CTGGCCTTTC	TGGTATTTCG	CGATCTTCAG	CAGCAACTCG	ACTTCCTCGT	300
ACTTCGCCAG	CCATTTCGCG	AAGCGTCCGG	CCGCATGGCG	CTGATCGTCG	TCGACGATCT	360
GGTTCATGA						369

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

TCTGGGTTAG	CGAAGAACCC	CTTACTCTTG	CAACTGATTT	TTATCTATTA	TGTGCTCCCA	60
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AGTATTGGGA	TTCGTTTAGA	CCGCCTTCCT	GCAGCTATTA	TTGCCTTTGT	TCTCAACTAT	120
GCAGCTTACT	TTGCAGAAAT	TTTCCGTGGG	GGAATTGACA	CTATTCCAAG	AGGACAGTAT	180
GAGGCCGCCA	AGGTCTTGAA	GTTTAGCCCT	TTTGACAGAG	TGCGCTATAT	TATCTTGCCC	240
CAAGTGACCA	AGATCGTTCT	TCCTAGTGTC	TTTAATGAAG	TTATGAGTTT	GGTCAAGGAT	300
ACTTCTTTGG	TCTATGCTCT	CGGAATTTCA	GACCTTATCT	TGGCTAGTCG	AACAGCTGCT	360
AACCGCGATG	CTAGTCTAGT	TCCTATGTTT	TTGGCAGGAG	CCATTTATTT	GATTTTGATT	420
GGGATTGTGA	CAATTATTTT	CAAAAAAGTT	GAGAAGAAGT	ATAGTTATTA	TAGATAG	477

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GTCTGTCTAG	CTATAGATAT	ATTAAGTTTG	ATAAAATTC	TTGGAGATTT	TGTTATGGAT	60
TATAATTTCA	ATTTGGAGCA	TCCTTTCTTT	TTCCTAATA	ATGATTATAG	TACAGATACT	120
AGCATAAAGT	ACCAAGTAAG	TCTGCCTTTT	AATTGGCAGC	AAGTAATGAA	TAATGATGAG	180
TGGGTTTATC	AATACCCTAT	TGGAAAAATTT	GTTGAAAGAC	AAGGGTGGAA	AATACACATT	240
AGTTCAGAGT	ATAACAGTTC	ACATGAATTG	TTACAAGATG	TAGCAAAAAAT	TTGCCATGAA	300
ATGCGAATTC	CATTTAAACA	TCTTAGTACA	GAAGACAAAT	TTATCATGCG	AAACGGGAAA	360
TTGGTTAGTC	GAGGATTTTC	TGGTAAATTT	ATTACATGTT	ATCCAAATCA	AAATGAATTA	420
GAGTCGGTTT	TGCAAGGTT	AGAAAGTGCC	TTAAAGCAAT	ATAATGGACC	ATATATTTTA	480
AGCGATAAAC	GTTGGGATGA	AGCACCAATA	TATCTGAGGT	ATGGTGTGTT	TAGGCCGTCA	540
AGGGATGATG	AAAAGAAGGT	TGCTATTGAT	GAATTAATTG	TTGGCGATGA	AGTTGTTAAA	600
GATGAACGTT	TACCAGTATT	TAAAATTCCA	AAAGGTATAG	TGCCCCCTGA	CTTTTGAAT	660
AAATGGCTTG	ACAAGAAAGA	TAAAAAACAG	GGAGACTTTC	CCTTTATTAT	AGATAATGCA	720
ATTAGATTTT	CAACAGTGG	TGGGATATAT	AATGCTAGGC	TAAAAAGAAGA	TGGGAAAAAA	780
ATAATTTTAA	AAGAGGCTAG	ACCGTATACA	GGTCTAGGAT	TTGATGGTAC	TTATTCTTCA	840
GAGAAATTAG	CTTCGGAGTG	CAAAGCACTA	AAAAATCTAA	ATGAATGGAG	TGAGACGCCT	900
AAAATATACT	GGCACGGTAA	GATCTGGGAG	CACACCTTCT	TAGGAATTGA	ACATATGAAG	960
GGCGTTCCAC	TAAATAGATG	GGTTACCAAT	AATTTTCCTT	TATATGAAGT	TGTTGATAAG	1020
ACCAAAGATT	ATCTATTGAG	AGTTTCAAAG	ATAGTAGAAA	AACTCATCGA	TTTAACGAAT	1080
AAGTTTCATT	CTGAAAATGT	ATATCATCAA	GATTTACATT	TAGGAAATAT	CTTGGTTAAG	1140
GATGAAGATG	AGATTAGTAT	AATAGACTGG	GAACAGGCTG	TCTTTTCAA	TGATGAAAAA	1200
GTTGTACATA	AAGTTGCAGC	CCCTGTTTTT	AGAGCATGGC	GAGAAACACT	TCCCAGTGAG	1260
ATAGATTGGT	ATGGTATTAG	ACAAATAGCT	CATTATTTAT	ACATGCCACT	AGTAACTACA	1320
TCGGATTTGA	CATACAACTA	TGTAAGTCAA	ACCAGGATAG	AAGGAAAAAA	ACTATTTGAG	1380
TCTTTGGGTT	ATACAAGAGA	ACATATAGAT	TATGTAGAAA	GTTTATTGTC	ATATCTAGAT	1440
TCTAAATGTC	CACAGATTGA	GAATATTTCC	AGGAAAAAAG	TTTTAAAACC	CATGCATGAG	1500

ATTAGAACTA TCGAGAGTGA GCAAGATATA CAAGATTTTA TTATAAAAGC TTTTCTTTTA	1560
GTGAACTGA	1569

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 930 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GAAAGACTAG CCCTCAGCTT CCAGACAAAA TCAAAGCCTT TTAGGCTTTT TTTTGTTATA	60
CTAGAAAAGT ATATTTATAG AATTTTGTCT CTATTTTGGG GGAAATCAGA CGTTTTTCTA	120
GTAAGTACTG TAAAAGTTTT GAAAAAGAAA GGAAGTATCA TGTCAGTATT AGAGATCAAA	180
GATCTTCATG TTGAGATTGA AGGAAAAGAA ATTTTAAAAAG GGGTTAACCT GACCCTGAAA	240
ACAGGAGAAA TTGCCGCTAT CATGGGACCA AATGGTACAG GTAAATCGAC TCTTCTGCC	300
GCTATCATGG GAAATCCAAA CTATGAAGTA ACTAAAGGTG AAGTTTGTGTT TGATGGCGTA	360
AACATCCTTG AGTTGGAAGT GGATGAGCGT GCGCGTATGG GACTTTTCCT TGCTATGCAA	420
TACCCATCAG AAATCCCTGG AATTACCAAT GCTGAGTTTC TTCGTGCCGC TATGAATGCG	480
GGTAAAGAAG ATGATGAGAA GATTTCAAGT CAGTATTTTA TTAATAAGCT AGATGAAAAA	540
ATGGAATTGC TCAACATGAA AGAAGAAATG GCAGAGCGTT ACCTCAACGA AGGCTTCTCT	600
GGTGGTGAGA AAAAACGCAA TGAAATTCCTT CAACTTTTGA TGTTGGAGCC AACATTTGCT	660
CTTTTGGATG AGATTGACTC AGGTCTTGAT ATTGACGCTC TTAAAGTTGT GTCTAAAGGT	720
GTCAATGCCA TGCGTGGTGA AGGTTTGGT GCTATGATCA TTAATACTA CCAACGTCCT	780
TTGAACTATA TCACACCTGA TGTGGTACAC GTGATGATGG AAGGTCGTGT TGTCCTTCT	840
GGTGGTCCAG AATTGGCTGC GCGTTGGAA CGTGAAGGAT ACGCAAACT AGCTGAAGAA	900
CTTGGCTACG ACTACAAGGA AGAATTGTAA	930

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

CATTTTATAG	CAATTGCAGT	TATTGATTGG	CTACTATTTG	CATTTTTTAT	CATTAGACTC	60
GAGACATCTT	TTGAGTGGCT	CTTGCTCTCT	GATTTAATTT	TCTTCCTTAC	TCAAGGACTC	120
CTGCTATTTT	TCTTGATCGT	CCGACTCAAA	CATCAATTCG	CTGAGATTTA	TCCTCAAATC	180
AATAAAAAGA	TTCGCTTCTA	CTATTTAGGG	GTTCTCACCA	TTGATTTTCT	ATTTTTTGTT	240
CTCTTAGCCT	TCATTAGTTC	TCAGCGTTTT	TCATCTCTTA	TGCCAATCAT	CACTGCTTGC	300
CATTCTACTT	TTTATTATAT	GACAGCTGAC	TACCTAAGAG	AAAACATATC	AGACTTTTAC	360
GACAAACACA	TCTCTTTATG	GGAGTGTCTC	TAA			393

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GCGCGTTCAG	CTGGGATGCA	CTATGATGCA	AGCTACATTT	CATTTGATGG	GATATTAAGA	60
AAGGAGATTC	TCATGACACT	TTTAGATGTA	AAACACGTTT	AAAAAATTTA	TAAAACACGT	120
TTTCAGGGCA	ACCAAGTAGA	AGCCCTCAAG	GATATTCACT	TTACCGTCGA	AAAGGGTGAC	180
TACGTTGCCA	TCATGGGTGA	GTCTGGTTCT	GGTAAATCAA	CTCTTCTCAA	TATTCTAGCT	240
ATGCTGGATA	AACCAAGTCG	TGGTCAGGTT	TACTTGAATG	GAACTGACAC	CGCAACCATT	300
AAAAAATTCAC	AGGCCTCTAG	CTTCCGTCGT	GAAAAGTTGG	GCTTTGTCTT	CCAAGACTTT	360
AACTTGCTAG	ATACTCTATC	TGTAAAGGAC	AATATCTTGC	TTCCGCTTGT	CTTGTCAAGA	420
AGACCTATTA	CAGAGATGAT	GAAGAAATTG	GTGGTGACAG	CTGAGAATCT	GGGAATAAAC	480
CAATTACAAG	AGAAGTACCC	TTACGAGATT	TCTGGTGGCC	AGAAACAGCG	TGTAGCAGTA	540
GCACGCGCCA	TCATCACTGA	ACCTGAAATT	CTCCTTGCGG	ACGAACCGAC	AGGAGCTCTT	600
GACTCCAAGT	CATCTGCAGC	CTTACTTGAT	GTCTTTGATG	AAATCAATGA	GCGCGGCCAA	660
ACCATTCTCA	TGGTAACCCA	CTCAACAGCA	GCAGCTAGCA	GAGCTAAACG	TGTACTCTTT	720
ATCAAAGACG	GCATTCTTTA	CAATCAAATC	TACCGTGGAG	AGAAGACAGA	ACGTCAGATG	780
TTCCAAGAAA	TCTCTGATAC	CTTGACTGTC	ATGGCAAGCG	AGGTGAATTA	G	831

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1038 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1038
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

ATGAAATCAG	CAGTATATAC	AAAGGCAGGT	CAGGTTGGAC	TTGCTAGCAT	TGAACGTCCG	60
CAAATAATAG	AAGCGGATGA	TGTGATTATT	CGTGTGGTTC	GTGCGTGCGT	TTGTGGTTCA	120
GATTTATGGA	GGTACCGTAA	TCCAGAAAACG	AAAGCTGGAC	ATAAAAAATAG	TGGACACGAA	180
GCGATTGGGA	TTGTTGAAGA	AGCTGGGGAA	GCCATTACGA	CGGTGAAACC	AGGTGATTTT	240
GTGATTGTCC	CTTTTACACA	TGGATGTGGT	GAGTGTGATG	CCTGTCTTGC	TGGATTTGAC	300
GGTTCCTGCG	ACAATCATAT	TGGTAATAAT	TTGGGGGGTG	ATTTTCAGGC	AGAATATATT	360
CGCTTCCACT	ATGCAAACTG	GGCGCTGGTT	AAAATCCCTG	GTCAACCTTC	TGATTATACA	420
GAAGGGATGC	TCAAGTCCCT	TTTGACTCTT	GCAGATGTCA	TGCCGACAGG	CTATCATGCA	480
GCGCGTGTTG	CAAAATGTTCA	AAAAGGGGAC	AAGGTTGTTG	TTATCGGTGA	TGGGGCTGTT	540
GGTCAATGTG	CTGTCATCGC	GGCTAAGATG	CGTGGAGCAT	CACAAATTAT	CCTTATGAGC	600
CGTCATGAAG	ACCGTCAAAA	GATGGCTATG	GAGTCAGGTG	CGACAGCTGT	TGTTGCAGAA	660
CGTGGTCAAG	AAGGAATTAC	CAAGGTGCGT	GAAATCCTCG	GCGGAGGAGC	AGACGCAGCA	720
CTTGAATGTG	TTGGTACGGA	GGCTGCTATA	GAACAGGCGC	TAGGTGTTCT	TCATAATGGA	780
GGGCGTATGG	GCTTTGTAGG	AGTCCCACAC	TATAATAATC	GTGCTCTTGG	TTCGACATTT	840
ATGCAAAATA	TCTCTGTAGC	AGGTGGGGCA	GCTTCTGCTA	CAACATACGA	TAAGCAATTT	900
TTACTAAAAG	CCGTCCCTGA	TGGTGATATC	AATCCAGGTC	GCGTCTTTAC	TTCAAGTTAT	960
AAACTGGAAG	ATATCGACCA	AGCCTATAAA	GATATGGATG	AACGTAAGAC	AATTAAGTCT	1020
ATGATTGTAA	TCGAATAA					1038

(2) INFORMATION FOR SEQ ID NO:468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GCGGCCACAG	CCCGGCCCGG	GCTTCCCGGC	GAAAACCGCA	GCCGAGGTCG	CGTCCACGGC	60
GCAGGCCAGT	GTCCAGGTCT	CGCCGCCCGC	GCCGACAGCG	GGCGGCGAAG	GCCGCGGAGA	120
GGAGCGTCGG	CAACCCGGAG	AAACCGATCC	ATCCGCACTG	CCCCCGACG	ACCAAGCGCC	180
TGTGCCATTG	CCTGCCATGC	AAACCCCGG	CGACCGCCTG	CTGGCACGCC	TGCTGGCATC	240
GAGCGGGAGC	CGGCCACTGC	CGCTGGCCGA	TCTCGCGCGC	CTGCTAGATG	CCGTGCAGGG	300
GCGCATCCAG	GTCGCCAGCG	CAGCCGAAAG	CCATGCGGCG	CGCCTGCAGG	TGCGACTGCC	360
CCAGCTCGGC	GCCGTGGAGG	TGCAGGTCCT	GCATGGCCAT	GGCCAGTTGC	AGGTCGTCTT	420
CACCACGAGC	CGGGAGGTCC	C				441

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

AGAATAACAG	CAATATTAAA	AAGATCAGGA	CTGATAATAA	ACAAAAAGAA	AGTACAACGA	60
CTAGTTCAAA	AGCTAAACT	TCAAGTAAAA	AGTTATTCAA	GAAATCTAG	AAAATACTCA	120
TCCTACAAAG	GACAGGTAGG	AAAAATATCA	GACAACAAAA	TAAAAAGAAA	TATTTATTAC	180
CGAAAAAAG	GGGAAATCGA	GTCAAGTACC	AACAGGCTCA	TCTATTCCAA	AAAGATATTT	240
ACTCGATGGA	AAAACTCCTA	G				261

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

AAAATGACAG	CAGGACAAAC	TAAATTAGCC	ACTATGGTTA	ATCCAGAAGT	AATGGCGGAT	60
ATGGTAGCCG	CTAAATTACC	TAAATTGATT	AAATTTACAC	CGCTAGCGTA	TGTAGAGACA	120
AAGCTTGAAG	GTCAACCAGG	TAGCACTTTA	ACAGTGCCAG	CATGGGAGTA	TGCAGGAGAC	180
GCTACTGAAA	TTGAAGAAGG	CCAAGCAATT	ACGCCAGACC	AATTGACTAC	TAAAAAGACT	240
ACTATGACCA	TCAAAAAAGC	AGGTAAAGGT	TATGAAATTA	CCGATGAGTC	TCTTTTGTCA	300
GGTCTTGGTG	ACCCACTAGG	TCAAGCGACT	TACCAGCTTG	GTTTAGCTAT	TGCCAACAAG	360
ATCGATAATG	ATTTGGTAGC	GGTAGCTAAA	ACTGCAACAC	AACATATTAC	AGAAACTCCA	420
ACAACTCTTG	AGGCAATCGA	TAAAGCTCTA	GATATCTTTG	AGGACGAAGA	AGATGCACAG	480
TATGTTGCTA	TCATCAACCC	TAAAGATGCT	ACTAAGCTAA	AAACTGCAGT	AGCAAAAGAA	540
TGGATTAAAG	GTTTCAGAGCT	TGGAGCAAAT	ATGGTTGTTT	CTGGAACCTT	CGGTGAAGTT	600
GATGGTGTGC	AAATCGTGCG	CTCTAAAAAA	GTTGATGAAG	GTAAAGGCTT	CCTTGTTAAA	660
GTGTCACCAA	GTCAAACTCA	GACAGACGAC	GCTAACAAAT	ATGGAGCTTT	TGTTATCTTG	720
CTTAAACGTG	ATGTGGCTAT	CGAAACAGAC	CGCGATATCT	TGAAGAAGAC	TACCGTAATC	780
ACAGGTGATG	AACACTACGG	CGTTTACCTT	TACGACCCTA	CACGAGTTGT	AAAATTCGGT	840
GGCGCGTAA						849

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

AAATGGACAG	CAGTACAAGA	GCTTGAGAGA	ACTTTAAGAG	GTGTTGAGAT	GATTACTATT	60
AAAAAGCAAG	AAATTGTCAA	GCTAGAGGAT	GTTTTGCATC	TCTATCAGGC	TGTCGGTTGG	120
ACAAATTATA	CCCATCAACC	AGAGATGCTG	GAGCATGCCT	TATCGCATT	ATTAGTAATT	180
TATCTGGCAC	TTGATGGTGA	TGCTGTGGTG	GGCTTGATTC	GTTTGGTTGG	AGATGGATTC	240
TCATCAGTTT	TTGTACAGGA	TTTGATTGTT	TTACCAATCT	ATCAGCGTCA	AGGGATTGGT	300
AGTGCCCTAA	TGAAAGAGGC	CTTAAAAGAT	TACAAAAGATG	CTTATCAAGT	CCAGCTGGTG	360

ACAGAAGAGA CAGAAAAAAA CGTGGGATTT TATCGTTCTA TGGGCTTTGA AATCTTATCC	420
ACCTATAATT GTATAGGGAT GACTTGGGCG AATCGAGAAA AATAA	465

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

AGGTACCAAG CCAAGAAAAAG TATTGCAGCA ATAAAAAATA GCTTCTTTCC AAGGTTGGAA	60
GGAGCTATTT TACTGGCTAT TGATTACTTT TATACTCTTC GCAAATCTCT TCAAACCACG	120
TCAGCTTTGC CTTGCCGTAT ATATGTGACT GACTTCGTCA TGTCTTATCT ACAACCTCAA	180
AACAGTGTTT TGAGCAGCCT ACGGCTAGCT TCCTAG	216

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

AAAAACAAG CTTATGATGA AAAAAATAAA AAAGTCATCT ATTTATTGCT AGATGAAAAA	60
AGGAAGAACT ATGTAGAAGA TAAGAGACAA AATTTCCCTA GTCTCCCTAA CTGGAAAAATG	120

GATTTATTTT	CAGAAGAAGA	AAAAAGGAAT	TATTTTCAAA	CCACATGTGA	AATTTCAAGT	180
AAAGACTCTG	CAATAAATAA	ATACAAAATG	GAAAAAATTA	TTAAGAGATC	AAATAAAGGA	240
AATGTTTATC	GGGCAATTAG	AAAATCGGAC	GGGCAAAAAG	TAATCATCAA	GCAGTCAAGA	300
CCTTTTGTGA	ATTATGATGC	TGAAGGAGAA	TGGACAGCTC	TTGATGATAT	AAAAAATGAA	360
GCTCATATGC	TAAAAAAATT	AGCCGATAAA	AGTTATACTA	CTAATTTAAC	TGATGAATTT	420
TATATCGTGG	ATGATTATTT	TCTTGTTTCA	GAACAAGTTG	ACGGGTTAAA	CTTTGAAGAA	480
TTTATTCGAG	AAACAGAACA	CTCCTTAAAT	ATTAGAGAAA	AAACACTGTA	TAACATTGTG	540
AATATAGTAA	GTGACATCCA	TAAACTGGGA	ATATAA			576

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

AAAATGCAAG	CCTTTTATAT	TAAAAAAGAG	AAAAAACTGT	CAAACGATTA	TCATGAAATA	60
AATACAGGAA	ATCAATCAAA	TTTTTACGAA	AATGTGAAAG	ATAATGAAAT	AAAATACTTT	120
TTAACCAAGG	TTTCAAACTT	ATTTTTC AAG	GAATTCCTGA	TGAAACAGTC	AAAAACAATC	180
AATCTAAAAAC	TTGCCCACTA	A				201

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

CAAATGTATT	TAGGAGATTT	GATGGAGAAA	GCCGAGTGTG	GTCAATTTTC	AATCCTTTCC	60
TTTCTATTAC	AAGAGTCTCA	GACGACCGTC	AAGGCTGTAA	TGGAAGAAAC	AGGATTTTCA	120
AAAGCAACCC	TAACCAAATA	TGTCACCCTG	CTCAATGACA	AGGCTTTGGA	TAGTGGCTTA	180
GAGCTGACTA	TTCATCAGA	AGATGAAAAT	CTGCCGTCTGT	CTATCGGTGC	AGCTACCAAG	240
GGGAGAGATA	TTCGGAGCTT	GTTTTTGGAT	AGTGCTGTTA	AATACCAGAT	TTTGTTTTAT	300
CTTCTCTACC	ACCAACAGTT	TTTAGCCCAT	CAGCTGGCTC	AAGAATTGGT	GATTAGCGAG	360
GCTACGCTTG	GTCGTCACCT	GGCTGGTTTA	AATCAGATTT	TGTCAGAATT	TGATTTATCC	420
ATCCAAAATG	GACGCTGGCG	AGGTCCAGAG	CATCAGATTC	GCTATTTCTA	TTTCTGTCTT	480
TTCCGAAAGG	TCTGGTCGAG	TCAGGAATGG	GAAGGTCACA	TGCAGAAACC	AGAGAGAAAA	540
CAGGAGATTG	CCAATTTAGA	GGAAATCTGC	GGTGCAAGTT	TGTCTGCGGG	GCAGAAATTG	600
GACTTGGTTC	TCTGGGCTCA	CATCAGTCAA	CAACGTCTTC	GGGTCAATGC	TTGTCAGTTT	660
CAAGTTATAG	AAGAGAAAAT	GCGAGGGTAT	TTTGACAATA	TCTTCTATCT	TCGTTTGCTG	720
AGAAAGGTTT	CGTCCTTTTT	TGCTGGGCAA	CATATTCCAC	TAGGAGTTGA	GGATGGTGAG	780
ATGATGATAT	TCTTCTCTTT	TCTCCTATCT	CATCGCATTC	TTCTCTTCA	TACTATGGAG	840
TATATTCTTG	GTTTTGGAGG	GCAGTTGGCA	GATTTACTGA	CGCAATTGAT	TCAAGAAATG	900
AAGAAGGAGG	AACTATTGGG	GGATTATACA	GAGGACCATG	TCACCTATGA	ACTCAGTCAG	960
CTTTGTGCTC	AAGTCTATCT	CTATAAGGGC	TATATTTTAC	AGGATCGCTA	CAAGTACCAG	1020
TTAGAGAATC	GTCATCCATA	TTTACTGATG	GAACATGATT	TTAAAGAGAC	AGCAGAGGAG	1080
ATTTTTCATG	CTCTACCTGC	TTTTCAACAG	GGGACAGATT	TAGATAAGAA	GATTCTCTGG	1140
GAATGGCTCC	AGTTAATCGA	ATATATGGCT	GAAAACGGTG	GCCAGCATAT	GCGGATTGGT	1200
CTGGATTTGA	CATCTGGTTT	TCTTGTCTTT	TCAAGGATGG	CAGCCATTTT	GAAACGGTAT	1260
TTGGAATACA	ATCGTTTAT	TACCATTGAA	GCTTATGACC	CTAGTCGGCA	TTATGATTTG	1320
CTGGTTACCA	ATAACCCGAT	TCATAAGGAAG	GAACAGACCC	CAGTCTATTA	TTTAAAAAAT	1380
GACTTGGATA	TGGAAGATTT	GGCAGGGATT	CGTCAGTTAT	TATTCACCTA	A	1431

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GTAGCAAAAG	CTAGGTGGAA	CAGCATTGAG	ATGTCTGTTA	CATTTTTTTAT	AGGAGAGCAA	60
AGATTGAAAA	CAAAAATTGG	ATTAGCAAGT	ATCTGTTTAC	TAGGCTTGGC	AACTAGTCAT	120
GTCGCTGCAA	ATGAAACTGA	AGTAGCAAAA	ACTTCGCAGG	ATACAACGAC	AGCTTCAAGT	180
AGTTCAGAGC	AAAAATCAGTC	TTCTAATAAA	ACGCAAACGA	GCGCAGAAGT	ACAGACTAAT	240
GCTGCTGCCC	ACTGGGATGG	GGATTATTAT	GTAAAGGATG	ATGGTTCTAA	AGCTCAAAGT	300
GAATGGATTT	TTGACAACCTA	CTATAAGGCT	TGGTTTTATA	TTAATTCAGA	TGGTCGTTAC	360

TCGCAGAATG	AATGGCATGA	AAATTACTAC	CTGAAATCAG	GTGGATATAT	GGCCCCAAAC	420
GAGTGGATCT	ATGACAGTAA	TTACAAGAGT	TGGTTTTATC	TCAAGTCAGA	TGGGGCTTAT	480
GCTCATCAAG	AATGGCAATT	GATTGGAAAT	AAGTGGTACT	ACTTCAAGAA	GTGGGGTTAC	540
ATGGCTAAAA	GCCAATGGCA	AGGAAGTTAT	TTCTTGAATG	GTCAAGGAGC	TATGATGCAA	600
AATGAATGGC	TCTATGATCC	AGCCTATTCT	GCTTATTTTT	ATCTAAAATC	CGATGGAACT	660
TATGCTAACC	AAGAGTGGCA	AAAAGTGGGC	GGCAAATGGT	ACTATTTCAA	GAAGTGGGGC	720
TATATGGCTC	GGAATGAGTG	GCAAGGCAAC	TACTATTTGA	CTGGAAGTGG	TGCTATGGCG	780
ACTGACGAAG	TGATTATGGA	TGGTGCTCGC	TATATCTTTG	CGGCCTCTGG	TGAGCTCAAA	840
GAAAAGAAAAG	ATTTGAATGT	CGGCTGGGTT	CACAGAGATG	GTAAACGCTA	TTTCTTTAAT	900
AATAGAGAAG	AACAAGTGGG	AACCGAACAT	GCTAAGAAAA	TCATTGATAT	TAGTGAGCAC	960
AATGGTCGTA	TCAATGATTG	GAAAAAGGTT	ATTGATGAGA	ACGAGGTGGA	TGGTGTTCATT	1020
GTTCTCTAG	GTTATAGCGG	TAAAGAAGAC	AAGGAATTGG	CGCATAACAT	TAAGGAGTTA	1080
AACCGTCTGG	GAAATCCTTA	TGGTGTCTAT	CTCTATACCT	ATGCTGAAAA	TGAGACCGAT	1140
GCTGAGAATG	ACGCTAAACA	GACCATTGAA	CTTATAAAGA	AATACAATAT	GAACCTGTCT	1200
TACCTTATCT	ATTATGATGT	TGAGAACTGG	GAATATGTAA	ATAAGAGCAA	GAGAGCTCCA	1260
AGTGATACAG	ACACTTGGGT	TAAAATCATC	AACAAGTACA	TGGACACGAT	GAAGCAGGCG	1320
GGTTATCAAA	ATGTGTATGT	CTATAGCTAT	CGTAGTTTAT	TACAGACGCG	TTTAAAACAC	1380
CCAGATATTT	TAAAACATGT	AAACTGGGTA	GCGGCCTATA	CGAATGCTTT	AGAATGGGAA	1440
AACCCTTATT	ATTCAAGGAGA	AAAAGGTTGG	CAATATACCT	CTTCTGAATA	CATGAAAGGA	1500
ATCCAAGGGC	GCGTAGATGT	CAGCGTTTGG	TATTAA			1536

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

ATTGAACGAG	CTTGTA AAAAG	CTATCGAAGA	AGAATTTGGT	GTAAC TGCAG	ATACTTCTGT	60
AGCTGTTGCT	GCAGCTNGAT	GCTTGATGCT	GGTGCTGCTA	AAGATTTCATT	CGACGTTGAA	120
TTGACATCTG	CAGGCGACAA	AAAAGTTGGT	GTTATCAAAG	TTGTACGTGA	AATCACTGGT	180
CTTGGTCTTA	AAGAAGCTAA	AGAACTTGTT	GACGGTGCAC	CAGCACTTGT	TAAAGATGGC	240
GTTGCAACTG	CAGAAGCTGA	AGAAATCAAA	GCTAAATTGG	AAGAAGCTGG	AGCTTCAGTT	300
ACTCTTAAAT	AA					312

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

AGGAGACGAG	CTAATGACTA	CAAAAAAGCT	AATATTACTA	TTGAAGAGTA	CATTGAAATG	60
TCTGAAGTTG	ATTTTAATGA	AGCTGTTAAT	TATGAATTTA	CATCTGACAC	TTGTCAATTA	120
GCAAATAGTA	TTTATCAATC	TCTTTTAAAG	TTTTTTTGATA	AGAAAAATTT	CTCTGGCGAT	180
TTAATTTTTA	CTTGAAAATC	TCCATCATT	GTCAAAGAAG	GGGATTATAT	TGGGAAAAGG	240
GATTCACAAG	TAGATAATCT	TAGAGTAATA	GGAAATATAT	TTCCGAATTA	TCTTACTAAT	300
CGAAAAATATA	GCCTCAATAT	GAATCGTAAT	GGCTGTATGG	GAGATTTTCC	TCATGACTTT	360
TTTGATATAT	ACCTAGATCA	TGTAGCAAAA	TATGCCTACG	AACAAAAAGT	TAATAATATT	420
AAAGAGTATT	ATCCTTTAAA	AAGAGCGATT	TTACACCAAG	AGAATGCATT	GTATTTTCGA	480
TTTTTTTCTA	ATTTTGACGA	CTTTTGTAGAA	AAAAATTATT	TAAAGACTAT	ATGGCAAGTT	540
TCTAAAGAAA	CTCCTTTTTC	TGAAATGGAT	TTTAATATGT	TTAAAAATAT	TTCAGAAAAG	600
ATAATCTTCG	AAAGAGGTAG	TAAAATGCTT	AATGATTTAA	AAAGTAATTA	TAAAAAATAG	660

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1011
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TATAATAGAG	CCATGAGTAG	AATTTTATAGAT	AATGAGATAA	TGGGGGATGA	GGAGTTAGTA	60
GAACGCACGC	TCCGTCCTCA	GTATTTACGT	GAATATATCG	GACAGGATAA	GGTCAAGGAC	120
CAGCTACAAA	TCTTTATTGA	AGCTGCCAAA	ATGCGGGATG	AAGCGCTGGA	TCATGTGCTC	180
TTATTTGGGC	CTCCAGGTCT	CGGGAAAACG	ACCATGGCCT	TTGTTATTGC	CAACGAACGT	240

GGAGTCAATC	TTAAGCAGAC	GTCGGGTCCA	GTCATTGAAA	AAGCCGGAGA	TCTGGTAGCT	300
ATTTTGAATG	AGTTAGAGCC	TGGGGATGTA	CTTTTATTG	ATGAGATCCA	TCGTTTGCCA	360
ATGTCAGTGG	AAGAGGTGCT	TTATAGTGCT	ATGGAGGACT	TCTACATCGA	TATTATGATT	420
GGGGCTGGTG	AGGGTAGTCG	TAGTGTTTCA	TTGGAGTTAC	CACCTTTTAC	CTTGATTGGT	480
GCGACGACTC	GGGCTGGTAT	GCTCTCCAAT	CCGCTACGGG	CACGTTTTTG	GATTACAGGC	540
CATATGGAGT	ATTATGCCCA	TGCTGACTTG	ACAGAAATTG	TCGAGCGGAC	GGCAGATATT	600
TTTGAGATGG	AAATCACTCA	TGAGGCAGCA	TCTGAGTTGG	CCCTACGTAG	TCGTGGGACC	660
CCTCGTATTG	CCAATCGTCT	CCTCAAGCGC	GTGCGCGATT	TTGCCCAGAT	AATGGGGAAT	720
GGGGTAATTG	ATGATATTAT	TACCGATAAG	GCTTTGACTA	TGCTGGATGT	TGACCATGAA	780
GGTTTGACT	ATGTGGATCA	AAAAATCCTT	CGTACCATGA	TTGAGATGTA	CAGTGGAGGA	840
CCTGTTGGTC	TAGGAACTCT	TTCTGTGAAT	ATCGCCGAAG	AGCGTGAGAC	AGTTGAAGAC	900
ATGTATGAGC	CTTACTTGAT	TCAAAAAGGT	TTTATCATGC	GGACACGGTC	TGGACGGGTG	960
GCGACTGCTA	AGGCATATGA	GCACTTAGGT	TATGAATACA	GTGAAAAATA	A	1011

(2) INFORMATION FOR SEQ ID NO:480:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...285
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

TTGAACAGAG	CTAATAGAGG	CGAAAAAATT	TCAGGTCCTC	CTTTGCTAGA	TGATAATGAG	60
GAAACTAAGA	TTTTACCAAC	CTCTTCTTCC	CGTTTTGGTT	ATGCCAATCC	TAAGGATCAT	120
GGTTTTAGCC	AGGAAACCTT	GAAGATTCAG	GTCGAACCAT	CTATTCATAA	AAGCCGTCGT	180
ATTGAAAATA	CCAAGAGAAA	TGTCTTCAAT	TCTAAGTTGA	ATAAAATCTT	ATTTGCGGTC	240
ATCTTTCTCT	TGATTTTGCT	TGTTTTAGCA	ATGAAACTTT	TGTAA		285

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

TCGATGAGAG	CACCTATGAG	CCCCTTCAAG	AAAATGGGCA	AGCCAAAGTC	AAGGAGGGCA	60
ATATCAGTTT	TGGAACATGT	GTGTATCTCG	TATGACGGTA	AACATCCGAT	TCTGGATGAC	120
ATTTCTTTCT	CTGTTAATAA	GGGTGAAACC	ATTGCCTTTG	TAGGTCATAC	AGGTTCAGGG	180
AAATCGTCTA	TTATCAATGT	CCTCATGCGC	TTTTATGAAT	TCCAGTCAGG	GAGAGTTCTC	240
TTGGATGATG	TGGATATCAG	GGATTTCAGT	CAAGAAGAGC	TGAGAAAAAA	CATCGGTTTG	300
GTTTTACAGG	AACCCTTCCT	CTATCATGGA	ACTATTAAGT	CCAATATCGC	CATGTACCAA	360
GAAATCAGTG	ATGAGCAGGT	TCAGGCTGCG	GCAGCCTTTG	TGGATGCAGA	TTCCCTTTATT	420
CAAGAACTTC	CTCAGGGGTA	CGACTCCCCT	GTTTCCGAGC	GTGGTTCGAG	CTTCTCTACT	480
GGGCAGCGCC	AGCTTTTTGC	CTTTGCTAGA	ACAGTCGCCA	GCCAGCCTAA	AATCCTGATT	540
TTGGATGAAG	CGACAGCCAA	TATTGACTCT	GAAACAGAAA	GTTTGGTTCA	AGCTTCTCTG	600
GCGAAGATGA	GACAGGGCCG	AACAACTATT	GCTATCGCTC	ACCGCCTTTC	TACTATTCAA	660
GACGCCAACT	GCATCTATGT	CTTGGATAAG	GGACGCATTA	TCGAGAGTGG	AACCCATGAG	720
GAACTCTTGA	CTCTGGGAGG	AACCTATCAC	AAGATGTATA	GTTTGCAGGC	AGGGGCCATG	780
GCCTATACTC	TTTGA					795

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

AACCAAGGAG	CGCTTCCTCT	AATCCATAAG	GAGGTATTTA	TGACGCACTA	CGTTGCCAAT	60
CCAGAGGTGG	TCATTCTCGA	GGGTGGCATC	ATGGGACAAG	AAGCTATCCT	CAAACCAAAG	120
ATTCGTGCAG	CCTTGAAAGA	AGTCTTGGTT	CCAAGTTTGG	CTGAGAACAC	AAGATTAGAA	180
TTTGCTCATC	ATCAAAACAC	TGCTGGTATG	CTTGGAGCCT	ACTATCATTT	TAAAATAAAA	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 693 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GAAGGAGGAG CAAGCATGAA AAAAATCTAT TCATTTTTAG CAGGAATTGC AGCGATTATC	60
CTTGCTTTGT GGGGAATTGC GACTCATTTA GATAGTAAAA TCAATAGTCG AGATAGTCAA	120
AAATTGGTTA TCTATAACTG GGGAGACTAT ATCGATCCTG AACTCTTGAC TCAGTTTACA	180
GAAGAAACAG GAATTCAAGT TCAGTACGAG ACTTTTGACT CCAACGAAGC CATGTACACT	240
AAGATAAAGC AGGGTGGAAC GACCTACGAT ATTGCCATTC CAAGTGAATA CATGATTAAC	300
AAGATGAAGG ACGAAGACCT CTTGGTTCCG CTTGATTATT CAAAAATTGA AGGAATCGAA	360
AATATCGGAC CAGAGTTTCT CAACCAGTCC TTGACCCAG GTAATAAATT CTCCATCCCT	420
TACTTCTGGG GAACCTTAGG AATTGTCTAC AACGAAACCA TGGTAGATGA AGCGCCTGAG	480
CATTGGGATG ACCTTTGGAA GCCGGAGTAT AAGAATTCTA TCATGCTCTT TGATGGGGCG	540
CGTGAGGTGC TGGGACTAGG ACTCAATTCC CTCGGCTACA GCCTCAACTC CAAGGATCTG	600
CAGCAGTTGG AAGAGACAGT GGATAAGCTC TATAAACTGA CTCCAAATAT CAAGGCTATC	660
GTTGCGGACG AGATGAAGGG CTATATGATT TAG	693

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GTAGCTTTGG CGAAAGAGCA AGATATTCCA TTTAAGCTCG ACATCTATCC ATTTTACGGA	60
TCGGACGCTT CAGCAGCGAT GTCAGCAGGT GCAGAGGTCA AGCATGCACT TCTTGAGACT	120

GGTATTGAGT CCACTCACTC TTATGAGCGG ACCCACATCG ATTCAGTAGT AGCGACTGAG	180
CGTATTGTTG ATGCTTATCT TAAGAGCGAG GCGGTATCAT AG	222

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

ATCTCCTTGG	CTTCATCGAA	GCCATCGTCG	ATTTCCCTATT	TTTCAGTCGC	TTTTGACGCC	60
CTTTGTATCA	TAAATAGAAT	TGGAGAGGTC	ATGGCTGATG	ACAAGCTAAG	AGCGACTCCT	120
GCAGCTAGAA	AGTTAGCAGA	TGATTTAGGG	ATAAACCTCT	ACGACGTTTC	TGGCTCAGGT	180
GCAAAACGGTC	GTGTCCACAA	AGAAGACGTG	GAAACTTATA	AAGACACAAA	CGTGGTTTCGC	240
ATTTTCGCCAC	TTGCAAAACG	AATTGCCCTC	GAACATAACA	TTGCTTGGCA	GGAAATCCAA	300
GGAACCGGTC	ATCGTGGTAA	AATCATGAAG	AAGGATGTTT	TGGCCCTGCT	TCCTGAAAAAT	360
ATCGAAAACG	ATAGCATCAA	ATCTCCTGCT	CAGATTGAAA	AAGTGGAAGA	AGTCCCTGAT	420
AACGTAACAC	CATATGGTGA	AATCGAGCGT	ATTCCAATGA	CACCAATGCG	TAAGGTTATT	480
GCCCAACGCA	TGGTTGAATC	TTACTTGACT	GCGCCAACCT	TCACCCTCAA	CTATGAAGTT	540
GATATGACTG	AAATGTTGGC	TCTTCGTAAG	AGGGTTCTTG	AGCCAATCAT	GGAAGCAACT	600
GGGAAGAAGA	CTACTGTAAAC	AGACCTTCTT	TCACTTGCAG	TTGTTAAGTC	TCTTATGAAA	660
CATCCATACA	TCAACGCTTC	ATTGACAGAA	GATGGCAAGA	CTATTATCAC	TCACAACTAT	720
GTCAATCTTG	CCATGGCAGT	TGGGATGGAT	AATGGATTGA	TGACACCTGT	TGTTTACAAT	780
GCTGAGAAGA	TGAGTCTTTC	AGAACTGGTT	GTAGCCTTTA	AGGATGTTAT	TGGCCGTACC	840
TTGGATGGTA	AATTGGCTCC	AAGTGAGTTA	CAAAATTCAA	CATTACAAAT	CAGTAATTTG	900
GGAATGTTTG	GTGTTCACTC	CTTTGGCCCC	ATTATTAACC	AACCCAACTC	AGCTATCCTT	960
GGTGTCAAGT	CGACAATCGA	GAAGCCAGTT	GTCGTCAATG	GTGAAATTGT	GATTCGCCCA	1020
ATCATGAGTT	TAGGATTAAC	CATTGACCAC	CGTGTCTAG	ATGGTATGGC	TGGTGCTAAG	1080
TTTATGAAGG	ACTTGAAAAGA	GTTGATTGAA	ACCCCAATCT	CAATGTTGAT	TTAA	1134

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

ANGGNATTGG	CCATTACAGG	ATTCCTTATG	AATAAGATGA	ACAAGGTGAT	GCTGACGATG	60
TTTGGCTTAG	TGATGCTCCC	CCTACTATTT	GCTTGTAAGTA	ACAATCAATC	GGCTGGAATT	120
GAAGCCATAA	AGTCCAAAGG	AAAATTGGTT	GAGCCCTCA	ATCCAGATTT	TGCTCCATTT	180
GAATATCAAA	AAGTGGTTGA	TGGGAAAAAT	CAGATTGTGG	GTTTCAGATAT	CGAATTAGCC	240
AAGGCTATCG	CAACAGAACT	AGGTGTCGAA	TTGGAACTAT	CTCCTATGAG	TTTTGACAAT	300
GTACTGGCTA	GCGTTCAATC	AGGAAAAGCT	GACCTTGCCA	TATCAGGTGT	TTCTAAGACA	360
GATGAACGGA	GCAAGGTGTT	TGATTTTTTC	ACTCCCTACT	ATACTGCAAA	AAATAAACTC	420
ATTGTCAAAA	AATCTGATTT	AGCCACTTAT	CAGTCTGTCA	ACGATTTGGC	GCAGAAAAAG	480
GTCGGAGCGC	AGAAAGGTTC	GATTCAAGAG	ACGATGGCGA	AAGATTTGCT	ACAAAATTCT	540
TCCCTCGTAT	CTCTGCCTAA	AAATGGGAAT	TTAATCACAG	ATTTAAAAATC	AGGGCAAGTG	600
GATGCCGTTA	TTTTTGAAGA	ACCCGTTGCC	AAGGGATTG	TGGAAAATAA	TCCTGATTTA	660
GCAATCGCAG	ACCTCAATTT	TGAAAAAGAG	CAAGATGATT	CCTATGCGGT	AGCCATGAAA	720
AAAGATAGCA	AGGAATTGAA	AGAGGCAGTC	GATAAAACCA	TTCAAAAAGTT	GAAGGAGTCT	780
GGGGAATTAG	ACAACTCAT	TGAGGATGCC	TTTAAAGCGT	CCATTGAAAA	ATAG	834

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

ACTTGGCTGG	CTGGATTATC	CCCAACCAAA	ATCACTACCA	AACCAGGCAC	TAGACCTGTT	60
TCTTCCTTTA	ATTTTGCAGT	CTTTTCAGCC	AACTGCCCCCT	GCAATTTGGC	CGCTAAAGCT	120
TTCCCATCAA	TAATCTGTGT	CATATCACTT	CTCTTTTCTT	TCAAAATATCT	TCCATTATAC	180
CAAAAACTGC	AAGTGCCCTC	TAACACTTCT	TTCCTAGGTT	ATCCTATAGT	TTCAAACTAT	240
AAGAAAAAGC	TCTGGTTGAA	CTTTTCACTA	ATCTTGCTCT	GA		282

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

CCAAGGCTGG	CAATACCGAC	ACGATTCTTA	TCATCGGTTT	CTAAGAGTAA	GGGAATTCAA	60
GCATCTATGT	CACGCAAGGG	AAACAGCCAA	GACAACGGTA	TGATGGAGTC	CTTCTTTGGG	120
ATTCTGAAAT	CGGAAATGTT	TTATGGCTAT	GAGAAAAACAT	TTAAATCACT	TAATCAATTG	180
GAACAAGCTA	TTGTAGACTA	TATTGATTAC	TACAACAATA	AACGAATTAA	GGTAAAACTA	240
AAAGGACTTA	GCCTTGTGCA	ATACAGAACT	AAATCCTTCG	GATAA		285

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GAAATTATGG	CCCTACCAAC	TATTGCCATT	GTAGGACGTC	CCAATGTTGG	GAAATCAACC	60
CTATTTAATC	GGATCGCTGG	TGAGCGAATC	TCCATTGTAG	AAGATGTCGA	AGGAGTGACA	120
CGTGACCGTA	TCTATGCAAC	GGGTGAGTGG	CTCAATCGCT	CTTTTAGTAT	GATTGATACA	180
GGAGGAATCG	ACGATGTAGA	TGCTCCTTTC	ATGGAACAAA	TCAAGCACCA	GGCAGAAATT	240
GCCATGGAAG	AAGCAGATGT	TATCGTTTTT	GTCGTGTCTG	GTAAGGAAGG	AATTACTGAT	300

GCAGACGAAT	ACGTAGCTCG	TAAGCTTTAT	AAGACCCACA	AACCAGTTAT	CCTCGCAGTC	360
AACAAGGTGG	ACAACCCTGA	GATGAGAAAT	GATATCTATG	ATTTCTATGC	TCTCGGTTTG	420
GGTGAACCAC	TGCCTATCTC	ATCTGTCCAT	GGAATCGGTA	CAGGGGATGT	ACTAGATGCT	480
ATCGTAGAAA	ATCTTCCAAA	TGAATATGAG	GAAGAAAATC	CAGATGTCAT	TAAGTTTAGC	540
CTGATTGGTC	GTCCAAACGT	TGGAAAATCA	AGCTTGATCA	ATGCTATCTT	GGGCGAAGAC	600
CGTGTTATTG	CCAGTCCTGT	TGCTGGAACA	ACTCGTGACG	CTATTGATAC	CCACTTTACA	660
GATACAGATG	GTCAAGAGTT	TACCATGATT	GATACGGCTG	GTATGCGTAA	GTCTGGTAAG	720
GTTTATGAAA	ATACTGAGAA	GTACTCTGTC	ATGCGTGCCA	TGCGTGCTAT	TGACCGTTCA	780
GATGTGGTCT	TAATGGTCAT	CAATGCGGAA	GAGGGGATTC	GTGAATACGA	CAAGCGTATC	840
GCTGGATTTG	CTCATGAAGC	TGGTAAAGGG	ATGATTATCG	TGGTCAACAA	GTGGGATACG	900
CTTGAAAAAG	ATAACCACAC	TATGAAAAAC	TGGGAAGAAG	ATATCCGTGA	GCAGTTCCAA	960
TACCTGCCTT	ACGCACCGAT	TATCTTTGTA	TCAGCTTTAA	CCAAGCAACG	TCTCCACAAA	1020
CTTCTGGGA	TGATTAAGCA	AATCAGCGAA	AGTCAAAATA	CACGTATTCC	ATCAGCTGTC	1080
TTGAACGATG	TCATCATGGA	TGCCATTGCC	ATCAACCCAA	CACCGACAGA	CAAAGGAAAA	1140
CGTCTCAAGA	TTTTCTATGC	GACCCAAGTG	GCAACCAAAC	CACCAACCTT	TGTTATCTTT	1200
GTCAACGAAG	AAGAACTCAT	GCACTTTTCT	TACCTACGTT	TCTTGAAAAA	TCAAATCCGC	1260
AAGGCCTTTG	TCTTTGAGGG	AACACCGATT	CATCTCATCG	CAAGAAAGCG	TAAATAA	1317

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

CAATCTATGG	CTCGCAAAGA	GACCATGGCA	GAAAGGAAAT	ATTGCAAAAT	GAAAAAAGAT	60
ATCCATCCAG	AATATCGCCC	AGTTGTCTTC	ATGGACACAA	CTACTGGTTA	CCAATTCCTT	120
AGCGGTTCAA	CAAAACGCTC	TAACGAAACA	GTTGAGTTTC	AAGGCGAAAC	TTACCCATTG	180
ATCCGTGTGG	AAATTTTCATC	AGACTCACAC	CCATTCTACA	CTGGACGTCA	AAAGTTTCACT	240
CAAGCAGATG	GACGCGTGGA	TCGTTTCAAC	AAAAAATACG	GTCTCAAATA	A	291

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GAATCAATGG	CTAAGGAAAG	AGTGGATGTA	CTAGCTTATA	AACAGGGGTT	GTTTGAAACG	60
AGAGAGCAGG	CCAAGCGAGG	TGTGATGGCT	GGCCTAGTCG	TAGCAGTCCT	TAATGGAGAA	120
CGGTTTGACA	AGCCAGGAGA	GAAAAATCCA	GATGACACCG	AATTAAAACT	CAAGGGGGAG	180
AAACTCAAGT	ATGTCAGCCG	TGGTGGTTTG	AAACTGGAAA	AGGCCTTGCA	GGTCTTTGAT	240
TTGTCGGTGG	ATGGCGCGAC	TACGATTGAT	ATCGGGGCCCT	CTACTGGAGG	TTTTACCGAT	300
GTCATGCTAC	AGAATAGTGC	CAAGTTGGTC	TTTGACAGTCG	ATGTTGGTAC	CAATCAGTTG	360
GCTTGGAAT	TACGCCAAGA	CCCACGAGTT	GTCAGTATGG	AGCAGTTCAA	TTTCCGCTAT	420
GCTGAAAAGA	CTGATTTCGA	GCAGGAGCCG	AGCTTTGCCA	GTATTGATGT	GAGTTTCATT	480
TCCCTTAGTC	TGATTTTGCC	AGCCTTGAC	CGTGTCTTGG	CTGATCAAGG	TCAGGTGGTA	540
GCATTGTCA	AACCTCAGTT	TGAGGCAGGA	CGTGAGCAGA	TTGGGAAAAA	TGGAATTATT	600
CGAGATGCTA	AGGTTTCATCA	GAATGTCCTT	GAATCTGTAA	CAGCTATGGC	AGTAGAGGTA	660
GGTTTTTCAG	TCCTTGGCTT	GGACTTTTCT	CCCATCCAAG	GTGGACATGG	AAATATTGAA	720
TTTTTAGCGT	ATTTGAAAAA	AGAAAAGTCA	GCAAGCAATC	AGATTCTTGC	TGAGATTAAA	780
GAAGCAGTAG	AGAGGGCGCA	TAGTCAATTT	AAAAATGAAT	AA		822

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

AAAAAATGG	CTAGTTTATA	CGAACTAACA	GGTCAGTTCC	TGACAATTTA	CCAATTGGAT	60
ATCGATGACG	AAACAAAAGC	AGACACGCTT	GAGGCCATCG	ATTGGCAAGA	ACAATTTGAA	120
CAGAAAGCAG	AAGGATATGC	CCATGTTATC	AAGAATCTAG	AAGCCGACGT	GGCAATGTAC	180
AAGGCTGAGG	AAGAGAGCTT	CAAAGCCAAAG	AAACAGGTGG	CACAGAAAAA	GCTGGATTAT	240
GTCAAGGATA	ACATTATGGC	AGCTATGAAT	GTCACGGGGC	AAACCGAAGT	TAAGAGTGGT	300
GCCCTGATTA	TAAAAATTGC	TAAGAATCCA	GAATCAGTCA	AGGTCAACGA	AGACGACCTT	360

CCGAAAAAAT ATTTTACAAA AAAAGTGACG CTTGCGCCGG ACAAAAAAAC ACTCAAAGAG	420
TTGCTTAAAT CTGGCAAGAA AGTCAAAGGT GCGGAGCTTG TCCGGACAGA AAAGTTGGTG	480
ATTAAGTAA	489

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...501
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

ATGAAGACGG CTTTATAAT CATTGATGTT CAGAATGTTT TAGTAGAAAC TGGGTTCAG	60
ACAAAAAGTC TATTGGAAAA AATTTCTTAT TTACAAAACC AGGCTAGAAG CAAGAATATT	120
GAAATTATCT ATGTTCAACA TATTGAGAAC TCTGAAGCTC AAACATCAGA AGATTGGCAG	180
TTATCTGCGC TTTTAAATCG AAAACCTGCT GAAAAGGTCT TTCAGAAGAA GTATAACAGT	240
ATTTTCAAAG AAACCTGGCTT AAAAGAATAC TTGGATAAAC AGGGGATTGA AAAATTAGTT	300
TTATGTGGTA TGCAGACAGA ATATTGTGTG GATACCTCTG TCAAGGTTGC CTTTGAATAT	360
GGCTATCAGC TTATTGTTCC AGAAGGTGCT GTCACAACCT TTGATGGGGA TGACATTCCA	420
GCAGAAACGA TTAATGAATT TTATGAGGAC ATTTGGGAGG AGCGCTTTGC AGATGTCCTA	480
GATTACAAAC ATATTTTCTA A	501

(2) INFORMATION FOR SEQ ID NO:494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

CAGCCTGCGG	CTAGCTTCCT	AGTTTGCAC	TTGATTTTCA	TTGAGTATTA	TCTTATCTCA	60
AGCCCATTTG	AGCGAGCTTG	GTTTGATATT	TGTTTTGATC	AACCAGCAAG	CCCAAGCCTC	120
CATAAACATC	ATAGGCGTCT	ACCCAGTCAC	CCAGTTCTGG	AATCGTCAAT	TTTTCAATAC	180
CATTTTTTGC	TCCATCCAAA	ACAGATAAAC	CGTTTGTTAG	GAGGAAAGTA	TAAGGTACGT	240
TGGTTGAGGT	CATAG					255

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

TCCACAGCGG	CTTATTCCAA	GTATACCACT	TGGGCTTTGG	CAGTAGCTAA	CTGCGCTAAA	60
TATAATATAA	GGAGGAGTAA	AATGAAGACA	GTTCAATTTT	TTTGGCATT	TTTTAAGGTC	120
TACAAAGTCT	CATTTGTAAG	TGTCATCCTG	ATGATTGTTC	TGGCGACTTT	TGCCCAAGCC	180
CTCTTTCCAG	TCTTTTCTGG	ACAAGCGGTG	ACGCAGCTAG	CCAATTTAGT	TCAAGCTTAT	240
CAAAATGGCA	ATCCAGAACT	TGTATGGCAA	AGCCTATCAG	GAATCATGGT	CAATCTTGGC	300
CTGCTGGTTT	TGGTTCTATT	TATCTCTAGT	GTAATATACA	TGTGTCTCAT	GACGCGCGTG	360
ATTGCAGAA	CGACCAACGA	GATGCGCAAA	GGCCTCTTTG	GTAAGCTTGC	TCAGTTGACG	420
GTTTCTTTCT	TTGACCGTCG	ACAAGATGGC	GATATCCTGT	CTCATTTTAC	CAGTGATTTG	480
GATAATATCC	TACAAGCCTT	TAACGAAAGC	TTGATTCAGG	TCATGAGCAA	TATTGTTTTA	540
TACATTGGTC	TGATTCTTGT	CATGTTTTTCG	AGAAATGTGA	CGCTGGCTCT	CATCACCATT	600
GCCAGCACCC	CATTGGCTTT	CCTTATGCTG	ATTTTCATCG	TGAAAATGGC	ACGCAAATAC	660
ACCAACCTCC	AGCAGAAAAG	GGTAGGGAAG	CTCAACGCCT	ATATGGATGA	GAGCATCTCA	720
GGCCAAAAAG	CCGTGATTGT	GCAAGGAATT	CAAGAGGATA	TGATGGCAGG	ATTTCTTGAA	780
CAAAATGAGC	GCGTGCGCAA	GGCAACCTTT	AAAGGAAGAA	TGTTCTCAGG	AATTCTTTTT	840
CCTGTCATGA	ATGGGATGAG	CCTGATTAAT	ACAGCCATCG	TCATCTTTGC	TGGTTCGGCT	900
GTAATTTTGA	ATGATAAGTC	TATTGAAACA	AGTACAGCCC	TAGGTTTGAT	TGTTATGTTT	960
GCACAATTTT	CACAGCAGTA	CTACCAGCCT	ATTATCCAAG	TTGCAGCGAG	TTGGGGAAGC	1020
CTTCAGTTGG	CCTTTACTGG	AGCTGAACGA	ATTGAGGAAA	TGTTTGATGC	AGAGGAGGAA	1080
ATCCGACCTG	AAAAGGCTCC	AACCTTCACT	AAGTTGCAAG	AAAAGTGTGA	AATCAGTCAT	1140
ATCGATTTTT	CATACTTGCC	TGATAAACCT	ATTTTGAAAG	ATGTCAGCAT	TTCTGCCCCCT	1200
AAAGGCCAGA	TGACAGCAGT	TGTTGGGCGG	ACAGGTTTCA	GAAAAACGAC	TATTATGAAC	1260
CTCATCAATC	GCTTTTATGA	TGTTGATGCT	GGTGGTATTT	ATTTTGATGG	TAAAGACATT	1320
CGTGGCTATG	ACTTAGATAG	TCTTAGAAGC	AAGGTGGGAA	TTGTATTGCA	AGATTCCGGTC	1380
TTGTTTAGCG	GAACGATTCG	AGACAATATC	CGATTTGGTG	TGCCAGATGC	TAGTCAGGAA	1440

ATGGTTGAGG	TAGCAGCAAA	AGCAACCCAC	ATTCACGACT	ATATCGAAAG	TTTGCCTGAT	1500
AAGTACGATA	CTCTTATTGA	TGATGACCAG	AGCATCTTTT	CAGCAGGGCA	GAAGCAATTG	1560
ATTTCAATCG	CTCGAACCCCT	GATGACAGAT	CCAGAAGTTC	TCATTCTCGA	TGAAGCAACT	1620
TCAAACGTA	ATACGGTGAC	AGAAAGCAAG	ATTCAACATG	CCATGGAGGT	GGTTGTAGCA	1680
GGTAGAACTA	GTTTCGTCAT	TGCCCACCGC	TTGAAAACCA	TTCTCAATGC	AGATCAGATT	1740
ATTGTCCTTA	AAGATGGAGA	AGTCATTGAA	CGTGGTAACC	ACCATGAACT	TTTGAAGCTA	1800
GGTGGCTTTT	ATTCAGAACT	CTATCACAAT	CAATTTGTTT	TCGAATAA		1848

(2) INFORMATION FOR SEQ ID NO:496:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

AATTCTCAGG	CGGAGGACAT	TCAAACGCTC	AAGATTAAAT	TTTCCATGGT	GGGATTTGGT	60
GAAGGTTTGC	TGAAAGGCTG	GCAAGCCATT	GATACCAAGA	TAGCGGATAT	ATTGCTCAAA	120
AGCATCAATA	TCAGACTGAC	TGAGGTCAGT	ATACAAATCA	GTTCTAAGAA	GATTGATCAA	180
ATCCTCCTGA	CGAAAACGGT	AACGTTTTTA				210

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GTAATCAAGG	CATTGATTGT	AGGAGTAGCA	ATAAACGGAA	TCAGCATAAT	CGGATTTAAA	60
ACTGTTGGAA	ACGTAAATAG	AATAGCTGTA	TTGATATTAA	AAATAGACGG	TATAATAGCT	120
AGCTTACCTA	ATGTTTTATT	CGCACGACTC	TTACTAAATA	GGAAGAGACA	AATCGCAAGA	180
CCAATAGTCG	CTCCACCGCC	ACCTATAAAT	ACAAATAAAT	CTTTAAACGG	TAATGTAATA	240
ATGTGTTGGA	GTGTTTGTC	TGCAGCCACA	GCTTCTTGGT	TTTCTGTAGT	AAATTGTAAC	300
CAAACCTGGT	CTACAAAAGC	ATTTAAAACT	TGTCCCCCAT	TAACTCCACA	GAACCAAAAG	360
AATGAGTTTA	CAATAACACA	TAGAATCATA	CCTGGAAGCG	TTCCTGCAAT	TAAC'TTAAGC	420
GGTGTTCCAA	CAATTGCACC	TAGGAATCCG	TTGAGACCTC	CTGCAACTCC	TGCCGCTTCA	480
AGACCTTTTA	AGACCAAAGC	CCACAAAACA	AAAGTAGTAA	AACCAGGTAA	AAGAGCTGAA	540
AATGATTTAC	TTACTACATC	TGGGACACCA	CTTGGCATT	TTATCGTAAT	TCCGCGCTGG	600
ATAAACATAC	GATAA					615

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

GAAGTTGAGG	CTTACTTGTT	GGATAAGTTA	AAACATCCCA	AGGTTGTGGC	TTTAGGTGAA	60
ATTGGCTTAG	ACTACCATTG	GATGACAGCG	CCTAAAGAGG	TGCAGGAGCA	GGTTTTTCGC	120
CGTCAGATTC	AGCTATCTAA	GGACTTGGAT	TTGCCTTTTG	TTGTCCATAC	CCGTGATGCG	180
CTGGAAGATA	CCTATGAGAT	TATCAAGAGT	GAGGGCGTTG	GTCTCTGTGG	TGGTATCATG	240
CATTCATTTT	CAGGGACGCT	TGAGTGGGCA	GAGAAAGTTG	TGGATCTTGG	TATGACCATT	300
TCCTTCTCAG	GAGTGGTGAC	TTTCAAGAAG	GCAACTGACC	TCCAAGAAGC	AGCTAAAGAG	360
TTACCTTTGG	ACAAGATGTT	GGTGGAAACA	GATGCGCCTT	ACTTAGCACC	TGTACCCAAG	420
CGTGGTCGTG	AAAATAAAAC	AGCCTATACT	CGCTATGTGG	TCGACTTTAT	CGCTGACTTG	480
CGTGGTATGA	CGACAGAAGA	GCTGGCGGTA	GCAACGACTG	CAAATGCAGA	ACGAATTTTT	540
GGATTGGACA	GCAAGTAA					558

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...501
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

ATAAAGGAGG	CAGATATGAA	TTTAAAACAA	GCTTTAATTG	ACAATGACTC	GATCCGACTA	60
GGTTTAGAGG	CTAACAATTG	GAAAGAAGCA	GTCAAGGTAG	CAGTAGATCC	CTTAATTGAA	120
AGTGGGGCAA	TTTGTCCAGA	GTATTACGAT	GCTATCATTG	AATCGACTGA	AGAGTATGGG	180
CCTTACTATA	TCTTGATGCC	AGGTATGGCT	ATGCCCCACG	CTAGACCTGA	AGCTGGTGTG	240
CAAAGTGATG	CCTTTTCATT	GATTACCTTA	CAAAATCCTG	TTGTATTTTC	AGATGGGAAA	300
GAGGTATCTG	TTTTGTGGC	ACTAGCAGCA	ACAAGTTCAA	AAATTCACAC	AAGTGTAGCC	360
ATTCCACAAA	TTATTGCCCT	GTTTGAATTA	GAAGATTCTA	TTGCACGTTT	ACAGGCTTGC	420
CAGACTAAAG	AAGATGTCTT	GGCTATGATT	GAAGAATCTA	AGGATAGCCC	TTATCTCGAA	480
GGATTGGATT	TGGAAAGTTA	G				501

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

AACATGAGGG	CAAAAGAAGT	ACAAGACTGG	TTTCCTGAGG	CTCGGATTTT	AGACCAACCA	60
GTAGAGAAAG	AGGGCTATCT	CACGCTCCCT	TTAGCTTCTC	AGCAGTGGAT	TTTGCTGGAG	120
GAAGCTGGGC	TCAGCGAGCG	TGAAAAGCAG	TTGGTTGCCC	TTTGACCCA	GCAGGAGCAG	180
GCTCGTTCGC	TAAACCCTTG	GTATTCCTAT	CTGGTTGAGG	GCAAGGGACA	GGCACCACAA	240
GTTTTTAAAA	AGATTTCAGT	GGTTTATTGC	CATCTTTCTT	ATTTTCAGCA	GGAAAATCTG	300
GCTTCTTGGC	TAGATATGAT	GCGGACTCTT	TTTCCGAATT	GTCAGACAGT	GCTACAGGTC	360
GGAGCTCAGG	ATTATGTTTT	CGTGCTTCAA	CAAGACAAAT	ACACTTCTGT	AAGAGATATT	420
TTAAGTGATA	CGATTGAAGC	GGTTGAGTAT	GACFTTGGAC	TTTCGTCTTT	TATCATGTTG	480
GGTCAGGTTT	GGTCTCAGAC	GGGACATCAA	GCCCTATCAG	ACTTAATCAA	AGCTGAGCGG	540

GATTTGTTCA	AGACATGGTG	GCGTCAGGGT	CACCAAGGTG	TTCATACTTT	TTCTCAGCTC	600
TATCTTTGGA	GTATGGGAGA	AAGACTCGTG	GACTTGAAGC	CAATCAAGGA	ATGTCTACAC	660
CAGATGATTT	TGGATCAAGA	TCAGATTCAG	GAAATCATTC	TCTCTCTTTG	GGAAAATAGT	720
GCTGTTCTCA	CTAAACAGC	CCAGCAACTC	TATCTGCACC	GCAATTCTCT	CCAATACAAG	780
ATTGATAAAT	GGGAAGAGTT	GACAGGGCTT	CAGTTGAAAG	AGTTGACCGA	CCTGACCTTG	840
TGTTATCAAT	TGATTTTAGG	TTCTTTGTCA	ACTATAGTTG	GTTTGTA		888

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

AAAAAGAGGG	CATTTATGAC	CTATGAATAC	AAGAGTCACA	TTTATTTGGC	AGAGACAGCT	60
TTAAATGTAA	AGGATTTGGC	CAGTCAAACA	GCCTTTTATC	AGCAAGTTAT	TGGTTTAGAA	120
ATCTTATCTC	AAACTGAGAC	AGAGTCCATT	CTAGGCCTTG	GTGGAAAAGT	CTTGGTACAG	180
CTGATTCAAG	CACAAGAGAG	CGGAGAAAGT	AGGGAATATT	ATGGTCTTTA	CCATTTGGCC	240
ATTCTCTTGC	CCACACGCAA	GGCTTTAGCT	GATGTCTTGA	AACACCTGAC	AGATTTACAA	300
ATTCCTCTTG	TCGGCGGTGC	AGACCATGGT	TACAGTGAAG	CTATTTACTT	GGAAGATTTG	360
GAGGGAAATG	GCATTGAACT	CTATCGAGAT	AAGCCATTTT	CCACATGGTG	A	411

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GGGCGGGGGC	GCCGGACAAC	ATAAGCACGC	CATCCTCTAG	TCCTGTACTC	CTCCCCACCT	60
CCCCCGTCCC	CACTCTGGCG	CGAGGGGGCG	GACCCGCCGC	ACCCCCCAGC	GCAGCCGGCC	120
GCAGCCTCCC	CAGATCCGCG	GCAACCAAAC	GGNGCAGCNG	GCCACCACAC	ACGCACCCCC	180
CCCCGCCCCG	GCCNCGCCC	ACCCGCCACA	ACCCAGAGCG	CGCCACGCAG	CCCAGCACAG	240
ACAGCAAGGC	GACGAGCCAC	CCCCGCCCCG	CACGGGACCC	CCGGGCCCCC	GCCCCGCGAC	300
CCCNCGCCCC	CCACAGGGAG	AGAAAAACCA	GCCACCCCGA	CCCACCAACG	CACCACCGNG	360
GTCCAGCCTC	ACCAANGANA	TTCCAACNAA	GTCAATAA			398

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

TCGTTCCATT	TAGATAGAGA	GGAAATACAT	ATGAGAATTT	TTGCTAGTCC	TTCTAGATAT	60
ATTCAGGGGG	AAAAATGCCCTT	GTTTGAAAAT	GCCAAATCAA	TTTTGGATTT	GGGAAATTAC	120
CCTATTCTAT	TATGCGATCA	GTTGGTTTAT	GATATTGTTG	GAAAAACGATT	TGAAGATTAC	180
CTACATAGGT	ATGGTTTCCA	TATTGTTCTG	GCGCTATTTA	ATGGTGAAGC	TTCTGACAAT	240
GAAATCAATC	GAGTTGTTGC	CTTGGCTGAG	AAAGAAAATT	GTGATAGTAT	TATCGGTCTT	300
GGTGGGGGAA	AGACGATTGA	TAGCGCAAAA	GCTATTGCAG	ATTTGATTGA	AAAGCCTGTT	360
ATTATTGCTC	CAACAATTGC	ATCGACCGAC	GCACCTGTAT	CTGCTTTATC	TGTTATTTAT	420
ACAGATGAAG	GTGCATTTGA	TCATTATCTA	TTTTATTCTA	AAAATCCAGA	TTTAGTTTTG	480
GTTGATACAA	AAGTTATTTT	ACAAGCCCCC	AAGCGTTTAT	TAGCGTCTGG	TATTGCAGAT	540
GGTTTAGCAA	CTTGGGTTGA	GGCGCGTGCG	GTTATGCAGG	CAAATGGAAA	AACTATGTTG	600
GGACAACAGC	AAACATTGGC	TGGAGTTGCA	ATTGCGAAGA	AATGTGAAGA	AACGCTGTTT	660
GCAGATGGTT	TACAGGCTAT	GGCAGCTTGT	GAAGCTAAAG	TGGTGACACC	AGCATTAGAA	720
AATATTGTTG	AAGCTAATAC	TTTATTGAGT	GGTCTAGGTT	TTGAAAGTGG	AGGATTAGCT	780
GCGGCGCATG	CAATTCATAA	TGGTTTTACT	GCATTGACAG	GTGACATTCA	TCATTTAACA	840
CATGGTGAAA	AAGTAGCTTA	TGGAACTTTA	GTACAACTAT	TATTGGAAAA	TAGACCTAAA	900
GAAGAACTTG	ATAAGTATAT	TGAGTTTTAC	AAAAAAATTG	GTATGCCAAC	AACTCTAAAA	960
GAAATGCATT	TGGATCAAGT	TGGATATGAT	GATTTAATAA	AAGTTGGTAA	ACAAGCAACT	1020
ATGGAGGGTG	AGACAATTCA	TCAGATGCCG	TTTAAGATTT	CGCCTTCAGA	TGTTGCTCAA	1080
GCTATTATCG	CTGTAGATGC	CTATGTAAAT	TCAAAATAA			1119

(2) INFORMATION FOR SEQ ID NO:504:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

ATCACACATT TAGGAGGAAA TTTTATGAAG AAAAAAATAC TTATCATTTT CATCTTGTAT	60
CTAATCATGT CCATCTTTCT TTATCCGCTT AGGGAAAGTA TTTGGTATCA GCTATTTTAT	120
ACCATAGCCT ATGTGATTGC AGTTATGATC TATTTTGCTT TAACTAAAAA GAAAGGAGCA	180
AAGAAATGA	189

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GGCTGGACCN CGGTGGTGCG TTGGTGGGTC GGGGTGGCTT GGTTTTCTCT CCCTGTGGGG	60
GGCNGGGGGT CGCGGGGCGG GGGCCCGGGG GTCCCCTGCG GGGCGGGGGT GGCTCGTCGC	120
CTTGCTGTCT GTGCTGGGCT GCGTGGCGCG CTCTGGGTTG TGGCGGGTGG GCGNGGGCCG	180
GGGCGGGGGG GGGTGCGTGT GTGGTGGCCN GCTGCNCCGT TTGGTTGCCG CGGATCTGGG	240
GAGGCTGCGG CCGGCTGCGC TGGGGGGTGC GGCGGGTCGC GCCCCTCGCG CCAGAGTGGG	300
GACGGGGGAG GTGGGGAGGA GTACAGGACT AGAGGATGGC GTGCTTATGT TGTCCGGCGC	360
CCCCGCCC	368

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1092 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1092
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GATTGTAATT	TTCTTACGGG	CATGATTCTC	TCCTTAACAG	TACATACCTA	TTTTATCATT	60
TTTTCGGCAG	AGAATTATTA	CAGAAAGGTT	ACAAAAAGAA	TAAAGTCCCT	TTTCATTTTC	120
AAAGCATGGC	TGATTTTGGA	GAAATGTGGT	ATAATTTTTC	TTATGGAAAA	GATTGTCATT	180
ACAGCAACTG	CTGAAAAGTAT	TGAACAAGTT	GAACAACTAC	TCGAAGCTGG	CGTAGACCGT	240
ATCTATGTCG	GTGAGAAAAG	TTTTGGCCTT	CGTCTGCCAA	CGACCTTTAG	TTATGACCAA	300
TTACGTGAAA	TCGCTAAGTT	GGTTCATGAT	GCTGGTAAGG	AATTGATCGT	TGCGGTCAAT	360
GCTCTCATGC	ACCAAGATAT	GATGGACCGT	ATCAAGCCTT	TCTTAGACTT	CTTGGAAGAA	420
ATCAAGACAG	ACTATATTAC	GATTGGGGAT	GCAGGCGTCT	TTTACGTAGT	TAACCGCGAT	480
GGTTATTTCAT	TTAAGACCAT	CTACGATGCT	TCAACCATGG	TAACTAGCAG	TCGTCAGATT	540
AACTTCTGGG	GACAAAAGGC	TGGCGCATCT	GAGGCTGTTT	TGGCGCGTGA	AATTCCATCA	600
GCTGAACTTT	TCAAAATGCC	AGAAATTTTG	GAAATTCCTG	CTGAAGTTTT	GGTTTACGGT	660
GCTAGTGTCA	TCCATCATTC	TAAACGTCCG	CTCTTGCAAA	ACTACTATAA	CTTTACACAT	720
ATCGATGATG	AAAAGACGCA	TAAACGTGAC	CTCTTCTTGG	CTGAGCCAAG	TGATCCAGAG	780
AGCCACTATT	CCATTTTGTG	AGATAATCAT	GGGACCCATA	TCTTTGCCAA	CAATGACCTT	840
GATTTGATGA	TCAAATTAAC	AGAATTGGTG	GAGCATGGCT	TTACTCGCTG	GAAACTAGAA	900
GGGCTCTACA	CTCCTGGTCA	GAACTTTGTT	GAGATTGCAA	AACTCTTTAT	CCAAGCGCGT	960
AACTTGATTG	AAGAGGGCAA	CTTTAGCCAT	GATCAAGTCT	TCTTGCTGGA	TGAAGAAGTT	1020
CGTAAACTTC	ACCCTAAAAA	CCGTTTCCTT	GATACAGGAT	TTTATGACTA	CGATCCTGAC	1080
ATGGTTAGAT	AA					1092

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

TTCTGTTTTT	TTTATTATA	CTCAATGAAA	ATCAAAGAGC	AACTAGGAA	GCTAGCCGCG	60
GGTTGCTCAA	AGCACTGCTT	TGAGGTTGTA	GATAGAACTG	ACGAAGTCAG	CTCAAAACAT	120
GTTTTTGAGG	TTGTAGATGA	AACTGACGAA	GTCAGCTCAA	AGCACTGCTT	TGAGGTTGTA	180
GATGAAACTG	ACGAAGTCAG	TAACCATACA	TACGGTAGGG	CGACGCTGAC	GTGGTTTGAA	240
GAGATTTTCG	AAGAGTATTA	A				261

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

AAGCTAAATT	TTATGAAGGC	TATATTCTTT	ATTATTCTCT	TCGCTTTTCA	AACCTATCTT	60
ATTTATCTAT	CCATAAGTAT	CTCCGATAAA	AAACAAAAGA	CTATTGAATT	AACATCATTG	120
AATTGTTTTG	TCATATTATT	TCTAATCTAT	GATAAAATTAA	TTTTTCTCTT	TATTGCTTAT	180
GTTTTTTTGA	TAATTTTAT	ATTAAACTTG	TTCCGTA	ACT GA		222

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1032 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1032
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

ATAAAAAATT	TAGAAAATTT	AAGAATAGAA	AAGAGAACAA	ATCTTATGGC	AAAAGATATT	60
CGTGTCTTAC	TTTACTACCT	TTTACTCCA	ATTGAAAATG	CAGAGCAATT	TGCTGCAGAC	120
CACTTGGCTT	TCTGTAAATC	AATCGGCCTT	AAAGGCCGTA	TCCTAGTCGC	TGACGAGGGA	180
ATTAACGGAA	CAGTTTCAGG	TGACTATGAA	ACAACTCAA	AATACATGGA	CTACGTTTAC	240
AGCCTTCCAG	GAATGGAAGA	TCTCTGGTTC	AAGATTGACG	AAGAAAGTGA	ACAAGCCTTC	300
AAGAAGATGT	TTGTTTCGCTA	CAAGAAAGAA	ATTGTCCACC	TTGGTTTGGA	AGACAACGAC	360
TTTGACAATG	ACATCAACCC	ACTTGAAACA	ACAGGTGCTT	ACTTGTCTCC	AAAAGAGTTC	420
AAAGAAGCGC	TTCTTGATAA	AGATACCGTT	GTCCTTGACA	CACGTAACGA	TTATGAGTAC	480
GACCTAGAAC	ATTTCCGTGG	GGCTATTCGC	CCAGATATTC	GCAACTTCCG	TGAGTTACCA	540
CAATGGGTCC	GTGACAACAA	AGAAAAATTC	ATGGACAAGC	GTGTCGTGGT	TTACTGTACA	600
GGTGGTGTTT	GCTGTGAGAA	ATTCTCAGGC	TGGATGGTTC	GTGAAGGTTA	CAAAGATGTT	660
GGCCAATTGC	ACGGAGGAAT	CGCAACTTAC	GGTAAAGACC	CAGAAGTTCA	AGGTGAGCTT	720
TGGGATGGAA	AAATGTACGT	ATTTGACGAG	CGTATCGCCG	TTGATGTCAA	CCATGTCAAC	780
CCAACCATCG	TAGGGAAAGA	CTGGTTTGAT	GGAACACCAT	GTGAACGTTA	TGTCAACTGT	840
GGAAATCCCT	TCTGTAACCG	TCGTATCTTG	ACATCAGAAG	AAAATGAAGA	CAAGTACCTT	900
CGTGGATGCT	CACACGAGTG	CCGTGTTTAC	CCACGTAACC	GCTATGTTTC	AAAAAATGAA	960
TTGACACAAG	CTGAAGTGAT	TGAGCGCCTA	GCCGCTATCG	GTGAAAGCTT	GGATCAAGCA	1020
GCTACTGTAT	AA					1032

(2) INFORMATION FOR SEQ ID NO:510:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...984
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

TTCCATTTTT	ATTACGGGGG	CTTTCCTTAT	TATTTGACAA	ACCCTATTGT	TACTTTCTTA	60
AATAAAGTCT	GTAAACTCAA	TCGTTTGCTT	GGTATTTTAA	TTACCTTGTTG	TACTTTGGTC	120
TGGGGAATGG	TCATAGGTGT	TGTCTATCTC	TTACCTATTT	TGATTAATCA	GTTATCTAGT	180
TTGATTATAT	CTAGTCAAAC	TATTTATAGT	CGAGTACAAG	ACTTAATCAT	AGACTTATCT	240

AATTATCCTG	CGCTCCAGAA	TTTGGATGTA	GAAGCTACAA	TTCAGCAGTT	AAACTTATCC	300
TATGTTGATA	TTCTTCAAAA	TATCCTAAAT	AGCGTATCAA	ATAGTGTGGG	GAGCGTCTTG	360
TCAGCTCTTA	TCAGTACTGT	TTTGATTTTG	ATTATGACTC	CAGTTTTTTT	GGTTTATTTT	420
TTATTAGATG	GACATAAAAT	CTTGCCCATG	CTTGAAAGAA	CGATTCTAAA	GAGGGATCGC	480
TTGCATATTG	CAGGCTTATT	AAAGAATTTA	AATGCGACGA	TTGCTCGCTA	TATTAGTGGA	540
GTTTCGATTG	ACGCAATCAT	TATAGGTTGT	TTAGCTTATA	TTGGCTATAG	TATTATTGGT	600
TTAAAAATATG	CTTTAGTTTT	TGCCATTTTT	TCTGGTGTAG	CCAATTTAAT	TCCTTATGTG	660
GGGCCAAGTA	TTGGTTTGAT	TCCTATGATC	ATCGCAAATA	TATTCACTGA	TCCCCATAGA	720
CTGCTGATTG	CAGTGATTTA	TATGCTTGTT	GTTTCAGCAGG	TAGATGGCAA	TATCTTATAT	780
CCTCGAATCG	TAGGAAGTGT	TATGAAGGTT	CATCCAATCA	CGATTTTAGT	TTTACTTTTG	840
TTGTCAAGCA	ATATCTATGG	TGTAGTTGGA	ATGATTGTCG	CAGTGCCAAC	CTATTCTATC	900
TTGAAAGAAA	TTTCTAAGTT	CTTATCCCGT	TTGTATGAAA	ATCATAAAAT	AATGAAAGAA	960
CGAGAAAGAG	AATTAGCTAA	GTAA				984

(2) INFORMATION FOR SEQ ID NO:511:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...348
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

AAGTCATTTT	ATGGCTTATC	TACAAATTGAT	TCAGTTTATT	CTTATGCAAT	GCAGCACTTG	60
ACTAGCCAAA	ATTATCCGGA	CATTATTTTT	GTTTCAGGAG	ATGAAAAGGT	TCAGGGCTTG	120
ATTCGTGCGT	GCTATGAGAA	AGGAATTCTT	ATTCCAGATG	ATATTTCTAT	CATTGGATTT	180
AATAATATTC	CTATTTCTCA	GTATTATACT	CCAGCTTTGT	CTACAATTGC	TCCCAATTAT	240
GTTAAATTGG	CTAAAGAAAT	GATAGAGGGT	GTTTTAGCGA	TTATTAAAGG	GGAAAGTGTC	300
ACATCTGTTG	AAGTTTCTCC	TAAATTTGTT	AGGAGACAGA	TTTTCTAG		348

(2) INFORMATION FOR SEQ ID NO:512:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

ACTAAATTTT ATAGGAGGAA GACAATGGAT TGGTACGATT ATATGATACA GGCATCCAAA	60
CAATCACAAT TCAACGCAAG CCATTGGTTT CGCTATTTGC GAAAAGTTAT TTTTGAAGAC	120
TATTCTTATT TAACAAACCA AGATGTAGAA AAGTTGCTAG ACTCCAAAGA ACTAACCCGT	180
TTTCAAAAAA TTAGCTTGAA GTATGCCTTT CAAGAGCATA CTCCAACCTCA TAAATATGTG	240
ATTCATTAA ATAAACCTGC TAAGTTAACC AATGTTCAAA AATTGATGGA GAAATACAAA	300
CATGGATAA	309

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 690 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

AAGCATTTTC TATTTCACTC GTCAAAAGAG GAGGTTTATA GAATGAATGA AATAATTACA	60
TTAAAAAATA TTGAGTTGAA ATTAAAAAAA ACATGTGTTT TTCAAAACCT TAATTTTAGT	120
TGTAAACAGG GGGAAATTAT AGGAATTACT GGTGCGAATG GCTCAGGGAA AAGTGTATTG	180
TTTAAATTAA TAGCTGGTTT ATATAGTCCG TCTTATGGAG AAGTGTTAAT CAATGGGGAA	240
AATATTGTTC CTGAGAGAAA AATTCCAGCT AATTTGGGAG CTTTGATTGA AGAACCTGGT	300
TTTATAAATT ATTATAGTGG CTTTAAGAAT TTACAATATT TGGCAAGCAT ACGAGGAGTA	360
GTTGGTAATC AGGAAATCAA TGATACACTG AAAATAGTTG GTCTATATGA GCAAAAAGAC	420
CAGAAAGTTA AAACCTATTG GCTAGGTATG AGGAAAAAGC TAGGGATTGC TCAAGCAATT	480
ATGGAGAATC CCTCTATTCT TTTACTAGAT GAACCTATGA ATGCCTTGGA TAAATCAAGT	540
GTAGAAAATA TGAGAACATT GTTTAGAAAG CTCTCTAGTG AAAAAGGGAC AACAAATTTT	600
ATTGCTAGTC ATAGTGAAGA GGATATTCGT ATCTTATGTG ATAAAGTATA TGCAATAGAA	660
GATAAAGTAT GTACACTGTG TTCAGATTGA	690

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

ATTATTCCTTT	ATACTCGTAA	GCAAGAAGTC	CATAGTGTCC	TAGCCAGTAA	GAAGTCGGTG	60
AAGCTTTTTTT	ACAGTATGTT	ACTCTTAATT	AATGTGTTAG	GAGCTGTTCT	TGTTTTGTCA	120
GATAACTTGT	TCATCAAAAA	TACGCTGCAG	CAAGAATTAG	TTGACTTTTTT	ATTGCCATCC	180
TTCTTTTTTCC	TATTTGGGCT	AGATTTGCTG	ATTTTTTTTAC	CCTTGAAAAA	ATACGTGCGC	240
GATTTTCTTG	CTATGCTGGA	CAGAAAAAAG	ACAGTGTGTTG	TGACTATTTT	AGCAACACTT	300
CTTTTCTTAA	GAAATCCAAT	GACCATTTGTC	TCACTTCTGA	TTTATATTGG	ACTGGGCTTG	360
TTTTTTGCAG	CCTATCTTGT	CCCAAATTCG	GTTAAGAAGG	AAGTTTCCTT	TTATGGTCAT	420
ATTTTCCGAG	ATCTTGTATT	GGTCATTGTT	ACGCTCATTT	TCTTTTAG		468

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GTCATTCTTT	ACTACAAATA	TCTAGGCTTT	TCTTTAGAGA	AAATAGCAGA	GCTGTTAAAG	60
GAAGAAAGGA	CAGATTTATT	GCCCCATTTA	ACTAGGCAGT	TGGACTATCT	AACTCGCGAA	120
AGGCAACATC	TGGATACCTT	GATTTCCACC	TTGCAAAAAA	CTATTCAAGA	ACAAAAAGGA	180
GAAAGAAAAA	TGACCATTTGA	GGAAAAATTC	ACGGGATTTA	GCTATCAAGA	CAATCAAAAA	240
TATCACCAAG	AAGCGGTAGA	GAAATATGGT	CAAGAAAGTCA	TGGGACAAGC	GCTCGAACGC	300
CAAAAAGGTC	ACGAAGACGA	GGCTACGGCC	GCCTTTAACC	AAGTCTTTCA	AACTTTGGCA	360

CAAAATCTTC	AAGTTGGTTT	ACCTGCAACA	GCAACCGAAA	ACCAAGAGCA	AGCAGCCAAG	420
CTCTTGCAAG	CTATTCGCAC	TTATGGATTT	GACTGCTCTA	TTGAGGTATT	CGGTCATATC	480
GGTAAAGGTT	ACGTCTACAA	CCCAAATTTT	AAGGAAAACA	TTGACAAGTT	TGGTTCTGGA	540
ACAGCCCAGT	ACACGTCAGA	TGCCATTGCC	GGCTTACGTT	CAGACAAATG	CAGAATAAAT	600
AGACTAGGAA	TTTCCTAG					618

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

CTTTATCTTT	ATACCTTTCT	AAAAC TGTTT	GAGCAAATTT	TTCATAAAAA	TGAATCATT	60
TCCTATCAAC	CCATCCATGA	TATTTTCTTG	CTAAATATAA	TGGAGTCTCA	TAGTGTGAAA	120
GAGTTACAAG	TGGCTCTATC	CCGTGAGCAT	GTAGTTCATC	AAACAATTCA	TCATAATATT	180
TCAAACCAGC	TTCGTTAG					198

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

CTGAAGCTTT	ATCGGGTTCA	AAACTCGGCA	ATGAACTCTA	TCTGGGTTCT	AACTTCCAAG	60
AAGAAGTTGG	TCTGCGTGGC	GCTCATACCT	CTACAACCAA	GTTTGACCCA	GAAGTCTTCC	120
TCGCAGTTGC	TTGCTCACCA	GCAGGTGATG	TCTACGGTGG	TCAAGGCAAG	ATTGGAGATG	180
GAACCTTGA						189

(2) INFORMATION FOR SEQ ID NO:518:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 948 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...948
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GATTACATTT	ACTTGCATAC	GACGAAATGT	AAACATTTCT	GTTTAAAATT	AAGGATAAAA	60
TCAATGAAAA	AAGCAATGGT	AATTATCAAC	CCTACTTCTG	GTGGCGAGAA	GGCTTTGGAT	120
TACAAAGAAA	AGCTGGAGAA	TAAAGCAAAA	GAATACTTTG	AATATGTTGA	AACCAAAAATT	180
ACCGAAAAAG	CGCTGGATGC	AACACATTTT	GCTGAAGAAG	CTTCTCGTGA	GCAGTATGAT	240
GCAGTGGTTG	TGTTTGGTGG	AGATGGAAC	GTCAATGAAG	TCATTTCAGG	TATTGATGAG	300
AGAGACTACA	TTCCTAAGTT	AGGGATTATC	CCAGGCGGTA	CGGGTAACCT	CATTACAAAA	360
CTTTTGAAAA	TCAATCAAGA	CATCGATGGC	GCAATTGACG	AACTGGATTT	TGATTTAACC	420
AATAAGATTG	ATATCGGTAA	AGCAAATGAC	AACTATTTTG	GTTATATCTT	TAGTATCGGT	480
TCTCTGCCTG	AGGCGATTCA	CAATGTTGAA	ATAGAGGACA	AAACAAAATT	CGGTATTTTA	540
ACCTATGCTG	TAAATACCAT	GAAGTCTGTC	ATGACAGATC	AGGTCTTTAA	CATTAAGGTT	600
GAGACAGAAA	ATGGAAATTA	TGTTGGTGAA	GCTAGCCATG	TTTTGGTCCT	TTTGACAAAT	660
TACTTCGCTG	ATAAGAAAAT	CTTTGAAGAA	AACAAGGACG	GCTATGCCAA	CATTTTGATT	720
CTGAAAGATG	CCTCTATATT	CTCCAAATTA	TCCGTCATTC	CTGATTTATT	AAAAGGGGAT	780
GTTATCGCAA	ATGATAATAT	CGAGTATATC	AAAGCGCGTA	ATATTAAAA	CTCTTCAGAT	840
AGTGAATTGG	AGTCAGATGT	TGACGGAGAT	AAATCAGATA	ACCTACCTGT	AGAAATCAAA	900
GTCTAGCTC	AGCGAGTAGA	AGTATTTTCA	AAACCGAAAG	AGGATTAG		948

(2) INFORMATION FOR SEQ ID NO:519:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

CCTCCCTTTC	TAAAAAATAG	CAAGTTTTGG	GTCATTGATG	AAACTGATGA	AAGATTAGGA	60
CCATTCAATA	CATTTGAAGA	GGCTTATCAA	TCGTTGTTAT	TTTATTTAAA	AATGACTGAA	120
GATGAATATC	AGTCAAAC TA	TACGGCCCAG	GAAC TTGTTT	ATATTTACAA	AGAGGAGAAA	180
AAACCATGCC	GTGATGA					198

(2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1146
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

AACATGATTT	ACTTTGATAA	TTCGGCGACG	ACCAGGCCCT	ATCCAGAAGC	CCTTGAAACC	60
TATATGCAGG	TGGCTTCAAA	AATTTTAGGA	AATCCATCTA	GTCTCCATCG	TTTGGGAGAC	120
CAGGCAACAC	GAATTTTAGA	TGCTTCCCGT	CAACAGATTG	CAGATTTAAT	CGGTAAGAAA	180
AGTGATGAAA	TCTTCTTTAC	ATCTGGTGGG	ACAGAAGGGG	ATAACTGGAT	CATCAAGGGA	240
GTAGCATTTG	AAAAAGCCCC	GTTTGGCAAG	CACATCATCG	TATCAGCCAT	TGAACATCCA	300
GCAGTTAAGG	AATCAGCCCT	CTGGTTGAAA	GCTCAAGGTT	TTGAAGTGGA	TTTTGCTCCA	360
GTTGATAACA	AAGGATTTGT	GGATGTTGAG	GCGCTAGAAG	ATTTGATAAG	ACCTGATACG	420
ACCCTCGTTT	CCATCATGGC	AGTTAACAAT	GAAATTGGCT	CTGTTCAGCC	CATTGAGGCT	480
ATTTCAAAAC	TATTGGCAGA	CAAGCCAAC T	ATTTCCTTCC	ACGTTGATGC	GGTTCAGGCG	540
CTTGCCAAGA	TTCCGACTGA	AAAGTATCTG	ACAGAACGAG	TGGATTTCGC	GACTTTCTCT	600
GGTCACAAGT	TCCACGGAAT	CCGTGGTGTT	GGTTTTATCT	ATATCAAGTC	TGGCAAGAAG	660
ATTACGCCTC	TTTTAACAGG	TGGTGGTCAG	GAACGTGATT	ACCGTTCGAC	AACTGAAAAT	720
GTGGCAGGAA	TTGCAGCGAC	CGCTAAGGCT	CTCCGTTTAT	CTATGGAAAA	GCTAGATATC	780
TTTAGGAGCA	AGACTGGGCA	GATGAAGGCA	GTGATTCGTC	AAGCACTTCT	GGACTATCCG	840
GATATATTTG	TCTTTTCAGA	TGAGGAAGAC	TTCGCCCTC	ATATTCTGAC	TTTTGGAATC	900
AAGGGTGTTT	GTGGTGAGGT	CATTGTTTAC	GCCTTTGAAG	ACTATGATAT	TTTCATCTCA	960
ACGACCTCGG	CTTGTTTCGTC	CAAGGCTGGG	AAACCAGCCG	GAACCCTGAT	TGCTATGGGA	1020
GTGGACAAGG	ATAAGGCTCA	GTCAGCTGTG	CGTCTTAGTC	TAGACCTTGA	AAATGATATG	1080

AGTCAGGTCG AGCAGTTCTT GACCAAGCTA AAATTAATTT ACAATCAAAC TAGAAAAGTA	1140
AGATAG	1146

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

AAACGAAATT TTCACATCTT CACTTTTGTGTA AGTAGATATA GAGCTTCAAT CAGTACCTCT	60
ACTTGTA AAA GAATGTGTGA GATAGAAAGG ACAGGAAAAG GAATGAATGC AGATGATACA	120
GTAACCATTT ATGATGTCGC TCGTGAAGCA GGTGTTTCCA TGGCGACGGT CAGCCGTGTG	180
GTCAATGGCA ATAAAAATGT AAAAGAGAAT ACCCGTAAAA AAGTGCTAGA GGTAATTGAT	240
CGTTTGGATT ATCGTCCAAA TGCAGTTGCG CGTGGTCTTG CAAGTAAAAA GACAACCACT	300
GTCGGTGTGCG TGATTCCAAA TATTACCAAT GGTATTTTTT CGAGTTTGGC TAAGGGGATT	360
GATGATATTG CAGAAATGTA CAAGTACAAT ATTGTCCTAG CTAATAGCGA TGAAGATAAC	420
GAGAAAGAAG TTTCTGTTGT CAATACCCTC TTTTCAAAGC AGGTAGATGG CATTATCTAT	480
ATGGGTTATC ACTTGACAGA TAAAATTCGC TCAGAATTTT CGCGTTCACG TACTCCGATT	540
GTTCTCGCAG GAACTGTGCGA TGTGAGCAC CAGTTGCCAA GTGTCAATAT TGACTATAAG	600
CAAGCAACAA TTGATGCAGT GAGTTACCTT GCTAAAGAAA ATGAGCGTAT TGCTTTCGTT	660
AGCGGTCCGC TAGTGGATGA CATCAATGGT AAGGTTGCTT TAGTTGGCTA CAAGGAAACC	720
TTGAAAAAAG CAGGAATCAC TTATAGTGAG GGTGTTGGTAT TTGAATCTAA ATATAGCTAT	780
GATGATGGTT ACGCCTTAGC AGAGCGTTTG ATTTTCATCAA ATGCAACTGC AGCAGTTGTG	840
ACAGGTGATG AGTTGGCAGC AGGAGTCTTG AACGGTTTGG CTGATAAGGG TGTTCCTGTG	900
CCAGAAGATT TTGAAATTAT TACTAGTGAT GATTCACAAA TCTCACGCTT TACCCGTCCA	960
AACTTGACAA CGATTGCCCA ACCTCTTTAT GACCTTGGTG CCATTAGTAT GCGTATGTTG	1020
ACCAAGATTA TGCATAAGGA AGAGTTGGAA GAACGTGAAG TTCTCTTACC TCATGGTTTG	1080
ACAGAACGTA GCTCAACACG AAAACGTAAA TAG	1113

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

CAACGCTTTC	TATATGTGCG	AGAATATCGA	ACTTATGAAG	AAATTGCGGC	TGATTTTGGT	60
ATCCACGAAA	GCAACTTACT	CCGTCGGAGC	CAATGGGTTG	AAGTAACTCT	TGTTCAAAGT	120
GGTGTTACGA	TTTCAAAAAC	TCATCTTAGT	GCTGAGAATA	CGGTGATTGT	GGATGCAACA	180
GAGGTAAAAA	TAAATCGTCC	TAAAAAATC	AACTAG			216

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

CAGCGAAATT	TCGCCTATAA	TCTTTCAACT	TCACCAAAC	TAGAACAAGT	GAAAGCTATG	60
TTAAACCAGG	CCTTTACAGA	GAAACATTAT	GAGAATACCA	TTCTCCATAG	CGATCAAGGC	120
TGGCAATACC	AACACGATTT	TTATCACAGG	TTTTTAGAGA	GTAAGGGAAT	TCAGCCATCT	180
ATGTCACGCA	AAGGAAACAG	CCCAGACAAT	GGCATGATGG	AGTCCTTCTT	TGGCATCTTG	240
AAATCCGAAA	TGTTTTATGG	TTATGAGAA	AACTTTAGAT	CTTTAGAAAA	CCTTGAACAA	300
GCTATTGTGG	ACTACATTGA	TTACTACAAC	AACAAACGAA	TTAAGGTAAA	ACTAAAAGGA	360
CTTAGTCCTG	TGCAATACAG	AACTAAATCC	TTCGGATAA			399

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GCTATATTTT	CTGACTGTCCT	AAAAACAATG	GTGAAGCAGC	TAGTCCAGCA	GCCGCGGAAT	60
AATACAGGTT	CTAAATACCC	TTATACTATT	GATGTGACAG	GCGAGGTTGG	TGATTTGAAA	120
CAAGGTTTTT	CTGTCAACAT	TGAGGTTAAA	AGCAAAACTA	AGGCTATTCT	TGTTCCCTGTT	180
AGCAGTCTAG	TAATGGATGA	TAGTAAAAAT	TATGTCTGGA	TTGTGGATGA	ACAACAAAAG	240
GCTAAAAAAG	TTGAGGTTTC	ATTGGGAAAT	GCTGACGCAG	AAAATCAAGA	AATCACTTCT	300
GGTTTAACGA	ACGGTGCTAA	GGTCATCAGT	AATCCAACAT	CTTCCTTGGA	AGAAGGAAAA	360
GAGGTGAAGG	CTGATGAAGC	AACTAATTAG				390

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

TGGCCATTTT	TGCTATCTAC	ATGGGCCACA	AGGTTATCGC	GCTGGATCCT	GCGGCGGATT	60
GCCCGGCCCT	TCGCGTGGCG	GAAATCATTT	TGGCACCTTA	TAACGATGTG	GACGCCCTCC	120
GTCAGTTGGC	AGACCGTTGC	GATGTCCTCA	CTTATGAGTT	TGAAAATGTC	GACGCTGACG	180
GTTTGGATGC	CGTTATCAAG	GATGACAAC	CCCTCAAGAA	ACAGATTCTG	CCGCATTTTCG	240
CAAAATCGTA	TTTTAGAAAA	GGACTTTTTT	TCAAACAAGG	CTCAAGTCAC	TGTGGCACCC	300
TACAAGGTCG	TGACTTCTAG	CCTAGACTTG	GCAGATATCG	ACATGTCGAA	AAACTATGTC	360
CTCAAGACTG	CGACTGGTGG	CTACGATGGT	CATGGACAAA	AGGTTATTCT	TTCAGAAGCA	420
GACTTGGAAG	CAGCCTATGC	GCTAGCAGAC	TCAGACAGCT	GCGTCTTGGA	AGAATTTGTC	480
AACTTTGACC	TTGAGATTTT	TGTCATCGTG	TCAGGAAATG	GCAAGGAGGT	GACGTTTTTTC	540
CCAGTTCAGG	AAAATATCCA	CCGCAACAAT	ATCCTGTCTA	AGACCATCGT	ACCAGCCCCG	600
ATTTCTGAAA	GTCTAGTAGA	CAACCATAAG	ACTATGGCAG	TCGAATCGCA	GAACAAAAC	660

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...852
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

AAGGGAAATT	TTATGATCAT	AAAACGAATA	CTAAACCACA	ATGCCGTAAT	TGCGCAAAGT	60
AAAAAAGATA	TCGATATTCT	TCTTTTTTGG	AGGGGAATAG	CTTTTGGAAG	AAAAACTGGA	120
GATAAAGTAA	ATCCAATTGA	TATTGAGAAA	AGTTTTTTTC	TCAAAAATAG	AGATAATATG	180
ACCCGTTTTA	CAGAGATGTT	TATTAACGTT	CCTTTGGAGT	TGGTGTACAT	CACCGAAAAA	240
ATAATTAACC	TAGGTAAAAT	AACATTGGGT	AATAATTTTG	ATGAAATTAT	CTATATTAAT	300
TTAACGGATC	ATATTTCTTC	GAGCATAGAA	CGTTATAAAG	AAGGGATTAT	TATTTCGAAT	360
CCCCTACGCT	GGGAAATATC	GAAATATTAT	AAAGAAGAAT	TTGAACTTGG	GAAAAGGGCT	420
TTACAAATAA	TAAAAAAGA	GTTAGGTATT	GAACCTCCAA	TTGATGAAGC	TGCATTCATA	480
GCGCTACATT	TTGTTAATGC	TAATTTAGAA	AATAATTTTC	AAGAGTCGTA	TAAAATCACT	540
GAAATAATTA	TGGGAATTGA	GAAAATCATT	CAAGATTTCT	ATTGTACTGA	GTTTAACCAA	600
GATTCATTG	ATTATTATAG	ATTCATAACT	CATATAAAAT	TATTTGCCCA	TCGCTTGTT	660
GAAAAACAA	CTTATTGTGA	CGATGATGAT	GAAGACTTGT	TAGCATTAAT	GAAAAATAAA	720
TATCCTAGAG	AATATGAATG	TGGTGAACAG	GTGGCAATGT	TTATACAAAC	TGAGTACAA	780
TATTTGCTGA	CTTCTAGTGA	ATTAGTTTAT	TTGATGGCTA	ATATTCGTCG	CTTAACAAAA	840
AATTTAGATT	AA					852

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

TTTTTTTCTT	ACTGTTTTTA	TCCCTTTTAT	TGTGGTAAAA	TAAGACTATT	AAGTTTAAAG	60
AGGATCCCTA	TGAAATTACA	AAAACCAAAA	GGAACGCGAG	ATATTTTACC	TGCTGAATCT	120
GCTAAGTGGC	AGTATGTTGA	GGGCTTTGCC	CGTGAGATTT	TCAAGCGCTA	TAACTATGCA	180
GAAGTGCACA	CGCCTATTTT	TGAGCATTAC	GAGGTTATCA	GTCGCTCTGT	CGGAGATACA	240
ACGGATATCG	TAACCAAGGA	AATGTACGAT	TTTTATGACA	AGGGTGACCG	TCATATTACC	300
CTCCGTCCAG	AAGGAACTGC	GCCCGTTGTC	CGTTCCTATG	TGGAAAATAA	ACTCTTCGCC	360
CCAGAAGTGC	AAAAGCCAAG	CAAGTTCTAC	TATATGGGAC	CTATGTTCCG	TTATGAGCGT	420
CCACAGGCAG	GGCGCTTGCG	CCAATCCAC	CAGATTGGTG	TTGAGTGTTT	TGGCTCTAGC	480
AATCCAGCTA	CCGATGTGGA	AACAATCTCT	ATGGCAGCCT	ATTTTTTGAA	GGAAATCGGT	540
ATTCAAGGTG	TCAAATTGCA	CCTCAACACT	CTTGGAATC	CTGAGAGCCG	TGCAGCCTAC	600
CGCCAAGCCT	TGATTGACTA	TTTGACACCG	CTCAAGGAGA	CCTTGCTTAA	GGATAGCCAA	660
CGTCGCTTGG	AGGAAAAATCC	TCTTCGTGTC	TTGGACTCTA	AGGAAAAAGA	AGACAAGGTG	720
GCAGTAGAGA	ATGCGCCGTC	TATCTTGGAC	TTTCTTGATG	AAGAAAAGCCA	AACTCATTTT	780
GATGCTGTGC	GTCAGATGTT	GGAAAATCTT	GGAGTAGATT	ACATCATCGA	TACCAATATG	840
GTGCGTGGTC	TGGACTACTA	CAACCACACC	ATTTTCGAGT	TTATCACAGA	GATTGAGGGC	900
AATGACTTGA	CAGTCTGTGC	GGGTGGTCGC	TACGATGGTT	TGGTTGCTTA	CTTTGGAGGC	960
CCTGAACTG	CTGGATTG	TTTTGGGCTT	GGTGTAGAGC	GCCTGCTTCT	CATCCTTGAA	1020
AAACAAGGCG	TGGCCCTCCC	TATCGAAAAC	GCCCTAGATG	TCTATATCGC	AGTCTTGGGT	1080
GATGGAGCAA	ATGTCAAAGC	CCTAGAACTA	GTCCAAGCTC	TTCGCCAACA	AGGTTTCAAA	1140
GCAGAGCGTG	ATTACCTCAA	CCGTAAGCTC	AAAGCTCAGT	TCAAGTCAGC	AGATGTCTTT	1200
GCGGCTAAGA	CCCTCATCAC	CCTAGGAGAG	AGCGAAGTCG	AAAGCGGACA	AGTGACGGTC	1260
AAGAACAACC	AAACCCGAGA	AGAAGTGCAA	GTGTCACTTG	AGACAATCAG	CCAAAACTTC	1320
TCAGAAATCT	TTGAAAAACT	AGGATTTTAT	ACTCAATGA			1359

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

AATAATTCTT	ATTTGCTAGA	AAGGTGGAGA	GACATGCGCT	GGCTTTTTTCG	TTTGATAGGG	60
GCTTTCTTTT	CTTTTGTGTG	GCGTTTGTTT	TGGCGTCTGG	TTTGGATAGT	TGTGCTCTTA	120
TGTGTGCTTG	CTTTCGGACT	TCTCTGGTAT	CTGAACGGGG	ATTTTCAAGG	AGCGCTAAAG	180

CAAGCAGAAC	GGTCAGTAAA	AATTGGTCAA	CAAAGTATTG	ACCAATGGGA	GAAAAACAGGG	240
CAACTGCCTA	AGTTAAGCCA	GACAGATAGT	CACCAGCATT	CTGAAGGAAG	GTGGCCACAG	300
GCCTCTGCTC	GTATTTACCT	GGATCCGCAG	ATGGATTAC	GCTTTCAAGA	GGCTTATTTA	360
GAAGCAATCC	AGAACTGGAA	TCAAACCTGGT	GCTTTTAACT	TTGAACTCGT	GACTGAGTCT	420
AGTAAGGCGG	ATATTACCGC	TACGGAGATG	AACGACGGAG	GCACTCCTGT	GGCAGGAGAG	480
GCGGAAAGTC	AAACTAATCT	CTTAACAGGG	CAATTCTTGT	CCGTAACGGT	GCGGTGGAAT	540
CATTATTATT	TGTCCAATCC	ATACTATGGC	TACTCCTATG	AACGCCTTGT	CCATACGGCA	600
GAACATGAGT	TAGGTCATGC	GATTGGCTTG	GACCATACAG	ATGAGAAGTC	TGTCATGCAA	660
CCAGCAGGTT	CCTTTTATGG	TATCCAGGAA	GAGGATGTTG	CAAACCTCCG	AAAAATATAT	720
GAGACTAGTG	AGTAG					735

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

CTGAGATTTT	TTCATAGCAT	AAACTTCTTG	GAACTGGTAG	TAGTCACCAG	AGTAACGCGT	60
CAGCTGTTGA	TTTTCCACAT	GATAGACAAT	ATTGATAACG	TCATTGAGGA	ATGGAATATC	120
GTGCGAAATG	AGAACAAAGG	CATTCTCATA	GTTTTGGAGA	TAGCGCTTGA	GCCAATCAAT	180
ATGCTCAGCA	TCCAAGTAGT	TGGTCGGCTC	GTCCAACAGC	AAAAATATCAG	GCTTTTCAAG	240
GAGAAGTTTT	GCCAAAAGCA	CCTTGGTTCT	TTGCCACCT	GA		282

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

ACAGAACTCTT	ATAATAAACG	AGTTATAAAA	GCAAACACGA	TGACAGGATT	TATTCATTTT	60
AAAGATTTGG	ATGGTGCCAG	TGTTGGGAAT	AGTCATCCTT	CAACTTCACC	AGGCGGAACT	120
CATTATTTTA	AGACCAAGTC	TGCTATTAAA	ACTGAACCTC	TAGCTAGCGG	AACTGTGATT	180
GATTACTATT	ATCCTGGGGA	GAAGGTTTCAT	TATGATCAGA	TACTTGAAAA	AGACGGCTAT	240
AAGTGGTTGA	GTTATACTGC	CTATAATGGA	AGCTATCGTT	ATGTTCAATT	GGAGGCTGTG	300
AATAAAAATC	CTCTAGGTAA	TTCTGTTCTT	TCTTCAACAG	GTGGAACCTCA	TTATTTTAAAG	360
ACCAAGTCTG	CTATCAAAAC	TGAACCCCTA	GTTAGTGCAA	CTGTGATTGA	TTACTATTAT	420
CCTGGAGAGA	AGGTTTCATTA	TGATCAAATT	CTCGAAAAAG	ACGGCTACAA	GTGGTTGAGT	480
TATACGGCTT	ATAACGGAAG	TCGTCGCTAT	ATACAGCTAG	AGGGAGTGAC	TTCTTCACAA	540
AATTATCAGA	ATCAATCAGG	AAATATCTCT	AGCTATGGAT	CCAATAATAG	TTCAACTGTC	600
GGTTGGAAGA	AAATAAATGG	TAGTTGGTAT	CATTTCAAAT	CAAATGGTTC	TAAATCAACA	660
GGATGGCTGA	AAGACGGTTC	TAGCTGGTAT	TATTTGAAAT	TATCTGGTGA	AATGCAGACA	720
GGATGGTTAA	AGGAGAATGG	CTCGTGGTAT	TATCTGGGTA	GTTCAGGGGC	TATGCAAACA	780
GGGTCTACCA	GTATCGTCAG	AAGAGCATAA				810

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

ATGAACACTT	ATGAAGGTAA	TTTAGTAGCA	AACAATATTA	AAATAGGTAT	TGTTGTAGCG	60
AGATTTAATG	AATTTATAAC	TTCAAAATTA	TTATCTGGAG	CACTAGATAA	TCTCAAAAGA	120
GAGAATGTAA	ACGAGAAAGA	TATCGAGGTA	GCCTGGGTTC	CAGGAGCTTT	TGAAATACCA	180
CTGATTGCAT	CAAAAATGGC	AAAAAGTAAA	AAATATGATG	CAATTATCTG	CTTGGGAGCT	240
GTCATTAGAG	GGAATACAAG	TCATTATGAT	TATGTATGTA	GCGAGGTATC	TAAGGGAATC	300
GCCCAAATCA	GTTTAAATAG	CGAAATTCCT	GTTATGTTTG	GTGTGCTAAC	GACAGATACA	360
ATTGAACAAG	CCATAGAACG	AGCTGGTACC	AAAGCAGGAA	ATAAGGGTTC	TGAGTGTGCA	420
CAAGGAGCTA	TTGAAATGGT	CAACCTAATT	CGTACATTAG	ACGCATAG		468

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GTATCAACTT	ATCCTTTTTT	AAAAGAAAAA	TCCGAAGATA	TTTGGCCTTC	TTCGGATTTT	60
TTCTATTTTC	CACAGTTTCA	TGTAATTCAT	CTAGATGATG	AACAAATTAG	TTGTTCTTTC	120
CTCTACGGAA	TAGATAAAAT	GCCCCAAGTA	GCAAGAACCC	TAGACTTGCC	AAGATTGACT	180
GACCTTCTCC	TGTCTGAGGG	AGATTCTTTT	GATCCGAATG	GTTCTTTTCC	TCTTCAGATT	240
TTTCCTTTTC	TTTGAATTC	TGTACTTGTG	GCTGAGCTGC	TTGCTCTAGC	TTTTTAA	297

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 963 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

ATGGAACTT	ACTACAAAGC	CATTAACTGG	AATGCCATCG	AAGATGTCAT	CGACAAATCA	60
ACTTGGGAAA	AACTGACGGA	GCAATTTTGG	CTCGATACAC	GTATTCCCTT	ATCAAACGAC	120
TTGGATGACT	GGAGAAAGCT	ATCTAACAAA	GAGAAAGACT	TGGTCGGAAA	AGTTTTTGGT	180
GGTTTAACCC	TTCTTGACAC	TATGCAATCT	GAAACTGGGG	TTCAAGCCCT	TCGCGCAGAC	240
ATCCGTACAC	CACATGAGGA	AGCTGTTTTT	AATAACATCC	AATTTATGGA	ATCTGTCCAC	300
GCTAAATCTT	ACTCATCAAT	CTTTTCTACC	TTGAATACTA	AGGCTGAGAT	TGAAGAAATT	360
TTCGAATGGA	CCAATACCAA	TCCTTACCTA	CAAAAGAAGG	CTGAGATTGT	CAACGAAATC	420
TACCTAAACG	GCAGCCCACT	TGAAAAGAAA	GTTGCCAGCG	TCTTCCTCGA	AACCTTCCTC	480
TTCTACTCTG	GTTTCTTCAC	TCCCCTCTAC	TATCTCGGTA	ACAACAAACT	AGCCAACGTT	540

GCAGAAATCA	TTAAATTGAT	TATTCGTGAC	GAGTCTGTTC	ACGGAACCTA	CATTGGTTAC	600
AAATTCCAAC	TTGGTTTCAA	TGAATTGCCT	GAAGAAGAGC	AAGAAAAACT	CAAAGAATGG	660
ATGTACGACC	TACTCTATAC	TCTTTATGAA	AATGAAGAAG	GCTACACAGA	GAGTCTTTAT	720
GACGGTGTG	GTTGGACTGA	AGAGGTAA	ACCTTCCTTC	GCTACAATGC	CAATAAAGCT	780
CTCATGAACA	TGGGACAAGA	TCCACTTTTC	CCAGATTGAG	CTGAAGATGT	CAACCCAATC	840
GTTATGAACG	GTATTTCAAC	AGGAACCTCC	AACCATGACT	TCTTCTCTCA	AGTCGGAAAT	900
GGTTACCTTC	TTGGCGAAGT	TGAAGCCATG	CAAGACGATG	ACTATAACTA	CGGTTTAGAC	960
TAA						963

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

TGGAGGACTT	ACGTGCTTAA	GATTCGTTAT	CATAAACAGT	TTAAAAAAGA	TTTTAAGTTG	60
GCTATGAAGC	GTGGTTTGAA	GGCAGAAATTA	TTAGAAGAAG	TTTTGAATTT	TCTGGTTCAA	120
GAAAAAGAAC	ATCCTGCCAG	ATATCGTGAT	CATTTCATTGA	CGGCATCCAA	GCATTTTCAA	180
GGAGTTCGTG	AATGCCATAC	CCAGCCAGAT	TGGCTTTTGG	TTTATAAAGT	AGATAAGTCG	240
GAATTGATTT	TAAATTTGCT	GAGGACAGGC	AGTCACAGTG	ATTTATTTTA	A	291

(2) INFORMATION FOR SEQ ID NO:535:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

GTTTTTCTTC	TAACCTATCC	TTTCTATTTT	ATTCGGTTAT	TTGAACGGCT	CTTGTATCGT	60
TTGCAGACTT	CCTACTATGC	CTACTATGCA	AATTTTGAAA	GTAAACTGCC	TTATTTTACC	120
TACATTTTGT	CTACCTTTAC	GGTCTATGCA	ATGTGTATGT	ATCTAGCAAC	CAAGCCAAAG	180
AAATTGCAGG	CCACAGCAGT	GCTTGTCTCC	TTTATTGCAG	CTAATACTAT	TCATTTGGCA	240
ATTGGGACAC	GAAATCCCCT	TATTTTAAGT	ATTTTATTTG	CTTTTGTTTA	TTACTTTTATG	300
CGGGAGCAAA	CTGAAAAAGG	AAAATGGATT	GGGTTTAAAG	AAAAGTTAGC	GATTTTGTGA	360
GGTTCTCCTA	TTCTCATGTT	AGCGATGGGA	GTACTCAATT	ATGTACGGGA	TAATGTCCAA	420
GTTTCCCATA	CAGGTTTCTG	GGATATCTTA	CTTGACTTTA	TCTATAAACA	AGGGACTAGT	480
TTTGGTGTTT	TGGCTCGAGG	TTTTCTATTT	AACAGTAGCC	TCCCTTACCG	AGATTTCCGT	540
AATTTTACTT	TTGGTCCTGT	TCTTGATTAT	TTTGCAAGGG	GGAGTTTGGG	AGCCATTTTC	600
GGAGGAAAAG	CCTTTGAACA	TACAACCAAT	AGTGTGGAAC	TAGCTATTGA	TAGTAATAGT	660
TATGCCACCA	ATATATCCCTA	TCTTGTCTTG	AACAAGGAAT	ACTTGAAAGG	GCATGGTATC	720
GAAAGTAGTT	ATATCATGGA	GTTGTATACC	GACTATGGTA	TGATTGGAGT	CTTTCTGCTT	780
AGTTTCTTAC	TCGGCGTATT	ATATATAGCC	ATGCTGCAAG	TAGCCTATCG	CTCAAGGACA	840
ATCCTATTTG	CTTTATCCAT	ACTCATCTTG	AATAATCTAT	TCTTTATGCC	AAGAAGCAGC	900
TTTTCAGAAA	GTTTCTTCAA	TTTATTTACA	ATGCAATTCT	GGGGAATTGT	TCTTGTGATT	960
ATATTTGTAG	CAAAAATGCT	TACAAAGGAA	AACTAG			996

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAGCTTCTTC	TGGACCCACT	CTACCGCCTA	CATGTTTCAG	TAATCTTTTT	AGAAAGAGAG	60
CAAGCCATTT	CAACCGAGGA	NTACCTCGCC	CACCTCTTTC	TCCATTTTCA	TAAAAACCAA	120
GACCATATCA	CCAGTCTGCT	ATTTTCCAAA	AATGACTACT	TCCTCCGTCA	ACTCCATAAA	180
GAGCTAGAAC	ACCATGTCTA	TTCCGTGCTA	GCTGATAATT	TAAAAGAAGC	CCACCCTAAT	240
ATGCTACTTT	CTTACCTCCA	ACACTTGGTC	GTGTCCAAC	TTATCGAGAC	ATTGACCTGG	300
TGGCTCAAAA	AAGGTCAAGA	TTTCACAGGC	CAGGAAGTTG	TCCAATTTTA	TCTAGACCTT	360
CTCATTCCTA	AAAAATTGA					378

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

AATGGTTATT	ATAAAAAATG	GTCTGAAATA	GATGATGATA	CTTTTCGAAA	ATCTTTTAC	60
GTCAGCTCAG	CTTTGCCTTG	CTGTGTTTTG	AGCAAGCTAC	GGTTAGCTTC	CGAGTTTGAT	120
TTTCATTAC	TAGAAATGAA	ACTGATGAGA	GATATCAGTA	GACATTTGAG	TCAGGATATT	180
ATGGAAAATG	ATAAAAAGAG	CTCGTGA				207

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1371 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

AAAATATATT	ATGAAAGAGC	TCTCATAATG	CTTTTAAATT	TCTTATTCAT	ATTTATTTTT	60
CTATTAATTA	TCATTACATT	TATATTATTT	GAGGGAGATT	TGTTTCAACC	CGCAGTAATT	120
TTAACTACTG	CTTATTTTAT	TTCGATTGCA	AGTGCTCTAG	TTAATAGAAA	TGTTTGGGGA	180
ACAGAACTCC	ATTTCAAAAC	CTTTGGTTTG	ATATTGCTAG	GGGTTGCTAC	ATTTATTATA	240
GTTTCCTTGT	TGACAAAATT	GTCGTACAAA	CCTAAAGTGG	AGGGAATTTC	GTATAAAGAA	300
TTAAAAGAAA	TAAATCCTTC	AAAGATAATA	TATGGCATTC	TTCTGATTCT	AAATCTTGTT	360
ATGCTATTTT	TTTATATCCA	TGAAATTCAG	AAAGTGGTAC	TGTTTTCAGG	TAGAGGTTTT	420
TCTAATATTA	CAGATTTGAT	AAGTAACTAT	AGGTACCTAT	CTTATTATTC	AAATGAAGTA	480

GAAGATCGTG	TAAGTGGAAAT	GATTAATCAA	CTAGCTAAAA	TTATTCCAGC	GA	540
TTTCTTTTAT	ATATATTTAT	AAATAATTAT	TTTATAACGA	AGCAAATAAA	GAAAAATTC	600
ATTTATTTGA	TTCCAATAGC	TATATTCTTT	GTCTATGCAA	TCATTAGTGG	TGGTAGACTG	660
CCCCTTATAA	GGTTAGTTAT	TGGA	ACTCTG	TTGATATTGT	ATATATACTC	720
AGTCATAAAT	CTCAACTTAC	CAGAAGTTTT	AAAATGATTA	CTCGCTCTCT	TTTTGCATTT	780
CTTATGTTGA	TAGTTTTATT	CTTTCTTTTA	AAATTGTAT	TAGGGCGTTC	TTCTCAGGAA	840
GATTTTATCA	GTTACATCAC	TCGTTATATG	GGAGGCTCAA	TTCAACTATT	TGATTTATTT	900
GTTATAGATC	CGATACGACG	TAACAAAGAA	CTAGGTGCAG	AAACTTTTTTC	GGGAATTTAT	960
GAGATGCTTG	CAAAATTAGG	ATTTGATAAT	AATATTATAA	AAGGCTTAGA	ATGGAGAATA	1020
TCGCCTAATT	ATTATTCTTT	AGGGAATGTG	TATACTGCAA	TTAGACGCTA	TTATTCAGAC	1080
TTTGGTGTA	TTGGTATTGT	AATTTGTCAG	AGTTTTACAG	CATGGTTGTA	TACTTTAGGT	1140
TATGAAAAAA	TTAGACATCA	TTCTTTAGTT	ACAAATGGTC	AAAGATTTAG	GTTGATTCTA	1200
TTAGCAGCTT	CATTTTATCC	ATTATTTTTA	AATAGTATCG	AGGATGTGTT	TTATATTTCA	1260
ATGGTTACCA	TTGGATATGG	AATCCAAATT	GTTATCTTTT	ATCTGGTTTT	TTGGGTTCTT	1320
CTGAAAGTTC	AGGTTGACTT	TAACAAAGGT	AAATTAAGGA	TAAATAGATG	A	1371

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

TCACTTCATT	ACGATTGTGA	CTCTGGTCGT	TTAGCCTAT	TCTCTCTTGA	TTGGAGTCAT	60
CCTATGATTC	GATTTTTAGT	TTAGCTGGC	TATTTTGAAC	TGACTATTTA	CCTCCATCTG	120
TCGGGCAAAC	TAAACCAGTA	CATCAACATG	CACTATTCCT	ATCTGGCCTA	TATCTCCATG	180
GTGCTTCTTT	TTATCTTGGC	TATCGTTCAA	TTGTATATCT	GGATGAAGCA	AGTCAAACCC	240
CACAGTCATC	TGAACAGCCG	ATTAGCCAAG	ATGACGAGTA	TTTCTCTTCT	GGCTATTCCA	300
CTTGTCATCG	GCTTAACTTT	CCCAACTGTT	AGCTTGGATT	CTCAGACTGT	TTCTGCTAAA	360
GGTTATCATT	TCCCCCTATC	GGAAGGAACG	GATCTAGCCA	TTCAGACAAG	CGAAGGGACG	420
ACAAGCCAAT	ATTTGAAACC	AGATACCAGT	TCTTATTTTT	CAAAATCAGC	CTATGAAAAG	480
GAAATGCGAA	CGGCGGCGGA	TAAATACTTA	TCCCAAGATA	GTATTCAGAT	CACTAATGAA	540
AACTATATGG	AAGTCATGGA	GGCTATCTAC	GACTATCCAG	ATGAGTTTGA	GGGCAAGACA	600
ATCCAGTTTA	CAGGCTTTGT	CTATAACGAC	CCAGTCATG	CCAATAGTCA	ATTTCTGTTC	660
CGATTCGGCA	TTATCCACTG	TATCGCAGAT	TCTGGTGTCT	ATGGATTGCT	GACCAAGGGC	720
AATACCCGGC	AGTATGAAAA	CAACACTTGG	ATAACAGCCA	AAGGAAAAC	GGTCAATCAC	780
TACCATAAAG	AACTCAAACA	AAACCTTCCA	ACCTTGGAAA	TCGACAGCTT	TACCAAAGTC	840
GATAAACCAG	AAAATCCCTA	TGTATATAGA	GCTTTTTTAA			879

(2) INFORMATION FOR SEQ ID NO:540:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

AGAACTCATT ATCCAAGTTG GATACGCTTA TTACATAGGA GAATACAAAT GAAATTTAGA	60
AAATTAGCTT GTACAGTACT TGCGGGTGCT GCGGTTCTTG GTCTTGCTGC TTGTGGCAAT	120
TCTGGCGGAA GTAAAGATGC TGCCAAATCA GGTGGTGACG GTGCCAAAAC AGAAATCAC'T	180
TGGTGGGCAT TCCCAGTATT TACCCAAGAA AAAACTGGTG ACGGTGTTGG AACTTATGAA	240
AAATCAAATCA TCGAAGCGTT TGA AAAAGCA AACCCAGATA TAAAAGTGAA ATTGGAAACC	300
ATCGACTTCA AGTCAGGTCC TGAAAAAATC ACAACAGCCA TCGAAGCAGG AACAGCTCCA	360
GACGTACTCT TTGATGCACC AGGACGTATC ATCCAATACG GTAAAAACGG TAAATTGGCT	420
GAGTTGAACG ACCTCTTCAC AGATGAATTT GTTAAAGATG TCAACAATGA AAACATCGTA	480
CAAGCAAGTA AAGCTGGAGA CAAGGCTTAT ATGTATCCGA TTAGTTCTGC CCCATTCTAC	540
ATGGCAATGA ACAAGAAAAT GTTAGAAGAT GCTGGAGTAG CAAACCTTGT AAAAGAAGGT	600
TGGACAACTG ATGATTTTGA AAAAGTATTG AAAGCACTTA AAGACAAGGG TTACACACCA	660
GGTTCATTGT TCAGTTCTGG TCAAGGGGGA GACCAAGGAA CACGTGCCTT TATCTCTAAC	720
CTTTATAGCG GTTCTGTAAC AGATGAAAAA GTTAGCAAAT ATACAAC'TGA TGATCCTAAA	780
TTCGTCAAAG GTCTTGAAAA AGCAACTAGC TGGATTAAAG ACAATTTGAT CAATAATGGT	840
TCACAATTTG ACGGTGGGGC AGATATCCAA AACTTTGCCA ACGGTCAAAC ATCTTACACA	900
ATCCTTTGGG CACCAGCTCA AAATGGTATC CAAGCTAAAC TTTTAGAAGC AAGTAAGGTA	960
GAAGTGGTAG AAGTACCATT CCCATCAGAC GAAGGTAAGC CAGCTCTTGA ATATCTTGTA	1020
AACGGGTTTG CAGTATTCAA CAATAAAGAC GACAAGAAAG TCGCTGCATC TAAGAAATTC	1080
ATCCAGTTTA TCGCAGATGA CAAGGAGTGG GGACCTAAAG ACGTAGTTCG TACAGGTGCT	1140
TTCCCAGTCC GTACTTCATT TGGAAAACTT TATGAAGACA AACGCATGGA AACAATCAGT	1200
GGCTGGACTC AATACTACTC ACCATACTAC AACACTATTG ATGGATTTGC TGAAATGAGA	1260
ACACTTTGGT TCCAATGTT GCAATCTGTA TCAAATGGTG ACGAAAAACC AGCGGATGCT	1320
TTGAAAGCCT TCACTGAAAA AGCAAACGAA ACAATCAAAA AAGCTATGAA ACAATAG	1377

(2) INFORMATION FOR SEQ ID NO:541:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 609 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

```
GTCGGTCTTC TTGAGTGCCC CACTTTTCTT TTAAAAAAGG AGTTTTTTTAT GTTGAAAAAA 60
TGGCAGTTAA AAGATGTTAT CTTGCTTGCT TTCTTGCTA TCTTTTTTGG TGGGGTTTTTC 120
GTTGGTTCAG GATATGTGTA TAATATTCTC AGTCTACTCT TAACACCTCT TGGTTTGCAG 180
GCCTTTGCCA ATGAAATCCT CTTCGGTCTC TGGTGTATGG CTGCGCCCAT TGCTGCCATC 240
TTTGTTC CGA GAGTCGGAAG TGCAACGATT GGAGAAGTGC TAGCTGCGCT TGCTGAAATC 300
CTTTATGGTA GCCAATTTGG TCTAGGAGCT CTTTGTGCTG GCTTGGTTCA AGGTTTGGGA 360
AGTGAATTTG GTTTTATCGT AACTAAGAAT CGCTATGAAA GTTGGCTCTC TCTAACTGCT 420
AATAGTATTG GGGTTACGCT TGTTAGCTTT GTCTATGAAT ACATTAAGTT AGGTTACTAC 480
GCCTTTTCCC TTCCGTTTGT CCTTTCCTTA CTTGTGGTAC GTTTTATTTT TGTTTATTTT 540
TTCTGTACCA TCTTGGTTCG TGCCATTGTC AACTCTATC ATCAGTTTGC AACTGGAGGA 600
AAAGCATAG 609
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(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

```
CGAGATAATT ATTATAATCC TGTGATTGTT CAACCATTAG TTTTAATTGG GCGCCTGAT 60
GTAAAAGAAA TGCCTAAAGA TTGGACTGAA TTAGGTAGTA AGTATAAAGG TAAATATTCA 120
ATTTATGGTC TTCAAGGTGG TACAGGACGG GCAATTCTAG CAAGTATCTT AGTTCGTTAC 180
CTTGATGAAA AAGGAGATTT AGGCGTATCA GAAAAAGGAT GGGAAAGTGC AAAAGAATAC 240
TTTGCAAAATG CCTATACTCT TCAAAAAGGT GAAAGCTCAG TTGTTAAAGC GTTAGATAAA 300
GAAAGCCCAA TTCAATACGG TATGATCTGG GGTTCCTGGAG CGTTAATTGG ACAAAAAGAA 360
CAAAATGTTG AATTCAAAAGT TATGACTCCT GAGATTGGTG TACCATTTGT AACTGAACAA 420
ACTATGGTTT TAAGCACTAG TAAAAACAA GCGTTAGCTA AAGAATTTAT TGATTGGTTT 480
GGTCAATCAG AAATTCAAGT AGAATATAGT AAAAAATTTG GATCTATTCC TGCAATAAAA 540
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GATGCCCTAA AAGAGTTACC TGAAGATACG AAAAAATTTG TTGATCAAGT GAAACCACAA	600
AATATTGACT GGGAAAGCTGT TGGAAAGCAT TTGGATGAAT GGGTAGAAAA AGCTGAATTA	660
GAATACGTAA AATAA	675

(2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

AATATGAATT ATTTTCGAAA ACGTAGGGAG AGACAAGCGA AATCTAATAG TGGAATTTAC	60
TGTCCCGCAG CTAATCGTTC CAAAATTCAA TATGAAACTA AAGAAAAAGC TGACCATGCG	120
GTTCAATATG ATAACGGAGG TTTAGTTAGA AGCTATTATT GTCGTACATG TCGGTGTTGG	180
CATACTACTT CAAAATCTAA TAAACCTCCG CTAAGTTTGA AAAACTATGG TCTGAAACTC	240
TTTGGTTTAG ATAAATCAGA ATAG	264

(2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

CAGCACCTTC TACACCATCA GAAAGTGGGG AAATCGAAGA TGACGAATTC TAATTACAAA	60
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CTTACAAAAG	AAGATTTTAA	TCAAATCAAC	AAACGTAGCT	TGTTTACTTT	CCAATTAGGT	120
TGGAACTACG	AACGTATGCA	AGCTTCTGGT	TACCTTTACA	TGATCTTGCC	TCAGTTGCGT	180
AAAATGTATG	GTGATGGAAC	TCCTGAATTG	AAAGAAATGA	TGAAAAGTTCA	TACTCAATTC	240
TTCAATACTT	CACCATTCTT	CCATACCATT	ATCGCTGGTT	TTGACCTTGC	CATGGAAGAA	300
AAAGATGGTG	TAGGTTCAAA	AGACGCCGTT	AACGGTATCA	AGACAGGTTT	GATGGGACCA	360
TTGCTCCTC	TTGGGGATAC	AATCTTTGGT	TCAGTTGTAC	CTGCTATCAT	GGGGTCAGTC	420
GCAGCAACTA	TGGCTATCGC	TGGCCAACCT	TGGGGGATCT	TCCTTTGGAT	TGCAGTTGCA	480
GTAGCGTATG	ACATCTTCCG	TTGGAAACAG	TTGGAATTTG	CTTACAAAGA	AGGGGTTAAC	540
CTTATCAACA	ACATGCAAAG	TACCTTGACA	GCTTTGATTG	ACGCTGCATC	CGTACTTGGT	600
GTCTTCATGA	TGGGTGCTCT	TGTAGCAACA	GTGATTAACT	TTGAAATTTT	TTACAAGTTG	660
CCAATCGGTG	AAAAGATGAT	TGATTTCCAA	GACATCTTGA	ACCAAATCTT	CCCACGTTTG	720
CTTCCAGCAA	TCTTTACTGC	CTTTATCTTC	TGGTTGCTTG	GTAAGAAAGG	TATGAACTCT	780
ACTAAAGCTA	TCGGTATTAT	TATCGTACTT	GCTTTGGCTC	TTTCTGCCCT	TGGTCACTTT	840
GCACTTGGA	TGTAA					855

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

AAATTACTTC	TTTCCTTAAC	AATAAGGAAA	AAGAATGCGT	TTTCATCTTT	TGGTTTGAGG	60
TTTATAATAA	GAGTATCAAA	GTCAGGAGGA	AAAAAGATGA	CTACTTTTAA	AGATGGATTT	120
TTATGGGGTG	GTGCTGTTGC	TGCTCATCAA	CTTGAAGGTG	GATGGCAAGA	AGGTGGCAAG	180
GGAATTAGTG	TTGCTGATGT	TATGACTGCT	GGTCGTCATG	GAGTAGCTCG	TGAAATTACT	240
TTGGGAGTTT	TAGAGGGTAA	ATATTATCCA	AATCATGAGG	CGATAGATTT	TTATCATCGT	300
TATAAAGAAG	ATATAGCACT	TTTTGCTGAA	ATGGGATTCA	AGTGCTTCCG	TACCTCTATT	360
GCATGGACAC	GTATCTTTCC	AAAAGGTGAT	GAGTTAGAGC	CGAATGAAGA	AGGATTACAG	420
TTTTATGATA	ATCTTTTTGA	TGAATGCTTA	AAGAATGGTA	TTGAACCTGT	CATCACTCTA	480
TCTCATTTTG	AAATGCCTTA	TCACTTAGTG	ACCGAATATG	GTGGTTGGAA	AAATAGGAAA	540
TTGATTGATT	TCTTTGCTCG	TTTTGCAGAA	GTCATATTTA	AACGTTACAA	AGATAAGGTT	600
AAATATTGGA	TGACTTTCAA	TGAAATCAAT	AATCAAGCGA	ATTATCAGGA	AGATTTTGCA	660
CCATTACTA	ACTCAGGTAT	TGTATATGAG	GAAGGTGATA	ATAGAGAGGC	AATTATGTAT	720
CAAGCAGCAC	ATTACGAATT	AGTTGCTTCT	GCACGAGCTG	TAAAAATTGG	TCATGAGATT	780
AATCCAGATT	TTCAAATAGG	TTGTATGATT	GCGATGTGTC	CAATTTATCC	AGCTACTTGC	840
AATCCTAAGG	ATATCTTAAT	GGCAATGAAA	GCTATGCAAA	AGCGTTATTA	TTTTGCTGAT	900
GTGCATGTTT	TAGGTAAAATA	TCCTGAGCAT	ATTTTCAAGT	ATTGGGAACG	AAAAGGTATT	960
TCAGTTGATT	TTACTGCCCA	GGATAAAGAA	GATTTACTTG	GTGGGACTGT	AGATTACATT	1020
GGTTTCAGTT	ACTATATGTC	CTTTGCTATC	GACTCTCATC	GTGAAAATAA	TCCTTATTTT	1080

GATTATCTTG	AAACAGAAGA	TTTAGTGAAA	AATAATTATG	TTAAGGCTTC	TGAATGGGAG	1140
TGGCAAATTG	ATCCAGAAGG	TTTGCGTTAT	GCGTTAAATT	GGTTTACAGA	CCACTATCAC	1200
TTACCACTCT	TTATTGTTGA	AAATGGTTTT	GGAGCTATAG	ATAAAGTTGC	AGCAGATGGT	1260
ATGGTACATG	ATGATTATAG	AATTGAATAT	CTAGGTGCCC	ATATTCTGTA	AATGAAAAAG	1320
GCTGTAGTTG	AAGATGGTGT	TGATTTAATG	GGTTATACTC	CATGGGGATG	TATTGATTTA	1380
GTTTCAGCTG	GTACCGGTGA	AATGCGGAAA	CGTTATGGCT	TTATTTATGT	AGATAAAGAT	1440
GACAATGGGA	AGGGAAGTTA	TAATCGTTCC	CCGAAAAAAT	CTTTTGGCTG	GTATAAGGAA	1500
GTTATTTTCAT	CTAACGGTGA	ATCAGTAGAA	TAG			1533

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...196
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

AACACTTCTC	AAGAAAAAAC	ACAACAAGAT	GAAACGCCAA	AATCTAGCGT	CAAGGAAGAG	60
AAAAAAGAAG	ATCAGAAAAC	AGCAACTCAG	GACTCTACTA	CACCTGCTAC	AAGTAAACCT	120
GCCACTGAAA	ATGAAAAACA	GCCCAATACT	CCAACTTCAG	AAAATAATAC	TCAATGAAAA	180
TCAAAGAACA	AACTAG					196

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

ACACGATGTT	ACAGCCTTGA	ATGTTTCAGG	AAAACGTTC	TTAAACCACT	CACTTTTTC	60
AATAATAAAG	CTGGTTTGA	ACTCTTAGAT	CTGTCTTTTC	GACAGCTCAA	CCAAGACTGT	120
CTCATCGCTC	TTAAACTTCT	TTCTGACCCC	AATCGTGAAC	AATTTCAACA	CGATAATCGG	180
CAAGTAGAAC	TAAAAAATACT	GGCTAGACAT	ATTCATCGTC	TCAAGAAAAA	ACAGTCTGAT	240
TGGAAAAGTAC	AATACACTCG	TTGTCTTGAT	ATCATCTTTC	CTGAGTTGGA	TAAAATCGTT	300
GGAAAAGCATT	CAGAATATAC	CTACCAACTC	TTGACACGCT	ACCCTAATCC	TCAGAAAAGG	360
CTTGAGGCAG	GATTTGATAA	GCTGATAGAA	ATTAAGCGAT	TGACCGCTTC	TAAAATTCAG	420
GATATCCTCT	CAGTCGCACC	TCGTTCTATC	GGAACAACAT	CTCCTGCTCG	TGAATTCGAA	480
ATCATCGAAA	TCATCAAACA	TTACAAGAGG	CTCATTGACA	AGGCGGAAAC	ATGTGTCAAT	540
GACTTGATGG	CTGAGTTCAA	CTCGGTCATC	ACGACGGTTA	CTGGGATTGG	GGGTCGTTTA	600
GGGGCGGTCA	TTTGTAGCCGA	GATTCGAAAT	ATTCATGCCT	TTGATAATCC	TGCTCAATTA	660
CAAGCTTTTCG	CTGGACTGGA	TTCTTCTATT	TATCAGTCAG	GTCAGATTGA	TTTAGCTGGA	720
AGAATGATCA	AACGGGGTTC	CCCTCATCTG	CGGTGGGCAC	TCATACAAGC	TGCCAAAGCA	780
TGCCTCGCT	TTTCACCTGC	TTTAAAGGTC	TATCTTAAGA	CTAAGTTAGA	ACAAGGAAAA	840
CATTACAATG	TAGCCATCAT	CCACCTTGCA	AAAAAACTTA	TCCGAACCCT	GTTTTATATC	900
CTAAAAAAGA	GCTGCCATTT	GACGAACAAA	AAGTGA			936

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

TGTAATCGTT	ATCAAAAGTC	TAAAAAAGAA	TTTTTAGATG	GATATCAAAA	TAAAAAGGGA	60
GGAAATTATG	AAAAAGTTTT	CAAAAACATT	GAGAGACAAC	TGGATCTTTC	TCTTGATGGT	120
TTTGCCAGGG	GACTCTGGT	TGATTCTATT	CTTTTACATT	CCAGTATTTG	GGAACGTGGT	180
TGCCTTCAAA	GACTACCACA	TGACCAGTAA				210

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

TCCCAGCTTC	TTTTTATATA	TAAAATTTTA	CCCGTGCAAA	GACAGGGCCT	TAGCAGACTT	60
CTTTTTTACT	TCGTTACCCC	TTGCTTTTTT	TTTTTAGGTT	TGGGCGTTGG	CAGTTGGTTA	120
TACATAGCTA	AAATCAGGTC	TTATAGAAAC	ATCTTATTAT	CAAGTTCTTC	CACTCAAATC	180
ATTTCTTTGG	CACCTTTGTA	TGGAAACTCA	AAAGAAGATT	GGTCAATCTT	ATCTAAGACT	240
GCTTGACACG	GTTTAACTAA	AAGCGATCGT	CATAAATACC	GCCAATAA		288

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

TGGAGGCTTC	TCCCTTTCGA	GAAAGCTCTT	GTTATCATGG	ATAGAGGCTA	TGAAAGTTAC	60
AATCTCATGG	CTCATTTTCA	AGAAAAAGGT	TGGCTTTATA	TCATCCGTAT	TCGAGATGGA	120
AAACAATCCA	TGCCTTCCTC	CTTCAACTTG	CCAAATACGG	AGTGTTTTGA	TCAAAAAGTT	180
TCTCTAAAAA	TATCACGAAA	GCAAACTAAT	CAGCTCAAAA	AACTTTATCG	TGATTTTCCC	240
AATGACTATC	ATTTTATTCC	ACACAATTCT	ATTTTTGATT	TTCTTCCAGA	AACAAGTCGA	300
AAACAAGATC	CTGTAACACT	CTATGAACTT	CCTTTTCGTA	TGGTGCGTTT	AGAAGTGGAA	360
GAAGGAAAAT	ACGAAACTTT	AGTGACGAAT	ACAGACTATT	CAGTCCAAGA	ATTAAAAAAT	420
CTCTACGCCA	GTAGATGGGG	CATAGAGACT	AGTTTTCGTG	ACCTGAAATA	CAGTATTGGC	480
TTGGTCAATT	TTCACGCCAA	AAAGAAGGGA	GGGATCTCCA	AGAAATCTTT	GCTCGCTTTA	540
CAAATTTTAA	CTTTTGTCGT	TGGGTAA				567

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

TGGAGGCTTC	TCCCTTTTCGA	GAAAGCTCTT	GTTATCATGG	ATAGAGGCTA	TGAAAGTTAC	60
AATCTCATGG	CTCATTTTCA	AGAAAAAGGT	TGGCTTTTATA	TCATCCGTAT	TCGAGATGGA	120
AAACAATCCA	TGCCTTCCTC	CTTCAACTTG	CCAAATACGG	AGTGTTTTGA	TCAAAAAGTT	180
TCTCTAAAAT	TATCACGAAA	GCAAACAAAT	CAGCTCAAAA	AACTTTATCG	TGATTTTCCC	240
AATGACTATC	ATTTTATTCC	ACACAATTCT	ATTTTGTGATT	TTCTTCCAGA	AACAAGTCGA	300
AAACAAGATC	CTGTAACACT	CTATGAACTT	CCTTTTCGTA	TGGTGCGTTT	AGAAGTGGAA	360
GAAGGAAAAT	ACGAAACTTT	AGTGACGAAT	ACAGACTATT	CAGTCCAAGA	ATTAAAAAAT	420
CTCTACGCCA	GATAGATGGG	CATAGAGACT	AGTTTTCGTG	ACCTGAAATA	CAGTATTGGC	480
TTGGTCAATT	TTCACGCCAA	AAAGAAGGGA	GGGATTCTCC	AAGAAATCTT	TGCTCGCTTT	540
ACAAATTTTA	ACTTTTGTCT	TTGGGTAACC	TCGCAAGTTG	CCATCGACAG	TAGTCACAAA	600
AAACAAAGAT	ATAAAGTGTG	TTTCTCAGAT	GCGGCTTATG	CCTGCCGTTT	GTTTTTTAAC	660
GGTTCCTTTT	CTTCCCTCCA	GTGA				684

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

TGGAGGCTTC	TCCCTTTTCGA	GAAAGCTCTT	GTTATCATGG	ATAGAGGCTA	TGAAAGTTAC	60
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AATCTCATGG	CTCATTTTCA	AGAAAAAGGT	TGGCTTTATA	TCATCCGTAT	TCGAGATGGA	120
AAACAATCCA	TGCCTTCCTC	CTTCAACTTG	CCAAATACGG	AGTGTTTTGA	TCAAAAAGTT	180
TCTCTAAAAAT	TATCACGAAA	GCAAACTAAT	CAGCTCAAAA	AACTTTATCG	TGATTTTCCC	240
AATGACTATC	ATTTTATTCC	ACACAATTCT	ATTTTTGATT	TTCTTCCAGA	AACAAGTCGA	300
AAACAAGATC	CTGTAACACT	CTATGAACTT	CCTTTTCGTA	TGGTGCGTTT	AGAAGTGGAA	360
GAAGGAAAAAT	ACGAAACTTT	AGTGACGAAT	ACAGACTATT	CAGTCCAAGA	ATTAAAAAAT	420
CTCTACGCCA	GTAGATGGGG	CATAGAGACT	AGTTTTTCGTG	ACCTGAAATA	CAGTATTGGC	480
TTGGTCAATT	TTCACGCCAA	AAAGAAGGGA	GGGATTCTCC	AAGAAATCTT	TGCTCGCTTT	540
ACAAATTTTA	ACTTTTGTCG	TTGGGTAACC	TCGCAAGTTG	CCATCGACAG	TAGTCACAAA	600
AAACAAAGAT	ATAAAGTGTG	TTTCTCAGAT	GCGGCTTATG	CCTGCCGTTT	GTTTTTTAAC	660
GGTTCCCTTT	CTTCCCTCCA	GTTGAAAAAC	TACCTCAAGA	AACAGTTATC	TATTATTTCGA	720
CCGAATCGAA	AATATTCAAG	AAAGATAAAA	GCTCAATCGG	TAGTTGATTT	CATCTATAGA	780
GTAACATAA						789

(2) INFORMATION FOR SEQ ID NO:553:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

TGGAGGCTTC	TCCCTTTTCGA	GAAAGCTCTT	GTTATCATGG	ATAGAGGCTA	TGAAAGTTAC	60
AATCTCATGG	CTCATTTTCA	AGAAAAAGGT	TGGCTTTATA	TCATCCGTAT	TCGAGATGGA	120
AAACAATCCA	TGCCTTCCTC	CTTCAACTTG	CCAAATACGG	AGTGTTTTGA	TCAAAAAGTT	180
TCTCTAAAAAT	TATCACGAAA	GCAAACTAAT	CAGCTCAAAA	AACTTTATCG	TGATTTTCCC	240
AATGACTATC	ATTTTATTCC	ACACAATTCT	ATTTTTGATT	TTCTTCCAGA	AACAAGTCGA	300
AAACAAGATC	CTGTAACACT	CTATGAACTT	CCTTTTCGTA	TGGTGCGTTT	AGAAGTGGAA	360
GAAGGAAAAAT	ACGAAACTTT	AGTGACGAAT	ACAGACTATT	CAGTCCAAGA	ATTAAAAAAT	420
CTCTACGCCA	GTAGATGGGG	CATAGAGACT	AGTTTTTCGTG	ACCTGAAATA	CAGTATTGGC	480
TTGGTCAATT	TTCACGCCAA	AAAGAAGGGA	GGGATTCTCC	AAGAAATCTT	TGCTCGCTTT	540
ACAAATTTTA	ACTTTTGTCG	TTGGGTAACC	TCGCAAGTTG	CCATCGACAG	TAGTCACAAA	600
AAACAAAGAT	ATAAAGTGTG	TTTCTCAGAT	GCGGCTTATG	CCTGCCGTTT	GTTTTTTAAC	660
GGTTCCCTTT	CTTCCCTCCA	GTTGAAAAAC	TACCTCAAGA	AACAGTTATC	TATTATTTCGA	720
CCGAATCGAA	AATATTCAAG	AAAGATAAAA	GCTCAATCGG	TAGTTGATTT	CATCTATAGA	780
GTAACATAA						789

(2) INFORMATION FOR SEQ ID NO:554:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1077 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1077
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

AAGGAAAGTT	ACATCATGAA	TAAACGCGTA	CAAGCATTTC	TAGCTAAAAAT	GCAAGAAAAA	60
GAAGTAGATG	GTGTCATCAT	CAACAATCTT	AAAAACGTCT	ATTATTTGAC	TGGTTTTTGG	120
GGCTCAAACG	GAACAGTCTT	TATCAGCCGT	GACCGTCAGG	TCTTAGTGAC	AGACTCTCGC	180
TATATCATCG	CAGCTAAGCA	AGAAACCAGT	GGTTTTGAGA	TTGTGGCTGA	TCGTGATGAA	240
TTGGCTGTCA	TTGCAGGAAT	TGTTAAGGAC	ATGGGCTTGA	CTCGTATCGG	TTTTGAAGAT	300
GAGATTTTCA	TGTCTTATTA	CCACCGTATG	CAGGCAGCTT	TTGCAGGTTT	GGACTTGTTT	360
CCGCAAATC	AGTTTGTGGA	AGGTCTTCGT	ATGATTAAGG	ATGAGGCAGA	GATTGCAGCG	420
ATTCGCAAGG	CTTGTTCTAT	CTCAGACCAA	GCTTTCGCG	ATGCGCTTGA	CTTTATCAAA	480
CCAGGAAAAA	CTGAAATTGA	GATTGCCAAC	TTCCCTTGACT	TCCGCATGCG	TGAGTTGGGA	540
GCATCTGGCT	TATCTTTTGA	TACGATCCTA	GCTAGCGGTA	TCAATTCTTC	TAAACCCCAT	600
GCCCATCCAA	TGCACAAACC	AGTGGAGTTG	GGAGAAGCCA	TTACCATGGA	CTTCGGCTGT	660
CTCTATGACC	ACTATGTCAG	TGATATGACC	CGGACTATCT	ATCTAGGGCA	TGTTAGCGAT	720
GAGCAGGCAG	AGATTTACAA	TACGGTTCTA	AAAGCTAACC	AAGCCTTGAT	TGACCAAGCT	780
AAGGCAGGCT	TAGGTTTCCG	TGACTTTGAC	AAAATCCCTC	GTGATATTAT	CATTGAGGCA	840
GTTTATGGCG	ACTACTTTAC	TCACGGCATT	GGCCACGTA	TTGGTCTGGA	TATCCATGAG	900
GAACCCTACT	TTAGTCAGAC	TTCTACAGAA	ACTATTAAGA	CAGGTATGGC	CTTAACCGAT	960
GAACCAGGTA	TCTATATCGA	AGGCAAATAT	GGCGTTCGTA	TCGAGGATGA	TATCCTGATT	1020
ACAGAGACAG	GTTGTGAATT	ATTGACCCTA	GCTCCAAAAG	AGTTGATAGT	CATTTAG	1077

(2) INFORMATION FOR SEQ ID NO:555:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1053 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TATCAGGGTT	ATTCTAAGGA	ACAAATTGAG	CTCTTGGTGA	GCTTGCCTTC	CTTTGGAATC	60
ATGATGATGT	TACTGCTAAA	TGGTTTCTTA	GAAAAAATAT	TTCTTGAGCG	CTTACAGATT	120
AGTTTGGGCT	TGCTGATTTT	ATCATTGAGC	GGTACAGCTC	CCTTCTGGTA	CCAAGCCTAT	180
CCCTTTGTCT	TTGGAACACG	GCTTCTCTTT	GGTTTGGGTC	TTGGGATGAT	CAATGCCAAG	240
GCCATTTCTA	TTATCAGTGA	ACGCTACCAA	GGAAAAAGGC	GAATTCAGAT	GTTAGGGCTA	300
CGCGCTTCTG	CAGAGGTCGT	TGGAGCTTCT	ATCATTACCT	TGGCCGTCGG	TCAGTTGTTG	360
GCTTTTGGTT	GGACAGCTAT	CTTTCTAGCC	TATAGTGCTG	GATTTTTGGT	GCTGCCCCCTT	420
TATCTGCTCT	TTGTCCCTTA	TGGAAAATCA	AAGAAAGAAG	TCAAGAAAAG	AGCGAAGGAA	480
GCAAGTCGTT	TAATCGAGA	AATGAAAGGC	TTGATTTTTA	CCTTAGCTAT	CGAAGCGGCA	540
GTTGTAGTTT	GTACCAATAC	AGCTATTACC	ATCCGTATTC	CAAGTTTGAT	GGTGGAAGA	600
GGATTGGGGG	ATGCCAGTT	ATCTAGTTTT	GTTCTTAGTA	TCATGCAGTT	GATCGGGATT	660
GTGGCTGGGG	TGAGTTTTTC	TTTCTTGATT	TCTATCTTTA	AAGAGAAACT	GCTCCTCTGG	720
TCTGGTATTA	CCTTTGGCTT	GGGGCAAATC	GTGATTGCCT	TGTCTTCATC	CTTGTGGGTG	780
GTAGTAGCAG	GAAGTGTTCT	GGCTGGATTT	GCCTATAGTG	TAGTCTTGAC	GACGGTCTTT	840
CAACTTGTCT	CTGAACGAAT	TCCAGCTAAA	CTCCTCAATC	AAGCAACTTC	ATTTGCTGTA	900
TTAGGCTGTA	GTTTCGGAGC	CTTTACGACC	CCATTTCGTT	TAGGTGCAAT	TGGCTTACTA	960
ACTCACAATG	GGATGTTGGT	CTTTAGTATC	TTAGGAGGTT	GGTTGATTGT	AATCTCTATC	1020
TTTGTCTATG	ACTTACTTCA	GAAGAGAGCT	TAG			1053

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

CGAATTATTC	TTGTAAAAAA	ATGCCACGCT	ATGAAGGCTC	AAGCGATTGT	CACAAGTCAA	60
GGGAGAATTG	TTTCTTTGGA	TATCACTGTG	AACTATTGTC	ATGATATGAA	GTTGTTCAAA	120
ATGAGTTGCA	GAAATATCGG	ACAAGCTGGT	AAAACTTGG	CTGACAGTGG	TTATCAAGGG	180
CTCATGAAGA	TATATCCTCA	AGCACAAACT	CCACGTAAAT	CCAGCAAAC	CAAGCCGCTA	240
ACAGTTGAAG	ATAAAGCCTG	TAACCATGCG	CTATCCAAGG	AGAGAAGCAA	GGTTGAGAAC	300
ATCTTTGCCA	AAGTAAAAAC	GTTTAAAAATA	ATTTCAACAA	CCTATCGAAA	TCATCGTAAA	360
CGCTTCGGAT	TACGAATGAA	TTTGAGTGCT	GGTATTATCA	ATCATGAACT	AGGATTCTAG	420

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2556 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO.

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

AGGAACATTC	TAAAATATTC	GGAATTTAAA	GTAAGGAAAA	ACATGGCTAA	TATTTTAAAA	60
ACAATTATCG	AAAAATGATA	AGGAGAAAATC	CGTCGTCTGG	AAAAAGATGGC	TGACAAAGGTT	120
TTCAAATACG	AAGACCAAAT	GGCTGCTTTG	ACTGACGACC	AACTAAAAGC	AAAAACAGTT	180
GAATTTAAGG	AACGTTATCA	AAATGGAGAA	TCACTGGATT	CATTGCTTTA	CGAAGCATTT	240
GCGGTTGTCC	GTGAAGGTGC	CAAACGTGTC	CTAGGTCTCT	TCCCTTATAA	GGTTCAGGTC	300
ATGGGGGGGA	TTGTTCTTCA	CCATGGTGAC	GTGCCAGAGA	TGCGTACAGG	GGAAGGGAAA	360
ACCTTGACTG	CGACCATGCC	GGTATACCTC	AATGCCCTTT	CAGGTAAAGG	GGTTCACGTA	420
GTTACGGTTA	ATGAATACCT	GTCAGAACGT	GACGCGACTG	AGATGGGTGA	ATTGTACTCT	480
TGGCTTGGTT	TGTCAGTAGG	GATTAACCTG	GCTACCAAAT	CTCCAATGGA	GAAAAAAGAA	540
GCCTATGAGT	GTGATATTAC	TTACTCAACT	AACTCAGAAA	TCGGATTTGA	CTACCTTCGT	600
GACAACATGG	TCGTTTCGCG	TGAAAACATG	GTACAACGTC	CGCTTAACTA	TGCCCTGGTC	660
GATGAGGTTG	ACTCTATCTT	GATTGACGAG	GCTCGTACAC	CTTTGATTGT	ATCAGGTGCC	720
AATGCGGTTG	AAACCAGTCA	GTTGTATCAC	ATGGCAGACC	ACTATGTAAA	ATCTTTGAAC	780
AAAGATGACT	ACATCATCGA	TGTGCAGTCT	AAGACTATTG	GTTTGTCTGA	TTCAGGGATT	840
GACAGGGCTG	AAAGCTACTT	CAAACCTGAA	AACCTCTATG	ACATCGAAAA	CGTGGCTTTG	900
ACCCACTTTA	TCGATAACGC	CCTTCGTGCC	AACTACATCA	TGCTTCTCGA	TATTGACTAT	960
GTGGTGAGCG	AAGAGCAAGA	AATCTTGATT	GTCGACCAAT	TTACAGGTCG	TACCATGGAA	1020
GGTCGTCGTT	ATTCTGATGG	ATTGCACCAA	GCTATTGAAG	CCAAAGAAGG	TGTGCCAATC	1080
CAGGATGAAA	CCAAGACATC	TGCCTCAATC	ACGTACCAAA	ACCTTTTCCG	TATGTACAAA	1140
AAATTGTCTG	GTATGACGGG	TACAGGTAAG	ACTGAGGAAG	AAGAATTTCC	TGAAATCTAC	1200
AACATTTCGTG	TTATTCCAAT	CCCAACAAAC	CGTCCTGTTT	AACGTATTGA	CCACTCAGAC	1260
CTTCTTTATG	CAAGTATCGA	ATCTAAGTTT	AAAGCGGTTG	TCGAAGACGT	TAAGGCTCGT	1320
TACCAAAGG	GTCAACCTGT	CTTGTTGGT	ACAGTAGCGG	TTGAACTAG	TGACTACATT	1380
TCTAAGAAAT	TGGTTGCAGC	TGGTGTTCCT	CACGAAGTCT	TGAATGCCAA	AAACCACTAT	1440
AGAGAAGCCC	AAATCATCAT	GAATGCTGGT	CAACGTGGTG	CCGTTACCAT	CGCAACCAAC	1500
ATGGCGGGTC	GTGGTACCGA	CATCAAGCTT	GGTGAAGGTG	TTCGTGAACT	TGGAGGACTT	1560
TGTGTTATTG	GTACAGAACG	TCATGAAAGT	CGTCGTATCG	ATAACCAGCT	TCGTGGACGT	1620
TCAGGTCGTC	AAGGAGATCC	AGGTGAGTCA	CAATTCTACC	TATCTCTTGA	AGATGATTTG	1680
ATGAAACGTT	TTGGTTCTGA	ACGCTTGAAG	GGAATCTTTG	AACGTCTCAA	CATGTCTGAA	1740
GAGGCGATTG	AGTCTCGCAT	GTTGACGCGT	CAGGTTGAAG	CAGCGCAAAA	ACGTGTCGAA	1800
GGAAATAACT	ACGATACCCG	TAAACAAGTC	CTTCAATACG	ACGATGTCAT	GCGTGAACAA	1860
CGTGAGATTA	TCTATACTCA	ACGTTATGAT	GTCATTACTG	CAGACCGTGA	CTTGGCACCT	1920
GAAATTCAGG	CAATGATCAA	ACGCACGATT	GGTCGTGTCG	TTGACGGTCA	TGCGCGTGCT	1980
AAACAAGATG	AGAAACTAGA	GGCAATTTTG	AACTTCGCTA	AGTACAACTT	GCTTCCTGAA	2040
GATTCATATTA	CGATGGAAGA	CTTGTCAGGC	TTGTCGTGATA	AGGCCATCAA	GGAAGAGCTT	2100
TTCCAACGTG	CCTTGAAGGT	TTACGATAGT	CAGGTTTCAA	AACTACGCGA	TGAAGAAGCA	2160
GTTAAAGAAT	TCCAAAAAGT	TTTGATTCTA	CGAGTGGTGG	ATAACAAGTG	GACAGATCAT	2220
ATCGATGCC	TTGATCAATT	GCGTAACGCG	GTTGGACTTC	GTGGCTATGC	TCAGAACAAC	2280

CCTGTTGTTG	AGTATCAGGC	AGAAGGTTTC	CGTATGTTTA	ATGATATGAT	TGGTTCGATT	2340
GAGTTTGATG	TGACACGCTT	GATGATGAAA	GCACAAATTC	ATGAACAAGA	AAGACCACAG	2400
GCAGAACGTC	ATATCAGTAC	AACAGCGACT	CGCAATATCG	CTGCTCACCA	AGCAAGTATG	2460
CCAGAAGATT	TGGATTTGAG	CCAGATTGGA	CGCAATGAAC	TTTGCCCATG	TGGTTCTGGT	2520
AAGAAATTTA	AAAACGTCA	CGGTAAAAGA	CAATAA			2556

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GATGGCATT	TTGGAATTAA	AAAATACAGA	GAAACCAGCA	AAGACAAGGT	TCGCAAGCCA	60
TGGTTGGAGT	TTTTCGGCAA	CAAGCCCTTT	ACCCAGCAAC	CGCAACGAGC	CATTAGCCAA	120
GCAAAATCAAC	TGCTGGACTA	CAAGAGCTGG	TCCGAGGAGG	ACAGGAAAAT	GTTTAGTCAA	180
CTACATATGC	GAGAAGAACA	AGTCTTGTTA	GCACAGGACT	ATGCCTTGA	AACTGCTAGG	240
GCTGAAGACC	TTGAACAAGG	ACTAGAGCGT	GGGAAAGTTG	AAGGAAGGGC	AGAAAGGAAA	300
CTTTTGGCCT	TCCTAGACAT	AGTACGCCAA	GGTCTTCTGA	CTTCTGAGGT	TGCCAGCCAG	360
CAATTAGGTA	TGTCAGTATC	TGAATTTGAG	GCACTGTTGT	AA		402

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

AAAAGGAATT	TAAGTATGGA	AGAAATTCTC	TGTATTGGTT	GTGGAGCAAC	CATTCAGACG	60
ACAGATAAAG	CTGGTCTTGG	TTTTACCCCC	CAGTCGGCAC	TTGAAAAAGG	TTTGGAGACT	120
GGCGAAGTCT	ATTGCCAACG	CTGTTTCCGT	CTCCGCCACT	ACAATGAAAT	CACAGATGTC	180
CAGTTGACGA	ACGATGATTT	CCTCAAGCTC	TTGCACGAGG	TGGGAGACAG	TGATGCTTTA	240
GTGGTCAATG	TCATTGATAT	CTTTGATTTT	AATGGATCTG	TCATCCCAGG	TTTACCACGT	300
TTCGTCTCGG	GCAATGATGT	CCTCTTGGTA	GGAAATAAAA	AAGATATCCT	TCCTAAGTCA	360
GTTAAGTCTG	GTAAGATTAG	CCAGTGGCTC	ATGAAACGTG	CCCATGAAGA	AGGTCTTCGT	420
CCAGTCGATG	TGGTCCTAAC	TTCAGCACAA	AATAAACATG	CCATTAAAGG	AGTCATTGAC	480
AAGATTGAAC	ACTACCGTAA	GGGCCGCGAT	GTCTATGTGG	TCGGTGTGAC	CAACGTTGGA	540
AAATCAACTC	TAATCAATGC	TATTATCCAA	GAAATCACGG	GTGATCAGAA	TGTCATCACT	600
ACTTCACGCT	TCCCAGGGAC	AACCTTGGAC	AAAATAGAGA	TTCCGCTTGA	CGACGGATCT	660
TATATTTACG	ATACGCCGGG	AATTATCCAC	CGCCACCAGA	TGGCTCACTA	CTTGACGGCC	720
AAAAACCTCA	AGTATGTCAG	TCCTAAAAAG	GAAATCAAGC	CTAAGACCTA	TCAGCTTAAT	780
CCTGAGCAAA	CCCTATTTTT	AGGTGGTTTG	GGACGCTTTG	ACTTTATAGC	AGGAGAAAAG	840
CAAGGATTTA	CTGCTTTCTT	TGATAATGAA	CTCAAACTCC	ATCGTAGCAA	GCTTGAAGGA	900
GCTAGTGCTT	TCTACGATAA	GCACCTGGGA	ACTCTTCTGA	CACCACCAAA	TAGCAAGGAA	960
AAAGAAGATT	TCCCAAGGCT	AGTCCAGCAT	GTCTTTACCA	TTAAAGATAA	GACAGACCTA	1020
GTCATCTCAG	GCCTAGGATG	GATTCGTGTA	ACAGGCACAG	CAAAAAGTCGC	CGTCTGGGCA	1080
CCAGAAGGCG	TCGCCGTCGT	CACACGAAAA	GCAATTATTT	AA		1122

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

AAGAGGAATT	TTATGAGTAT	TAAACTAATC	GCTGTCGATA	TTGACGGAAC	CCTAGTCAAC	60
AGTCAAAAAG	AGATTACTCC	TGAAGTCTTT	TCTGCCATCC	AAGATGCCAA	AGAAGCTGGT	120
GTCAAAGTCG	TGATTGCAAC	TGGCCGCCCC	ATCGCAGGTG	TTGCCAAACT	TCTGGACGAC	180
TTGCAGTTGA	GAGACCAAGG	TGACTATGTG	GTGACCTTCA	ATGGTGCCCT	TGTCCAAGAA	240
ACTGCTACTG	GCCATGAGAT	TATCAGCGAA	TCCTTGACCT	ATGAGGATTA	TCTGGATATG	300
GAATTCCTCA	GTCGCAAGCT	CGGTGTCCAC	ATGCATGCCA	TTACCAAGGA	CGGTATCTAT	360
ACTGCAAATC	GCAATATCGG	AACATACACT	GTACACGAAT	CAACCCTCGT	CAGCATGCCT	420
ATCTTCTACC	GTACCCCTGA	AGAAATGGCT	GGCAAAAGAA	TTGTTAAATG	TATGTTTATC	480
GATGAACCAG	AAATTCTCGA	TGCTGCGATT	GAAAAAATTC	CAGCAGAATT	TTACGAGCGC	540
TACTCCATCA	ACAAATCTGC	TCCTTTCTAC	CTCGAACTCC	TTACAAAGAA	TGTAGACAAG	600
GGTTCAGCCA	TTACTCACTT	GGCTGAAAAA	CTCGGATTGA	CCAAAGATGA	AACCATGGCA	660

ATCGGTGACG AAGAAAATGA CCGTGCCATG CTGGAAGTCG TTGGAAACCC CGTTGTCATG	720
GAAAATGGAA ATCCAGAAAT CAAAAAATC GCCAAATACA TCACTAAAAAC AAATGACGAA	780
TCCGGCGTTG CCCACGCCAT CCGAACATGG GTACTGTAA	819

(2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GTCTATCTCT ATCAACTTTT CTTGGTTTTG TTCCTTTTAC TTGGTGGTTT AGCTCTCCTG	60
TTTTCTCTTT TAGCTTTAAC CAGCCATAAA TGGTATTACG TGAGATTTGG AAAACGTGTG	120
ATGCTTCTGT TATACTACCT ATTCGCTCAC AATAAGAGAG AACTTTTTTA CGAAAATCTA	180
TTGAATATGC CATAA	195

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GTCTATCTCT ATCAACCTTT CTTGGTTTTG TTCCTTTTAC TTGGTGGTTT AGCTCTCCTG	60
TTTTCTCTTT TAGCTTTAAC CAGCCATAAA TGGTATTACG TGAGATTTGG AAAACGTGTG	120

ATGCTTCTGT TATACTACCT GTTCGCTCAC AATAAGAGAG AACTTTTTTA CGAAAATCTA	180
TTGAATATGC CATAA	195

(2) INFORMATION FOR SEQ ID NO:563:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GTCTATCTCT ATCAACTTTT CTTGGTTTTG TTCCTTTTAC TTGGTGGTTT AGCTCTCCTG	60
TTTTCTCTTT TAGCTTTAAC CAGCCATAAA TGGTATTACG TGAGATTGG AAAACGTGTG	120
ATGCTTCTGT TATACTACCT GTTCGCTCAC AATAAGAGAG AACTTTTTTA CGAAAATCTA	180
TTGAATATGC CATAA	195

(2) INFORMATION FOR SEQ ID NO:564:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GTCTATCTCT ATCAACTTTT CTTGGTTTTG TTCCTTTTAC TTGGTGGTTT AGCTCTCCTG	60
TTTTCTTTTT TAGCTTTAAC CAGCCATAAA TGGTATTACG TGAGATTGG AAAACGTGTG	120
ATGCTTCTGT TATACTACCT GTTCGCTCAC AATAAGAGAG AACTTTTTTA CGAAAATCTA	180

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

TTTGACCTCT ATTCCCTCCAT ACACACCAGA GATGAACCCA TTGAACAAGT GTGGAAAGAG	60
ATTCGTAAAC GTGGATTTAA GAATAAAGCC TTTCGAACTT TGGAAGATAT CATGAATCAA	120
CTTCAAGATG TCATACAAAG ACTGGGAGAA GAGGTGATAA AGTCCATCGT TAATCGGAGA	180
TGA	183

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

CATTTGATCT ATACGCTAAT ATTAATGATA TTGTGGATGG CATTAGCTTT TGCAGGAGAT	60
ATGAGATTAT TTGTTAAAAGA TAATGATCAG AAAAAAGCTG AAATTAAAAAT TAGAATGCCT	120
GAAAAAATTA AGGAAACTAA ATCAGAAATAT CCCTATGTAT CAAGTTATGG GAATGTCATA	180
GAATTAGGGG AAGGAGATCT TTCAAAAAAC AAACCAGACA ATTTAACTAA AATGGAATCT	240

GGTAAAATCT	ATTCTGATTC	AGAAAAACAA	CAATATCTGT	TAAAGGATAA	TATCATTTCTA	300
AGAAAAGGCT	ATGCACTAAA	AGTGACTACC	TATAATCCTG	GAAAAACGGA	TATGTTAGAA	360
GGAAATGGAG	TCTATAGCAA	GGAAGATATA	GCAAAAATAC	AAAAGGCCAA	TCCTAATCTA	420
AGAGCCCTTT	CAGAAACAAC	AATTTATGCT	GATAGTAGAA	ATGTTGAAGA	TGGAAGAAGT	480
ACCCAAGCTG	TATTAATGTC	GGCTTTGGAC	GGCTTTAACA	TTATAAGGTA	TCAAGTGTTT	540
ACATTTAAAA	TGAACGATAA	AGGGGAAGCT	ATCGATAAAG	ACGGAAATCT	TGTGACAGAT	600
TCTTCTAAAC	TTGTATTATT	TGGTAAGGAT	GATAAAGAAT	ACACTGGAGA	GGATAAGTCC	660
AATGTAGAAG	CTATAAAAAG	AGATGGCTCC	ATGTTATTTA	TTGATACCAA	ACCAGTAAAC	720
CTTTCATGG	ATAAGAACTA	CTTTAATCCA	TCTAAATCTA	ATAAAAATTTA	TGTACGAAAT	780
CCAGAATTTT	ATTTAAGAGG	TAAGATTTCT	GATAAGGGTG	GTTTTAACTG	GGAATTGAGA	840
GTTAATGAAT	CGGTTGTAGA	TAATTATTTA	ATCTACGGAG	ATTTACACAT	TGATAACACT	900
AGAGATTTTA	ATATTAAGCT	GAATGTTAAA	GACGGTGACA	TCATGGACTG	GGGAATGAAA	960
GACTATAAAG	CAAACGGATT	TCCAGATAAG	GTAACAGATA	TGGATGGAAA	TGTTTATCTT	1020
CAAACCTGGCT	ATAGCAATTT	GAATGCTAAA	GCAGTTGGAG	TCCACTATCA	GTTTTTATAT	1080
GATAATGTTA	AACCCGAAGT	AAACATTGAT	CCTAAGGGAA	ATACTAGTAT	CGAATATGCT	1140
GATGGAAAAT	CTGTAGTCTT	TAACATCAAT	GATAAAAGAA	ATAATGGATT	CGATGGTGAG	1200
ATTCAAGAAC	AACATATTTA	TATAAATGGA	AAAGAATATA	CATCATTTAA	TGATATTAAA	1260
CAAATAATAG	ACAAGACACT	AAACATTAAG	ATTGTTGTAA	AAGATTTTGC	AAGAAATACA	1320
ACCGTAAAAAG	AATTCATTTT	AAATAAAGAT	ACGGGAGAGG	TAAGTGAATT	AAAACCTCAT	1380
AGGGTAACTG	TGACCATTTA	AAATGGAAAA	GAAATGAGTT	CAACGATAGT	GTCGGAAGAA	1440
GATTTTATTT	TACCTGTTTA	TAAGGGTGAA	TTAGAAAAAG	GATACCAATT	TGATGGTTGG	1500
GAAATTTCTG	GTTTCGAAGG	TAAAAAAGAC	GCTGGCTATG	TTATTAATCT	ATCAAAAGAT	1560
ACCTTTATAA	AACCTGTATT	CAAGAAAATA	GAGGAGAAAA	AGGAGGAAGA	AAATAAACCT	1620
ACTTTTGATG	TATCGAAAAA	GAAAGATAAC	CCACAAGTAA	ACCATAGTCA	ATTAAATGAA	1680
AGTCACAGAA	AAGAGGATTT	ACAAAGAGAA	GATCATTCAC	AAAAATCTGA	TTCAACTAAG	1740
GATGTTACAG	CTACAGTTCT	TGATAAAAAAC	AATATCAGTA	GTAAATCAAC	TACTAACAAT	1800
CCTAATAAGT	TGCCAAAAAC	TGGAACAGCA	AGCGGAGCCC	AGACACTATT	AGCTGCCGGA	1860
ATAATGTTTA	TAGTAGGAAT	TTTCTCTTGA	TTGAAGAAAA	AAAATCAAGA	TTAG	1914

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1244
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GTGTTTCCTA	TCTGAAAACT	GGTATCGAGT	CTGGACGATT	TCCGACGGGT	AGTGCCTGCC	60
TTCTATCCGT	CAACTACAGC	CTTGACTTTT	ACTGCAGCAA	GGACACCAT	CAACGAGCCC	120
TGCTGGAATT	ACGGCACGAA	CAATACCTCT	ATGCCAAGCC	TCAGAGTGGC	TACTATGTAT	180
TAGAACACGG	GCAACATCAA	GACCTAGAAA	TCGAGGTTAC	CGACGAACAT	GCCAGTGCCCT	240
ATGACGATTT	CCGACTCTGT	GTCAATGAAA	CCTTGATTGG	CCGAGAAAAAC	TACCTCTTCA	300

ACTACTATGA	CAATCAAGAA	GGATTAGAAG	ACCTAAGACA	GTCCATTTCAC	AAACTCCTCT	360
TTGAGCAAGC	TCTCTACTGC	AAGGCTAACC	AACTAGTACT	GACTTCTGGA	ACCCAACAAG	420
CCTTATTTAT	CCTCTCTCAA	ATATCCTTTC	CTAGACAAGC	CAAGGAAATC	TTGGTGGAAC	480
AGCCAACCTA	CCATCGGATG	AATCGCCTCT	TGATTGCACA	GGGGCTGGAC	TATCAAACGA	540
TTGAACGAGG	CATTGATGGG	ATTGACTTGG	AGGAGCTGGA	AGGCCACTTC	AAAACAGGAA	600
AAATTAAATT	TTTCTACACC	ATTCCCCGAT	TTCACTATCC	TCTGGGACAT	TCCTATTCTG	660
AGCAAGACAA	ACGATCTATT	CTTAACTTAG	CTGCCAAGTA	TGATGTCTAT	ATCGTAGAGG	720
ACGATTATCT	GGGTGATTTG	GACTCCAAGA	AGGGCCAAAC	CTTCCACTAT	CTTGATACAG	780
AGGAGCATGT	CATTTATATC	AAGTCCTTCT	CGACCAGCCT	TTTTCTTGCC	CTTCGTATTA	840
CAGCACTCAT	TCTTCCAAAT	GCTATCAAAG	AAGCATTTGT	GGCCTACAAA	AATATCCTAG	900
ACTACGACAG	CAACCTCATT	ATGCAAAAGG	CCCTGTCACT	CTATATTGAC	AGTCAATTGT	960
TTGAAAAAAA	TCGTTTGGCT	CGCTTGACCA	ATCATGAATC	TTACCAAAAA	CAAATCGAGG	1020
AAAGGATAAC	TAAAACACCT	TGTCCCCTTC	CTCATTATCC	CCTACACGAT	GGTTTATTGC	1080
TAGACCTGAG	ACAGTATCCT	AAAATCGCCA	GTCTCAAACA	CAGTCAACTG	GGCTTGGAAT	1140
TCTTTGAAGA	GGCCTATTTA	AGCACCTGTC	CTTATCAATT	TGCCAAGGTG	TCCCTAGACA	1200
ATCTGGAAAA	TGTTTTAAAC	TATTTAAAAG	CAGAATTGGA	ATGA		1244

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TCCGTTGTTC	TTGGGTTTGT	TCAAAAATCT	GCTCAGGTGT	CCCATCTTCA	ACAACCACAC	60
CGTCTGCCA	TAAAGATAAC	ACGATCTGCC	ACCTCACGGG	CAAATCCCAT	CTCATGTGTT	120
ACGATAACCA	TAGTCATCCC	TGACTTGGA	AGGTCTTGCA	TAACAGCCAA	TACCTCACCT	180
ACCATTTTCA	GATCCAAGGC	TGAAGTTGGT	TCGTCAAAGA	GCAAAAACATC	TGGTACCATA	240
GCCAACCCAC	GCGCGATGCA	ATCCGTTGTT	GTTGCCACCC	CGACAGACTC	TGTGGATAAG	300
CGTCTGCCTT	ATCTGGCAAA	CCAACTTTTT	CCAAAAGCTC	TTGGGCTCTC	TTCTCAGCAA	360
CTTCCCTGCT	TTACCTTTTA	G				381

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

ATCAACCCCT	ATAAAATCAG	AAATGCAAAA	TTATCAAGTA	TAAGACGTAA	TGAAGTATCT	60
TTTATATTTT	AAGCATATAA	TTTAATACCT	TCCCTGCCGG	TAATAGAAAA	TATAGCACTT	120
CCTTTGCGAT	TATCACAAAA	AAAATTAACT	ATTAAAAATG	TAGAAAACTT	ACTCAAAAGA	180
ATGAAGTTTA	ATGCTGGCTT	AAACGATTTT	GTTGGAACTC	TGTCTGGTGG	AGAACAACAG	240
AAGGTTGCTA	TAGCTAGAGC	GTTTATTGCT	GATAGTGATA	TAATATTTGC	TGATGAGCCA	300
ACTGGTGCTT	TAGACAGCGT	TTCTCGTGAA	GTAATTTTTG	ATTTATTGAG	AGAGTTAGTA	360
GGGGCGGGTA	AGTGTGTAAT	TATGGTAAAC	CACGATATAG	AATTGGCCTC	GAAACTGAT	420
CGTGCAATTAA	TATTGAAAAA	TGGAAAAATT	TTCAAAGAAC	TTCATAGACT	AGCGGGGAAG	480
AGTTGTATAA	AATCTTAG					498

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TCGATGCCCT	ACAAAAGACA	AAGGAGTTTT	TCAATGGCAC	TTTCTAAACT	AGATAGCCTT	60
TATATGGCAG	TGGTAGCAGA	CCATTGCAAA	AATCCACATC	ACCAAGGGAA	GTTAGAAGAT	120
GCTGAGCAAA	CCAGTCTCAA	CAATCCGACT	TGTGGGGATG	TCATCAACCT	CTCTGTCAAG	180
TTTGATGCAG	AGGACCGTTT	GGAAGATATT	GCTTTTCTAA	ATTTCAGGATG	CACGATTTCA	240
ACTGCTTCTG	CTAGTATGAT	GACAGATGCC	GTTTTAGGAA	AAACCAAACA	AGAAATTTTA	300
GAACTGGCGA	CTATTTTTTC	TGAAATGGTT	CAAGGGCAAA	AAGATGAGCG	TCAAGGCCAA	360
CTTGAGACG	CGGCATTCTT	GTCAGGTGTT	GCCAAATTCC	CTCAAAGAAT	CAAGTGTGCA	420
ACCCTAGCTT	GGAATGCCCT	TAAGAAAACA	ATTGAAAATC	AAGAAAAACA	GTAA	474

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...864
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

TTGTCTGCCT ATCAGGTCGT GGGGACAAGG ATGTGGTTCA AGTCAAAGAC CGCTTGGAAG	60
CAGATGCAGC AAAGAAGGGA GAAGCTCATG CCTAAGACAC TAACAGAAAA ATTGAATGCT	120
ATAAAAGCAA CTGGAAAAGG AATTTTTGTT CCCATATCA TGGCTGGTGA CCACGAGAAA	180
GGTTTGACG GTCTTGCTGA AACAAATTCAC TTTTATAGAAG ATTTGGGTGT CTCTGCAATT	240
GAAGTGGGTA TTCCCTTTTC AGACCCTGTT GCAGATGGAC CTGTTATCGA AGAAGCTGGC	300
TTGCGCAGTT TAGCCACCGG GACCTCTACC CAGGCTTTAG TTGAAACCTT GAAAACCAT	360
GAAACAGAGA TTCCACTGGT CATCATGACC TACTTCAATC CCCTCTTTCA GTACGGTGTG	420
GAGAACTTTG TCAAAGATCT GGCTGATACA GCTGTGAAGG GCTTGATTAT CCCAGACTTG	480
CCTCATGAAC ATGCCAATT TGTAGAACCA TTTTGGCAG ATACAGATAT CGCCTTGATT	540
CCTTTAGTAA GCTTGACCAC AGGAATTGAG CGCCAGAAAG AGTTGATTGA AGGGGCGGAG	600
GGATTTCATCT ATGCCGTTGC CATCAATGGA GTGACAGGGA AATCAGGCAA TTACCGTGCA	660
GATTTGGACA AGCACTTGGC GCAACTTCAT CAAGTGGCCG ACATCCCAGT CTTGACAGGT	720
TTTGGTGTAT CTAGTCAAGC CGATCTGGAA CGCTTCAATG CGGTGTCAGA TGGTGTATC	780
GTCGGTTCAA AAATAGTAAA AGCTCTCCAC CAAGGAGAGC CGATTCAAGG TTTTATCAGA	840
CAAGCAGTAG CTTACCAAAA ATAA	864

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

ATCAATCACT	ATTTCAATTCT	TTTCTTAGCA	AGAATGGTTG	CCCCCGCCAA	GGTAAGAAGA	60
CCTGCAATTT	CAAGTGCTAG	ATTTGAAATA	GATCCAGTTG	ATGGCAATGA	CTTCTTCGGT	120
TTATTTGTTG	CTTTTTCGTT	TGTTGAAGCT	TGGTTAGAAG	GTTGCTTGTC	CTTGCTTAAA	180
TTATTTGTAG	TTGATGGCTT	CTTATCATCT	GCTTGTGGCT	TGCTATTATC	TGGTTTTGGT	240
TTTTCTGGTT	GCGGTTTAAC	CTCTGGTTTT	GGTTTTTCTG	GTTGCGGTTT	AACCTCTGGT	300
TTTGGTTTTT	CCGGCTGCGG	TTTAACCTCT	GGTTTTGGTT	TTTCCGGCTG	CGGTTTAACC	360
TCTGGTTTTG	GTTTTTCCGG	CTGCGGTTTA	ACCTCTGGTT	TTGGTTTTTC	CGGCTGCGGT	420
TTAACCTCTG	GTTTTGGTTT	TTCCGGCTGC	GGTTTAACCT	CTGGTTTTGG	TTTTTCCGGC	480
TGCGGTTTAA	CCTCTGGTTT	TGGTTTTTCC	GGCTGCGGTT	TAACCTCTGG	TTTTGGTTTT	540
TCCGGCTGCG	GTTTAACCTC	TGGTTTTGGT	TTTTCCGGCT	GCGGTTTAAC	CTCTGGTTTT	600
GGTTTTTCTG	GTTGCGGTTT	AACCTCTGGT	TTTGGTTTTT	CCAGCTGCGG	TTTAACCTCT	660
GGTTGA						666

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

AAAAATGGTTC	TAAGAGGAGT	TCCTATGTCT	CAAATTGATC	TACAAAAAATT	AAC TAAGAAA	60
AACCAAGAGT	TTGTCCACAT	TGCTACCCAA	CAATTCATCA	AAGATGGGAA	AACAGACGCT	120
GAAATCCAGA	CTATTTTTGA	GGAAGTCATT	CCCCAAATCC	TTGAGGAGCA	ATCTAAAGGT	180
ACAACTGCCC	GTTCCTTATA	CGGCGCACCA	ACTCATTTGGG	CTCATAGCTT	CACTGTCAAA	240
GAGCAGTACG	AAAAAGAGCA	TCCAAAAGAA	AATGATGATC	CAAAACTGAT	GATTATGGAC	300
TCAGCTCTTT	TCATCACTAG	CCTCTTTGCC	CTTGTCAGCG	CCCTCACAAC	CTTCTTTGCG	360
GCAGATCAAG	CTTTCGGCTA	TGGATTGATT	ACTCTTCTAT	TAGTTGGACT	GGTTGGTGGA	420
TTTGCCTTCT	ACTTGATGTA	CTACTTTGTT	TACCAATACT	ATGGACCAGA	TATGGATCGC	480
AGTCAACGTC	CACCTTTCTG	GAAATCTGTA	CTAGTTATCC	TAGCTTCTAT	GTTCCTTTGG	540
TTGCTTGTCT	TCTTTGCAAC	AAGCTTCCTA	CCAGCTAGCC	TTAACCCAGT	ACTGGATCCA	600
TTGCCACTAG	CTATTATTGG	AGCAGCCCTC	CTAGCCCTTC	GCTTCTATCT	CAAGAAACGC	660
TTGAATATCC	GTAGTGCAAG	TGCAGGACCA	ACACGCTATC	AAGAATAA		708

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1557 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

CATTCAA	ACT	ATCAAG	GATG	GGATAT	GAAA	TATAGG	AAAT	TTCAGT	TATT	GATGT	CCAAG	60
TATGGC	TTTA	GTCTTT	CGAT	TATGCT	ACTT	GAAC	TTTG	TC	TTT	TGG	TCTCT	120
TATTTA	GGAC	GCATGG	CTCC	CATTTT	TATG	ATTACT	GTCC	TCATT	CTACT	GATTAT	CAATC	180
ACAATC	ATTT	CAATATT	CAA	CCGTA	AATA	CACTC	CTGAG	ATAAG	GTAAC	CTGGT	TGTTA	240
GTAGCC	TTTG	TGCCAG	TATT	TGGTCC	CCTTG	CTCTAT	CTGA	TGTTT	TGGTGA	AAGGC	GATTG	300
TCCAAAA	AAG	AAATCAA	AACA	ACTGA	AAGA	CTAGG	CTCTA	TGCAT	TTCCA	AGAAG	CAAAAT	360
AGCCAG	CTAC	TAAAAG	AGAA	ATTAAA	AGAA	AGTGAC	AAGG	CAGCT	TATGG	AGTCAT	CAAG	420
TCCTTA	TATTGA	GTATGG	AATAC	CAATG	CTGAC	ATCTAT	GATC	AAACT	GCCTC	TACAT	TTTTT	480
CCTAAC	CGGAG	AAGCTA	TGTG	GAAAA	AAGAT	G	TAGA	AAGAT	C	TTAAAA	AAGGC	540
ATTTTC	TTGG	AATATT	ACAT	TATAGA	AAGAA	GGTTT	GATGT	GGAAT	CGCAT	ACTAGA	TATA	600
CTAGAG	CAAA	AGGTAG	CTCA	GGGTG	TAGAG	GTTAA	GATGC	TCTAT	GATGA	TATCG	GCTGT	660
ATGGCT	ACTT	TAACAG	GAGA	TTATG	CACAT	CGACT	TCGTC	AGCTG	GGCAT	CGAGG	CCCAT	720
AAATTCA	ATA	AAGTTA	TATCC	TCGTT	TGACA	GTGGC	TTATA	ATAAC	CAGAG	TCATAG	AAAA	780
ATATTGA	TG	TTGATG	GTCA	GATAG	CCTAT	ACTGG	TGGG	TCAAT	CTGGC	AGATGA	GTAC	840
ATTAACC	ACG	TCGAGA	GATT	TGGT	TATTG	AAGGA	TAGTG	GAATT	CGCTT	AGACG	GACTA	900
GCAGTA	AAAAG	CCCTGA	CACG	CTTAT	TTTTG	ACCACT	TGGT	ACATTA	ATCG	AGGAG	AAAT	960
AGTGAT	TTTG	ATCAAT	TATCA	TTTAG	AAAAAT	CATTCT	TATCC	CGAGT	GACGG	TTTAAC	CATT	1020
CCATAC	CGGAA	GTGGAC	CCAA	GCCAAT	TTTTT	CGAGC	GCAGG	TAGGG	AAAAAA	AGTTT	ATCAG	1080
AGTTTA	ATCA	ATCAAG	CAAC	AGAAT	CGGTC	TATATT	ACGA	CACCT	TATTT	GATTAT	AGAT	1140
TATGAT	TTAA	CAGAGA	CAAT	CAAAA	ATGCA	GCTAT	GAGAG	GGGTC	GATGT	TCGAAT	TATC	1200
ACCCCT	TACA	TACCAGA	TAA	GAAGT	TCATT	CAGTT	AGTCA	CGAGA	GGAGC	TTATC	CCGAC	1260
TTTCTT	TCTG	CTGGT	GTTCG	GATTT	ATGAG	TATAG	TCCAG	GTTT	TATTCA	TAGTA	AGCAG	1320
ATGTTG	GTAG	ACGAAG	ATTT	TGCGG	TGGTG	GGGAC	AATCA	ATCTC	GACTA	CCGGAG	CTTG	1380
GTACAC	CATT	ATGAAA	ATGC	AGTCT	TACTC	TATAAA	AACTC	CTTCT	AATAAG	GGAAAT	CGCC	1440
CGAGAT	TTTC	GAAAT	TATATT	TGCAG	ATTCT	CAGGA	AGTCT	ATCCT	CATTC	TATCA	AAACG	1500
AGCTGG	TATC	AAAAG	CTTGT	AAAAG	AAATC	GCCCAG	CTAT	TCGCCC	CTAT	CTTATA		1557

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

AAACTGGACT	ATAACTTATT	AGACTTCCTG	CGAAACAAAA	CATGGTATAG	TAGTTCTATG	60
AATTATGAAG	CAAGTAAACA	ACTAACCGAT	GCACGATTTA	AGCGTCTTGT	TGGTGTTTCAG	120
CGCACCACCTT	TTGAAGAGAT	GTTAGCTGTG	TTAAAAACAG	CTTATCAAAA	AAGTCGGACA	180
AGCTGGTAA						189

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

ATGATGGACT	ATCCTTATGC	TACCTGTTGC	TCTCTTAACG	ATGAAGTGGC	TCACGCTTTC	60
CCTCGTCATT	ATATCTTGAA	AGATGGTGAT	TTGCTCAAAG	TTGATATGGT	TTTGGGGAGG	120
TCCATTGCTA	AATCTGACCT	AAATGTCTCA	AAATTAAACT	TCAACAATGT	TGAACAAATG	180
AAAAAATACA	CTCAGAGCTA	TTCTGGTGGT	TTAGCAGACT	CATGTTGGGC	TTATGCTGTT	240
GGTACACCGT	CCGAAGAAGT	CAAAAACCTG	ATGGATGTAA	CCAAAGAAGC	TATGTACAAG	300
GGTATTGAGC	AAGCTGTTGT	TGGAAATCGT	ATCGGTGATA	TCGGTGCGGC	TATTCAAGAA	360
TACGCTGAAA	GTCGTGGTTA	CGGTGTAGTG	CGTGATTTGG	TTGGTCATGG	TGTTGGCCCA	420
ACTATGCACG	AAGAACCAAT	GGTTCCTAAC	TATGGTATTG	CAGGTCGTGG	ACTCCGTCTT	480
CGTGAAGGAA	TGGTCTTAAC	CATTGAACCA	ATGATCAATA	CAGGCGATTG	GGAAATTGAT	540
ACAGATATGA	AAACTGGTTG	GGCGCATAAG	ACCATTGACG	GTGGATTGTC	ATGTCAGTAT	600
GAACACCAAT	TTGTCATTAC	GAAAGATGGA	CCTGTTATCT	TGACTAGCCA	AGGTGAAGAA	660
GGAACCTATT	AA					672

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1332 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

ATGAAACGCT	ACCTTCAATT	TTGGCTAGTC	AATCTAAGTG	TTAGCCTCAT	TCTGATTGCA	60
GGGATGGCAT	TAACCTGGAT	CAGTAAAGGC	ATCGGTCTCT	TTCTTCTAGC	CCTTTCTTTG	120
GGACAAGGTG	GCTACTGGCT	CTTTTGCCCT	TGGAAATGGG	AAGTTGCTTT	TGAGACCTTG	180
CACCAACCTC	TCTTGACCAA	TAGTGAATAC	TTTTTAGAAA	AAGGGCAAGA	AGACTTAAAG	240
TCTTTGGCTC	AGTATGTGTC	TGCCCTAAAA	ACCAAAGTCT	CCCAACAGGA	TCAGCAATAC	300
AAGGACCTAC	CCGAAACAAT	GGAGGTTCTT	CTGTCGCACC	TAACCATGGG	GACGTTTTTA	360
GTTTCCGCTC	AAGGTCAGAT	GTTATTATCC	AGTCGCTCTC	TGCCTCATTA	TTTTCCCGAT	420
GTGGACGGCG	ACATAAGTTC	ACTTGATGAC	CTCAAACGGA	TGGATATTCG	AAATTTAGTT	480
CACCAAGCCT	TTGATCAAAA	AACAAGGTTA	AAACAAAAAG	TAAGTGGGTT	TCATGAGGGT	540
GACTTGATTT	TAGAAGTGAC	AGCAGTTCCC	GTTTTTAGCC	CCACCCAATC	TGTGGAAGCT	600
GTGCTCGTCT	TGCTATATGA	TTTAACAACG	ATTAGAACTT	ATGAAAAGTT	AAATTTAGCC	660
TTTGTCTCAA	ATGCCTCCCA	TGAATTGAGG	ACACCAGTTA	CTTCGATTAA	GGGCTTTGCT	720
GAAACCATTA	AGGGGATGTC	AGCTGAAGAA	GAAGCGCTCA	AGGATGACTT	TCTAGACATT	780
ATTTACAAAG	AAAGCTTGCG	TCTTGAGCAT	ATTGTTGAGC	ATCTTCTTAC	CTTATCTAAG	840
GCTCAACAAA	TGCCTATACA	ATGGACGACC	CTTTCTTTGG	CAGAATTTGT	ACAGGATTTG	900
ACTCAAAGCT	TGCAACCTCA	GCTCAAGAAG	AAGGATTTAC	AGCTAAAGGT	GCAGGTGCCA	960
GATGATGTCA	CCCTCGTATC	AGATAGTCAA	TTACTTTCCC	AAATCTTACT	CAATCTTTTA	1020
TCCAATGCCA	TCCGTTACAC	TGAACAAGGG	GGAAAAATTG	AGGTCAAGAC	CCAAAAGGTG	1080
AACGAAGGCA	TTAAGATTTT	TGTATCAGAT	ACAGGGATTG	GTATTAGTCA	ATTAGAGCAG	1140
GATCGTATTT	TTGAACGTTT	TTACCGAGTT	AATAAAGGTC	GAAGCAGACA	AACTGGTGCC	1200
ACTGGTCTTG	GCCTTGCCAT	TGTCAAAGAA	CTCAGTCAAT	TATTAGGTGG	CCAAGTCACG	1260
GTGACGAGTC	AGCTTGGCAG	AGGCAGTTGC	TTCACGATTT	TTCTTCCTAA	CCAATCTTTC	1320
GCACAGGACT	AA					1332

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 507 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

AATTTTGGCT	ATAACATCAC	GACCTGTAGT	TCCTCTTATA	GTCTAGGAGA	TTGGGTTGTG	60
ATTGGAGTCG	TTGCGAGAGA	GAATGCCGCA	GAGCAGATCA	AACAGTATCA	AAAATTTACT	120
GTGAATATTT	CTGATGAAAC	TTCTATGCTT	GCGATGGAGC	AGGCTGGTTT	TATCAGTCAT	180
CAGGAGAAAT	TGGAACGTTT	GGGAGTGCAT	TATGAAATTT	CTGAACGAAC	TCAGATTTCT	240
ATTTTAGACG	CCTGTCCACT	TGTTTTAGAT	TGTCGGGTAG	ATAGGATTGT	TGAGGAAGAC	300
GGTATTTGCC	ACATCTTTGC	CAAGATTCTT	GAGCGACTTG	TTGCCCCAGA	ATTCTTGGAT	360
GAAAAGGGAC	ATTTTAAAAA	TCAACTGTTT	GCCCCAACCT	ATTTTCATGGG	AGATGGATAT	420
CAGCGCGTTT	ATCGCTATCT	GGACAAGCGT	GATAGATATGA	AGGGCAGTTT	CATCAAAAAA	480
GCGAGGAAGA	AGGATGGCAA	GAAGTGA				507

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1800 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GCGAATTTAT	ATCTAAAAGG	GATATTAAAG	AAAGGAGATA	TGCTTATGAA	GATTTACAAA	60
AAACTATTTG	CTTATGTCCA	AGATAAGAAA	TATCTTGGGG	TTTTGGCCAT	AATTTTTTCT	120
GCTATATCTG	CTGCACTTAC	AGTATATGGA	TATTATTTAA	TCTACAAATT	TCTAGATAAG	180
TTAATAATTA	ATTCAAACCT	ATCCGGTGCA	GAGAGTATAG	CATTAATAATC	TGTTATTACA	240
CTAACAAAGTG	GAGCGATATT	TTATTTTGTC	TCAGGAATGT	TTTCACATAT	CTTGGGATTC	300
AGGCTTGAAA	CAAATTTAAG	AAAAAGGGGA	ATCGATGGTC	TGGAAAAAGC	AAGTTTTTAGG	360
TTCTTTGACT	TAAATCCATC	TGGTCAAATA	AGAAAGATTA	TAGATGACAA	TGCTGCACAA	420
ACTCATCAGG	TGGTAGCACA	CATGATTCCC	GATAGTTCTC	AGGCAATAAT	CACACCCGTA	480
CTTGTAATTG	CACTTGGCTT	TATAGTAAGT	ATAAGAGTTG	GCATAATTTT	GCTTGCTCTT	540
ACTATAATTG	GTGGCTTAAT	TTTAGGGGCA	ATGATGGGCG	AGCAAGAATT	TATGAAGATA	600
TACCAAGAAT	CCCTATCTAA	ACTAAGTGCT	GAAACTGTTG	AGTACGTGAG	AGGAATGCAA	660
GTTGTAAAAA	TATTTAAAGC	AAATGTAGAG	TCTTTTAAAA	GCTTTTATAA	GGCGATAAAA	720
GATTACTCAA	AGTATGCTTA	TGATTATTCC	CTATCTTGTA	AAAGGCCTTA	TGTTTTGTAT	780
CAATGGTTAT	TTTTTGGACT	GATTGCAATT	TTAATTATTC	CTATAGTTTA	TTTTATGACT	840
AGCTTAGCTA	GCGCAAAGGT	GATTTTACTT	GAGCTTATCA	TGATTTTATT	TTTATCAGGA	900

GTTCTCTTTG	TTTCATTCAT	GAGAATGATG	TGGTACTCCA	TGTATATTTT	TCAAGGAAAT	960
TATGCAGTAG	ATACTTTT	GGCGCTTTAC	GAAGATATGC	AAAAAGACAA	ATTAGTGCAT	1020
GGTAATGTCA	ATAATTTTAA	AAACTATAAT	ATAGAATTTG	AGAATGTTAG	CTTTGCTTAT	1080
AATGATAAAG	CTGTCAATTGA	AAATTTATCC	TTTAATTTAG	AAGAAGGAAA	GTCTACGCA	1140
CTTGTCGGTT	CATCTGGATC	AGGCAAATCA	ACAGTAGCAA	AACTTATATC	AGGTTTTTAC	1200
AATGTTAATA	AAGGAAGCAT	AAAGATAGGC	GGGATAGCAA	TAAGTGAATA	TTCTGACGAA	1260
GCCTTAATTA	AAGCCATTTT	CTTTGTTTTT	CAAGATTCAA	AATTATTCAA	GAAGAGCATT	1320
TATGATAATG	TAGCGTTAGC	TAATAAAGAT	GCGACGAAAG	ATGACGTTAT	GAGAGCCTTA	1380
AAATTAGCAG	GATGCGATTT	AATATTAGAC	AAATCCCAG	AAAGAGAAAA	TACAATCATA	1440
GGCTCAAAAG	GTGTTTATTT	ATCCGGTGGA	GAAAAACAAA	GAATTGCAAT	TGCTAGAGCA	1500
ATTTTAAAGG	ATTCCAAAAT	TATTATTATG	GATGAAGCAT	CAGCATCTAT	TGACCCAGAT	1560
AACGAGTTTG	AATTGCAAAA	AGCTTTTAAA	AATCTTATGA	AGGATAAAAC	AGTTATCATG	1620
ATTGCACACA	GGCTATCTAC	AATTAAAGAC	CTTGATGAAA	TTATTGTCAT	GGATAGTGGA	1680
AAAATTATAG	AAAGAGGGTC	TGACAAAGAA	TTAATGTCAA	AAGATACAAG	GTATAAGAGC	1740
CTGCAAGAGA	TGTTTAACAT	TGCGAATGAA	TGGAGGGTTT	CAAATGAAAG	AGTTTTATAA	1800

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

CGACTTTCTC	TGAAATATGG	TATGATAAAG	GATATACAAG	GAGATAAAAT	GAATAATAAT	60
TTACTGGTAT	TACAATCAGA	CTTTGGTCTG	GTTGATGGTG	CGGTATCGGC	TATGATTGGA	120
GTGGCTTTAG	AAGAGTCTCC	AACCTTAAAA	ATCCATCACT	TGACGCACGA	TATCACGCCT	180
TATAATATTT	TTGAGGGGAG	CTATCGTCTC	TTTCAGACGG	TGGATTACTG	GCCTGAGGGA	240
ACGACGTTTG	TATCGTTTGT	CGATCCAGGT	GTCGGTTCGA	AACGTAAGAG	TGTAGTTGCC	300
AAGACTGCAA	AAAATCAATA	CATTGTCACG	CCAGATAATG	GGACGCTTTC	CTTTATCAAG	360
AAACACGTTG	GCATTGTAGC	CATTCTGTAG	ATTTCTGAGG	TGGCCAATAG	GCGTCAAAAC	420
ACAGAGCATT	CTTATACCTT	CCACGGTCGT	GATGTCTATG	CCTATACTGG	TGCTAAACTG	480
GCCAGTGGTC	ACATTACTTT	TGAGGAAGTA	GGGCCAGAGC	TCAGTGTGGA	ACAGATTGTA	540
GAGCTTCCAG	TCGTAGCGAC	CATCATAGAA	GATCATCTGG	TGAAGGGAGC	CATTGATATT	600
CTGGATGTGC	GTTTCGGTTC	GCTTTGGACC	TCTATCACAC	GGGAAGAATT	TTACAAGCTG	660
GAACCAGAAAT	TTGGTGATCG	TTTTGAAGTG	ACCATCTATC	ATGCTGATAT	GCTGGTCTAT	720
CAAAATCAGG	TTGTCTATGG	CAAATCATTT	GCAGATGTGA	GAATTGGGCA	ACCCATCCTT	780
TACATCAACT	CTCTCTATCG	TTTAGGTTTG	GCTATCAACC	AAGGTTCCCT	TGCCAAGGCC	840
TATAATGTAG	GTGTCGGTTC	ATCTTGACC	ATTGAAATAA	AGAAAATAGA	AGGATAA	897

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

AGACTCTTAT ACCAGGAGAA AATTACCTAT CATGTTAAGG ATAATCAGCT AGAAGTAGAA	60
ACAGATAAAT ACACATATAC TGCCGCTAGA AATGGTAGTA AGGAAGTTGG TATTCAAGAG	120
TCAGATATAG CAGCAACTCT AAGTGCCGAT GAATATAATT CTAATCGCCA AACTTTTGAG	180
AGAGAATACA AATACAAAAG CAAATGCCCT TAA	213

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

TATAGCCTAT ATTATATAAA TAATCAATTG CGCAGAAATT TGGTAAGAAT TCATGCGTCA	60
ACTCATAAAG AACTACTTAA AAAATTCACA GTATTCATAA TTATTTTTCGA GGAGAAAAAC	120
AGTGAAAAAA AGAAAAAAGC TTGCTCTGTC TCTTATCGCT TTTTGGCTGA CGGCTTGTTT	180
AGTAGGCTGT GCTAG	195

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1806 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

AGTATACTAT	ATAAAGTAAA	CTATGATAAC	ATGGAGGTAT	TGTGTATGGT	TGACAAACAA	60
GTCATTGAAG	AAATCAAAAA	CAATGCCAAC	ATTGTGGAAG	TCATAGGAGA	TGTGATTTCT	120
TTACAAAAGG	CAGGACGGAA	CTATCTAGGG	CTCTGTCCCT	TTCATGGTGA	AAAAACACCT	180
TCTTTCAACG	TTGTAGAGGA	CAAGCAGTTT	TACCACTGTT	TTGGTTGTGG	TCGCTCAGGT	240
GATGTCTTTA	AATTCATCGA	GGAGTACCAA	GGGGTTACCT	TTATGGAGGC	TGTCCAAATC	300
TTAGGTCAGC	GTGTCGGGAT	TGAGGTTGAA	AAACCGCTTT	ATAGTGAACA	GAAGCCAGCC	360
TCGCCTCACC	AAGCTCTTTA	TGATATGCAC	GAAGATGCGG	CTAAATTTTA	CCATGCTATT	420
CTCATGACAA	CGACTATGGG	CGAAGAGGCC	AGAAATTACC	TTTATCAGCG	GGGTTTGACA	480
GATGAAGTGC	TTAAACATTT	TTGGATTGGT	TTAGCACCTC	CAGAACGAAA	CTATCTCTAT	540
CAACGTTTGT	CTGATCAGTA	TCGTGAAGAG	GATTTACTGG	ATTCAGGCCT	GTTTTATCTC	600
TCGGATGCCA	ATCAATTTGT	AGACACCTTT	CACAATCGCA	TTATGTTTCC	CCTGACAAAT	660
GACCAAGGAA	AGGTCATTGC	CTTCTCAGGT	CGTATCTGGC	AAAAAACGGA	TTCACAAACT	720
TCTAAGTATA	AAAACAGCCG	ATCGACTGCA	ATTTTTAACA	AAAGTTACGA	ATTATATCAT	780
ATGGATAGGG	CAAAAAATC	TTCTGGAAAA	GCTAGTGAGA	TTTACCTGAT	GGAAGGATTC	840
ATGGATGTTA	TTGCAGCCTA	TCGGGTGGA	ATCGAAAATG	CTGTGGCGTC	GATGGGAACG	900
GCCTTGAGTC	GAGAGCATGT	TGAGCATCTG	AAAAGGTTAA	CCAAGAAATT	GGTCTTGTT	960
TACGATGGAG	ATAAGGCTGG	GCAAGCCGCG	ATATTGAAAG	CATTGGATGA	AATTGGTGAT	1020
ATGCCTGTGC	AAATCGTCAG	CATGCCTGAT	AACTTGGATC	CTGATGAGTA	TCTACAAAAA	1080
AATGGTCCAG	AAGACTTGGC	CTATCTATTA	ACGAAAATC	GTATTAGTCC	GATTGAGTTC	1140
TACATTCATC	AGTACAAACC	TGAAAACAGT	GAAAATCTGC	AGGCTCAGAT	TGAGTTTATT	1200
GAAAAAATAG	CTCCCTTGAT	TGTTAAAGAA	AAGTCCATCG	CTGCTCAAAA	CAGCTATATT	1260
CATATTTTAG	CTGACAGTCT	GGCGTCCTTT	GATTATGCCC	AGATTGAGCA	GATTGTTAAT	1320
GAGAGTCGTC	AGGTGCAAAG	GCAGAATCGC	ATGGAAAGAA	TTTCCAGACC	AACGCCAATC	1380
ACCATGCCTG	TCACCAAGCA	GTTATCGGCT	ATTATGAGGG	CAGAAGCCCA	TCTACTCTAT	1440
CGGATGATGG	AATCCCCCTCT	TGTTTTGAAC	GATTACCGTT	TGCGAGAAGA	CTTTGCATTT	1500
GCTACACCTG	AATTTTCAGGT	CTTATATGAC	TTGCTTGGCC	AGTATGGAAA	TCTTCCTCCA	1560
GAAGTTTTAG	CAGAGCAGAC	AGAGGAAGTT	GAAAGAGCTT	GGTACCAAGT	TTTAGCTCAG	1620
GATTTGCCTG	CTGAGATATC	GCCGCAGGAA	CTTAGTGAAG	TAGAGATGAC	TCGAAACAAG	1680
GCTCTCTTGA	ATCAGGACAA	TATGAGAATC	AAAAAGAAGG	TGCAGGAAGC	TAGCCATGTA	1740
GGAGATACAG	ATACAGCCCT	AGAAGAATTG	GAACGTTTAA	TTTCCCAAAA	GAGAAGAATG	1800
GAGTAA						1806

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

CTTTGTATAT	ACTTTGTTAT	TCTTTTCTCA	TTAATAGTGT	CTAATGCACT	AGTTGCTTCA	60
TCTAAATA	CAATACTAGG	ATTATTTATT	AATGCACGTG	CCAGTGCTAT	CCGTTGCCTT	120
TGCCCACCTG	AAATATTTGA	CCCCATCTCT	GAGATGATAG	TATTAAATTT	CATCGGCATA	180
GCCATGATTT	CATCATAG					198

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

AGGTCCTCTC	TTAACAGTCA	ATTTGCTCAC	ATTTTtaggg	CAACTTCTTA	TTTTTCTGAT	60
TGGATTTGGA	CTTGTGGCCA	CAATTTTACG	AAGAAGTTTA	GTCAAGATTC	TCCTAAAATG	120
AAAATGGGCA	CTTACATTGT	TGTTGGGACT	ATAGTTCTTC	TAGTTGTTTT	AGGATATGTA	180
GGATTGGCAA	GCTACATACA	AGAAGGAGCC	TTTTATATTC	CGGCTCCCTG	GGATAGTTTG	240
TCTGTCTTTA	CGATTTGCT	AGTTATCGGT	ATTTGGAGTT	GGAAAGAAGC	GGTCTTTTCGT	300
CCCTTTGTCA	GTATGATTAT	TGCCCATCTT	GTGGTGGGTT	CTCTGCTCCG	TTATTATGAG	360
TGGATGGGAA	TTTCAAATGT	TTTCCTTACA	AAAGTTATTC	CTTTAGCTGT	CCTCTTTTATT	420
GGAATCTTTG	TCTTGTTCCG	TGGGTTTAAAG	AAGATAAAAT	GGAGTGAAGT	ATAG	474

(2) INFORMATION FOR SEQ ID NO:586:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

AAAGTGATAT ACTATATGGA TACAAAAATG ATGTCACAAT TTTCTGTTAT GGATAATGAA	60
ATGCTTGTTT GTACAGAGGA TGGGGATGTC TCTGATATTT ATAGAGGGTA CGCTAATCAG	120
AGAAGTCCAT TCGCTTCTTA CCCTTCTATA TTAAAAAATT CAGGTCCTTT TCCAGTAAGT	180
GGGTACTGCC TGGTGGTTA TCATGACCGT GGTATATATAG GAGCAGGTTT TCATTTATGT	240
GGAATATAG	249

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2589
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GATACAGTAT ACAGTTTTTC CTTTTNACAC ATTTCAAATT CTTTCAAAAA TGGTATAATA	60
GTAACATCAC AAAATTGGAG AGAGACCATG AGTTTTTACA ATCATAAAGA AATTGAGCCT	120
AAGTGGCAGG GCTACTGNAC AGAACATCAT ACATNTAAGA CAGGAACAGA TGCATCAAAA	180
CCTAAGTTTT ATGCGCTTGA TATGTTCCCT TATCCGTCTG GAGCTGGTCT GCACGTAGGA	240
CACCCAGAAG GTTATACTGC AACCGATATC CTCAGTCGTT ACAAACGTGC GCAAGGCTAC	300
AATGTCCTTC ACCCAATGGG TTGGGATGCT TTTGGTTTGC CTGCAGAGCA ATACGCTATG	360
GATACTGGTA ATGACCCAGC AGAATTTTACA GCGGAAAACA TTGCCAACTT CAAACGTCAA	420

ATCAATGCGC	TTGGATTTTC	TTATGACTGG	GATCGTGAAG	TCAATACAAC	AGATCCAAAC	480
TACTACAAGT	GGACTCAATG	GATTTTCACC	AAGCTTTACG	AAAAAGGCTT	GGCCTATGAA	540
GCTGAAGTGC	CAGTAAACTG	GGTTGAGGAA	TTGGGAACTG	CCATTGCCAA	TGAAGAAGTG	600
CTTCCTGACG	GAACCTCTGA	GCGTGGAGGC	TATCCAGTTG	TCCGCAAACC	AATGCGCCAA	660
TGGATGCTCA	AAATCACGGC	TTACGCAGAG	CGCTTGCTCA	ATGACTTAGA	TGAAC TAGAT	720
TGGTCAGAGT	CTATCAAGGA	TATGCAACGC	AACCTGGATTG	GTAAATCAAC	TGGTGCCAAT	780
GTAAC TTTCA	AAGTAAAAGG	AACAGACAAG	GAATTTACAG	TCTTTACTAC	TCGTCCGGAC	840
ACACTTTTCG	GTGCGACTTT	CACTGTCTTG	GCTCCTGAAC	ATGAATTAGT	AGACGCTATC	900
ACAAGTTCAG	AGCAAGCAGA	AGCTGTAGCA	GACTATAAAC	ACCAAGCCAG	CCTTAAGTCT	960
GACTTG GCTC	GTACAGACCT	TGCTAAGGAA	AAAAC TGGTG	TTTGGACAGG	TGCCTATGCC	1020
ATCAACCCTG	TCAATGGTAA	GGAAATGCCA	ATCTGGATTG	CGGACTATGT	TCTTGCTAGT	1080
TATGGAACAG	GTGCGGTTAT	GGCTGTGCCT	GCCCACGACC	AACGTGACTG	GGAATTTGCC	1140
AAACAATTTG	ACCTTCCAAT	CGTCGAAGTA	CTTGAAGGTG	GAGATGTCAA	AGAAGCTGCC	1200
TACACAGAGG	ATGGCCTGCA	TGTCAATTCA	GACTTCCTAG	ATGAACTCAA	CAAAGAAGAC	1260
GCTATTGCCA	AGATTGTGGC	TTGGTTGGAA	GAAAAAGGCT	GTGGTCAGGA	GAAGGTTACC	1320
TACCGTCTCC	GCGACTGGCT	CTTTAGCCGT	CAACGTTACT	GGGGTGAGCC	AATTCCAATC	1380
ATTCATTGGG	AAGATGGAAC	TTCAACAGCT	GTTCCCTGAAA	CTGAATTGCC	GCTTGTCTTG	1440
CCTGTAACCA	AGGATATCCG	TCCTTCAGGT	ACTGGTGAAA	GTCCACTAGC	TAAC TTGACA	1500
GATTGGCTTG	AAGTGACTCG	TGAAGATGGT	GTCAAAGGTC	GTCTGTGAAAC	TAACACCATG	1560
CCACAATGGG	CTGGTTCAAG	CTGGTACTAC	CTCCGCTATA	TTGACCCGCA	CAATACTGAG	1620
AAATTGGCTG	ATGAGGACCT	CCTCAAACAA	TGGTTGCCAG	TAGATATCTA	CGTGGGTGGT	1680
GCGGAACATG	CTGTACTTCA	CTTGCTTTAT	GCTCGTTTCT	GGCATAAAT	TCTCTATGAC	1740
CTCGGTGTTG	TTCCGACTAA	GGAACCATTC	CAAAAAC TCT	TTAACCAAGG	GATGATTTTG	1800
GGAACAAGCT	ACCGTGACCA	CCGTGGTGCT	CTTGTGGCAA	CCGACAAGGT	TGAAAAACGT	1860
GATGGTTCCT	TCTTTCATAT	AGAAACAGGG	GAAGAGTTGG	AGCAAGCGCC	AGCCAAGATG	1920
TCTAAATCGC	TCAAGAACGT	TGTTAACCCA	GATGATGTGG	TGGAACAATA	CGGTGCCGAT	1980
ACCCTTCGTG	TTTATGAAAT	GTTTATGGGA	CCACTCGATG	CTTCGATTGC	TTGGTCAGAA	2040
GAAGGTTTGG	AAGGAAGCCG	TAAGTTCCTT	GACCGAGTTT	ACCGTTTGAT	TACAAGTAAA	2100
GAAATCCTTG	CGGAAAACAA	TGGTGCTCTT	GACAAGGCTT	ACAACGAAAC	AGTCAAAGCT	2160
GTTACTGAGC	AAATTGAGTC	TCTCAAATTC	AACACAGCTA	TTGCCCAACT	TATGGTCTTT	2220
GTCAATGCTG	CTAACAAGGA	AGATAAGCTT	TATGTTGACT	ATGCCAAAGG	CTTTATTCAA	2280
TTGATTGCAC	CATTTGCACC	TCACTTGGCA	GAAGAACTCT	GGCAAACAGT	CGCAGAAACA	2340
GGTGAGTCAA	TCTCTTATGT	AGCTTGGCCA	ACTTGGGACG	AAAGTAAACT	GGTTGAAGAC	2400
GAAATCGAAA	TCGTTGTCCA	AATCAAAGGT	AAAGTCCGTG	CCAAACTCAT	GGTCGCTAAA	2460
GACCTATCAC	GTGAAGAAAT	GCAAGAAAT	GCTCTAGCGG	ATGAAAAAGT	CAAAGCAGAA	2520
ATTGACGGTA	AGGAAATCGT	GAAAGTGATT	AGTGTAACCA	ATAAATTTGGT	TAATATTGTT	2580
GTAAAAATAA						2589

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

CCATCATCTC	TTGTTTTTTT	GTGGTACAAT	AGAGCTATGA	AACATTTTGA	TACTATTGTC	60
ATCGGTGGGG	GACCTGCTGG	TATGATGGCT	ACGATTTCCA	GTAACTTTTA	TGGACAGAAA	120
ACCCTCCTCA	TCGAAAAAAA	TCGGAAACTT	GGAAAAAAAT	TAGCTGGGAC	TGGTGGGGGA	180
CGTTGCAATG	TGACCAACAA	TGGTAGCTTA	GACAACCTGC	TAGCTGGAAT	TCCTGGAAAC	240
GGACGCTTTC	TTTACAGTGT	TTTCTCCCAG	TTCGATAATC	ATGACATCAT	CAACTTTTTT	300
ACAGAAAAATG	GTGTTAAACT	TAAGGTCGAA	GACCACGGAC	GCGTCTTTCC	AGCCAGTGAC	360
AAGTCTCGGA	CTATTATCGA	AGCTTTGGAA	AAGAAAATCA	CTGAAC TAGG	TGGTCAAGTT	420
GCTACTCAAA	TAGAAATCGT	TTCTGT TAAA	AAAGTAGATG	ACCAGTTTGT	CCTTAAGTCA	480
GCGGATCAAA	CCTTCACTTG	TGAGAAACTC	ATTGTCACAA	CAGGTGGTAA	GTCTTATCCT	540
TCGACTGGTT	CGACTGGTTT	TGGTCACGAG	ATTGCTCGCC	ATTTTAAGCA	TACCATCACC	600
GATCTTGAGG	CTGCTGAAAG	TCCTTTATTA	ACAGATTTTC	CACATAAAGC	CTTACAAGGG	660
ATTTCTCTGG	ACGATGTGAC	CCTAAGTTAT	GGTAAGCATG	TCATCACTCA	TGATTTACTC	720
TTTACCCACT	TTGGTTTGTG	AGGTCCTGCT	GCCCTACGCA	TGTCTAGCTT	TGTCAAAGGT	780
GGGGAGGTTT	TCTCACTCGA	TGTTTTGCCT	CAACTTTC TG	AGAAGGACTT	GGTTACATTT	840
CTAGAAGAAA	ATCGGGAAAA	ATCCTTGAAA	AACGCTTTAA	AAACCTTGTT	ACCAGAACGC	900
TTGGCCGAAT	TTTTTGTACA	AGGATATCCT	GAAAAAGTCA	AACAGCTGAC	TGAAAAGGAA	960
CGAGAACAAC	TTGTCCAGTC	CATTAAAGAA	CTTAAAATTC	CTGTAACTGG	AAAAATGTCC	1020
CTTGCAAAGT	CCTTTGTTAC	CAAGGGTGGA	GTCAGTCTCA	AGGAAATCAA	TCCTAAAACC	1080
CTTGAAAAGTA	AGCTGGTACC	TGGCCTCCAC	TTTGCAGGCG	AAGTTATGGA	TATCAATGCC	1140
CACACGGGTG	GCTTTAACAT	CACTTCTGCC	CTCTGTACCG	GCTGGGTGGC	GGGAAGTCTG	1200
CATTATGATT	AA					1212

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

AAGAAATCTC	TAAATAAAGA	GGATACAATA	ATGGACATCT	GGGAAAAGAT	GTACGAAGAA	60
GCACAGAAAC	TATACAATCC	ACATGAAGTA	TCAGACTTTG	TTTATGCCAA	TCATGTTGTA	120
GCTGCAGTAG	AAGCAGAAGA	TGGACAAATA	TTTACAGGAT	TCTGTATGGA	GGGAACCTGT	180
GGTGTTTTCC	ATCTCTGCGC	AGAACGGGCG	GCCCTCTTCA	ATATGTACCA	ATTTTCAGGA	240
CAAAC TAAGG	TTAAGAAAGT	ATTAGCCTTT	CGAGACAAAC	CACCTTATGG	TGGAAGTTCA	300
GCCATGCCTT	GCGGTGCTTG	TAGAGAATTC	CTTTTAGAGC	TTAATGCTGA	AAATAAAGAT	360
GCAGAATTCA	TGATGGACTA	TAATATAAGA	AAAACAGTTA	AAGTCGCAGA	ACTAATCCCT	420

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

TTGATTTTCAT ATCACTGTTA TATAATGCTT NTTGATTNTA GTTTAGTATT AGTAAGCAGA	60
CTCAAAACTT TAGAAAATCT TTTGAGATCA TTGACAGGTG TATCGAATCC TACCACAGAT	120
TCAGCACGTC TGGTTTTGGC AGAGGCTAAG AAAGCTTTTG CAGATGATAG TTTGACAGAG	180
CAAGGTTTAC GTGATATCTT GCAAACAGTC AAAGATGCCA TTGCTTCCCT AGAGTCCATT	240
AAGGAAAGCC AGTCAGCAAC TAAGGATGGA GGACAAACAG CGGGCAAAGA AACAGCAGAT	300
AAGGATGTCC TTGAAAACCT TCAAGAAGAA CTTCAAAAAG CAGTTTTGTT CTTGGCAGAT	360
GAAAAAGGCT CTGAGCATAC TGAAGCAGAG TTGATTGATA ATCTTAAAGA GGTATTGCT	420
AAGTTGAAAG CAAACGCCTA A	441

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

AGTTGTTTCAT ATCTTATTTT AATTTACTAT AGTACAAAAC TAGAAAAGGA AAAAATCATG	60
ACCAAAACAA TTCTTGTTAC AGGTGGGACT AGCTACATTG GCTCCCATAC CGTTAAAGCT	120
CTTTTAAATG CTGGCTATCA GGTGCATGTC CTCGATAATC TCTCCACAGG AAATCGAGCG	180
GCTGTGGATA GTCGTGCTAG CTTTAAAGAA CTGGATGTTT ATGATGCTAG CGCCTTAAAA	240
GCTTACTTAA AAAAAAATCA AATTGATGCT GTCTTCCCTT TTCCAGTTGA AATTTTTTGA	300

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

AACGCATCAT ATCAAGCACG AAAATTCCAC GAGGTCAACT ACAGTCAGAA AGCTGAACAA	60
CAAGCCAAAA CGCCCAAAAA AGGCGGCAAA AAGCAAGCAC CTGCAAGCAA CGTGCCGAAA	120
TGGTCAAATC CTGATTATGT CAACGAATTA GACCCAAAAA TCGTTGATAT GCTAGTAGAA	180
TTTCACAAGT CACAAGGCAC TTTGGAAACT CCCGAGGCGC AAGCAGAAAT CGCCCAAAAA	240
CGTGAAGAAA TCGAGCAAAG GAGAGCTGAG CTTGAGGGTA AAAACAAGA GCTTTTGAAC	300
CGCTTGAACA AATAG	315

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

TTTATGTCTC	TTCAAAAATT	AGAAAATTAT	AGTAATAAAA	GTGTTGTGCA	AGAAGAAGTC	60
TTGATTCTAA	CAGAATTACT	GGAAGATATT	ACTAAAAATA	TGCTTGCCCC	AGAGACCTTT	120
GAAAAAATAA	TACAGTTGAA	AGAATTATCA	ACGCAGGAAG	ATTATCAAGG	TCTAAACCGT	180
CTAGTGACTA	GCTTATCAAA	TGATGAAATG	GTCTATATTT	CACGCTATTT	CTCTATCTTG	240
CCTCTTTTGA	TTAATATTTT	AGAGGATGTG	GATTTAGCTT	ATGAAATCAA	TCATCAAAAT	300
AATATTGATC	AGGACTATTT	AGGTAAATTA	TCTACAACGA	TTAAATTGGT	AGCAGAAAAG	360
GAAAAATGCCG	TTGAGATCCT	AGAACACTTG	AATGTTGTCC	CTGTTTTGAC	AGCCCATCCA	420
ACACAAGTGC	AACGCAAAAG	TATGTTGGAT	TTAACAAATC	ATATTCATAG	TCTTTTGCCT	480
AAATACCGTG	ATGTTAAGTT	GGGGTTGATC	AATAAAGATA	AATGGTACAA	TGATTTGCGT	540
CGTTACATCG	AAATTATCAT	GCAGACAGAC	ATGATTCTGT	AGAAAAAATT	AAAAGTGAAT	600
AACGAAATCA	CGAATGCTAT	GGAATATTAT	AACAGCTCCT	TTTTGAAAGC	TGTACCTCAT	660
TTGACGACGG	AGTATAAGCG	CTTAGCGCAA	GCGCATGGTC	TGAATTTAAA	ACAGGCTAAA	720
CCAATCACCA	TGGGTATGTG	GATAGGTGGT	GACCGTGATG	GAAATCCATT	TGTTACAGCA	780
AAGACCTTGA	AGCAGTCTGC	ACTCACTCAG	TGTGAAGTCA	TCATGAAC TA	CTATGATAAA	840
AAGATTTACC	AAC TTTATCG	TGAATTTTCT	CTTTCAACTA	GCATTGTCAA	CGTCAGCAAG	900
CAAGTCAGAG	AAATGGCTCG	TCAATCCAAG	GATAACTCTA	TTTACCGCGA	AAAAGAGCTT	960
TACCGTCGTG	CCTTGTTTGA	TATTC AATCA	AAAATTCAGG	CAACTAAAAC	CTATCTGATT	1020
GAGGATGAAG	AAGTTGGGAC	TCGTTATGAA	ACCGCCAATG	ATTTCTACAA	GGATTTGATT	1080
GCCATTTCGAG	ATTCTCTACT	AGAAAATAAG	GGTGAGTCCT	TGATTTTCAGG	TGATTTTGTG	1140
GAATTATTGC	AGGCAGTAGA	GATATTTGGT	TTTTACTTAG	CGTCAATTGA	TATGCGACAA	1200
GACTCTAGCG	TCTATGAAGC	CTGTGTGGCA	GAAC TCTTGA	AATCAGCAGG	AATTCATTCT	1260
CGTTATAGCG	AGTTGAGCGA	AGAAGAAAAG	TGTGACCTTC	TCTTGAAAGA	ATTAGAAAGA	1320
GATCCCCGAA	TTCTTTCTGC	GACTCACGCA	GAAAAATCAG	AATTATTAGC	AAAAGAATTA	1380
GCTATTTTGA	AGACGGCTCG	TGTTTTGAAA	GATAAGTTGG	GAGATGATGT	CATCCGTCAG	1440
ACCATCATTT	CACATGCAAC	CAGCCTTTCT	GATATGCTAG	AATTAGCTAT	TCTGTTAAAA	1500
GAAGTAGGAC	TGGTGGATAC	GGAAAGGGCG	CGTGTTCAGA	TTGTTCCCCCT	TTTTGAAACA	1560
ATTGAAGACT	TGGATCATTC	AGAGGAAACA	ATGAGAAAAT	ATCTTTCTCT	TAGCCTTGCC	1620
AAAAAATGGA	TTGACTCACG	AAATAACTAC	CAAGAAATCA	TGCTTGGCTA	CTCTGACAGT	1680
AATAAAGATG	GCGGTTACTT	GTCATCATGT	TGGACCCTCT	ACAAGGCTCA	ACAACAATTG	1740
ACTGCTATTG	GAGATGAATT	TGGCGTTAAG	GTTACCTTCT	TCCATGGTCG	TGGTGGTACT	1800
GTGCGTCGTG	GTGGTGGGCC	AACCTATGAA	GCCATTACAT	CTCAACCGCT	CAAGTCTATC	1860
AAGGATCGTA	TCCGCTTGAC	GGAGCAGGGT	GAAGTAATTG	GGAATAAATA	CGGTAACAAA	1920
GACGCCGCTT	ACTATAACCT	TGAAATGCTA	GTATCGGCAG	CTATTAACCG	TATGATTACT	1980
CAGAAGAAGA	GCGATACCAA	TACCCCAAAT	CGTTATGAAG	CCATTATGGA	TCAAGTAGTG	2040
GACCGTAGTT	ACGACGCTA	CCGTGATTTG	GTCTTTGGTA	ATGAGCATT	CTATGATTAT	2100
GTCTTCGAGT	CAAGTCCAAT	CAAGGCTATT	TCAAGTTTGA	ATATTGGTTC	TCGTCCAGCC	2160
GCTCGTAAGA	CTATTACTGA	AATCGGTGGA	TTGCGTGCCA	TCCCTTGGGT	ATTCTCATGG	2220
TCACAGAGTC	GTGTTATGTT	CCCTGGATGG	TACGGGGTTG	GTTCAAGCTT	CAAGGAATTT	2280
ATCAATAAAA	ATCCAGAGAA	TATTGCTATC	TTACGAGATA	TGTACCAAAA	TTGGCCTTTC	2340
TTCCAATCGC	TTCTTTCAAA	TGTTGATATG	GTTTTGTCAA	AATCAAATAT	GAATATTGCT	2400
TTTGAATATG	CTAAACTTTG	TGAAGACGAG	CAAGTTAAGG	CCATCTATGA	GACTATTTTA	2460
AATGAATGGC	AAGTTACTAA	GAACGTTATC	TTGGCTATTG	AAGGACATGA	CGAACTCTTA	2520
GCTGACAATC	CATATCTAAA	AGCTAGTCTG	GATTACCGTA	TGCCTTACTT	TAATATTCTC	2580
AACTATATTC	AGTTGGAGTT	GATTAAACGC	CAACGTCGTG	GAGAATTGTC	CAGTGATCAA	2640
GAACGATTGA	TTCATATCAC	CATCAACGGA	ATTGCGACAG	GATTGCGTAA	TTCAGGTTGA	2700

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1446
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

AAAATGACAT	ACGAAGTAAA	ATCTCTTAAT	GAAGAATGTG	GTGTTTTTCGG	TATTTGGGGA	60
CATCCAGATG	CTGCTAAGTT	GACCTATTTT	GGACTCCACA	GTCTTCAACA	CCGTGGTCAG	120
GAGGGGGCAG	GAATCCTCTC	CAACGATCAA	GGACAACTGA	AGCGCCATCG	TGACATGGGG	180
CTTTTATCAG	AAGTTTTTCAG	AAATCCAGCT	AATTTGGATA	AATTGACAGG	AGCTGGTGCG	240
ATTGGGCATG	TGCGTTATGC	GACTGCTGGC	GAAGCTTCTG	TAGATAACAT	CCAGCCCTTC	300
CTCTTCCGTT	TTCACGATAT	GCAGTTTGGC	TTGGCTCATA	ATGGAAATCT	GACCAATGCA	360
GCCTCTCTCA	AGAAAGAAAT	GGAACAAAGA	GGAGCAATTT	TCAGCGCGAC	TTCGGACTCT	420
GAAATCTTGG	CTCACCTCAT	TCGTGCGAGT	CATAATCCTA	GCCTGATGGG	CAAAATCAAG	480
GAAGCGCTCA	GCCTTGTCAA	AGGTGGTTTT	GCCTATATCT	TGCTGTTTGA	GAACAAGTTG	540
ATTGCGGCTC	TTGACCCTAA	TGGCTTTCGT	CCGCTTTCTA	TCGGGAAAAT	GGCCAACGGA	600
GCGGTGGTTG	TTTCCTCTGA	AACCTGTGCT	TTTGAGGTCA	TTGGTGCCGA	GTGGATTTCGT	660
GATTTGAAGC	CAGGTGAGAT	TGTGATCATT	GATGACGAGG	GCATTCAAGTA	TGACAGCTAT	720
ACAGATGATA	CCCGATTGGC	GATTTGTTCT	ATGGAGTATA	TCTACTTTGC	CCGCCCTGAT	780
TCTAATATCC	ACGGTGTCAA	TGTCCATACG	GCACGTAAGA	GAATGGGAGC	GCAATTGGCG	840
CGAGAATTTA	AGCATGAGGC	AGATATTGTA	GTTGGTGTGC	CCAATTCCTC	CCTAAGCGCG	900
GCTATGGGAT	TTGCGGAAGA	ATCAGGCTTA	CCAAATGAAA	TGGGTCTGAT	CAAAAACCAA	960
TACACCCAGC	GAACTTTTAT	CCAACCGACT	CAAGAATTGC	GGGAGCAAGG	AGTGCGGATG	1020
AAACTGTCTG	CTGTTTCGGG	TGTTGTCAAA	GGCAAACGTG	TGGTCATGGT	GGATGATTCC	1080
ATTGTACGTG	GAACAACCTC	TCGTCTGATC	GTTTCAGCTCT	TGAAAGAAGC	GGGTGCGACT	1140
GAGGTTACAG	TTGCCATTGG	AAGTCCTGCA	CTAGCGTATC	CATGTTTCTA	CGGGATTGAT	1200
ATCCAGACCC	GTCAGGAGCT	GATTGCAGCC	AATCATAACG	TCGAAGAAAC	TCGCCAAATC	1260
ATTGGTGCGG	ACAGTCTGAC	TTATCTTTCA	ATTGATAGCT	TGATTGAGTC	GATTGGTATC	1320
GAAACAGATG	CGCCGAACGG	TGGTCTCTGT	GTCGCTTACT	TTGACGGTGA	CTACCCAACG	1380
CCTCTCTATG	ACTACGAAGA	AGACTATCGT	AGAAGTTTGG	AAGAAAAGAC	CAGTTTTTTAC	1440
AAGTAG						1446

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GCCTGGACAT ATCCAAAGGG CAACAAC TTC ACTACTGTGT TCCTAAGGGC ACTATTTGGG	60
GATCAACAGT TGATAAGGAT TATGCTCTGG TTTCTTGTCT TGTTGCTCCT GGTTTTGAAT	120
GTTGAGGATT TTGAATTATT TGAAAGGGTA GATCTNACTG GCGACCTATC CAGAGCACAA	180
GGAGATGATT GA	192

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

AGCATGGCAT ATCAGGAACC AAATAAAGAT GGATTTTACG GAAAATTCGG CGGACGTTTT	60
GTCCCAGAAA CATTGATGAC AGCAGTTTTG GAGTTGGAGA AGGCCTACCG TGAAAGTCAG	120
GCAGACCCAA GTTTCCAAGA GGAATTAAAC CAACTTTTGC GCCAGTACGT GGGACGTGAA	180
ACTCCCTTT ACTACGCAA AAACCTTGACC CAGCATATCG GCGGAGCCAA GATTTATCTC	240
AAACGGGAAG ACCTTAACCA TACAGGAGCC CACAAGATTA ACAATGCCTT AGGACAAGTT	300
TGGCTTGCCA AACGCATGGG TAAAAAGAAA ATTATCGCAG AAACGGGTGC TGGTCAGCAC	360
GGTGTGGCAA CTGCAACTGC TCGGCCCTC TTTAACATGG AATGTACCAT CTACATGGGT	420
GAGGAAGATG TCAAACGCC AGCCCTCAAT GTCTTCCGTA TGGAGCTTTT GGGAGCTAAG	480
GTCGAGGCCG TGACAGATGG TTCGCGCGTG CTCAAGGATG CGGTCAATGC AGCCCTTCGT	540
TCATGGGTGG CTAATATCGA TGATACCCAC TATATCCTTG GTTCTGCCTT GGGGCCTCAT	600
CCATTTCAG AAATTGTTTCG TGA CTTCCTCA AGTGTCATTG GTCGAGAGGC TAAACAACAG	660
TACCGTGACT TGACAGGACA AAATCTGCCA GATGCCCTAG TAGCCTGTGT TGGTGGTGGG	720
TCGAATGCCA TCGGTCTCTT CCATCCCTTT GTAGAAGATG AGTCAGTAGC CATGTATGGA	780
GCTGAAGCGG CTGGACTTGG TGTGGATACG GAGCACCACG CAGCTACCTT GACCAAGGGT	840
CGTCCAGGTG TCCTTCACGG TTCCCTCATG GATGTGCTCC AAGATGCCCA TGGTCAAATT	900
CTTGAAGCCT TCTCTATCTC AGCAGGTTTG GACTATCCTG GTATCGGTCC AGAGCATTCT	960
CACTACCACG ATATCAAACG TGCCAGCTAT GTCCCTGTGA CAGACGAAGA AGCTTTGGAA	1020
GGATTTCAAC TCTTGCTCTG TGTGGAAGGG ATTATCCCAG CCTTGGAATC TAGCCATGCT	1080
ATCGCCTTTG CGGTGAAATT GGCCAAAGAA CTTGGACCAG AAAAGTCTAT GATTGTCTGC	1140
CTATCAGGTC GTGGGGACAA GGATGTGGTT CAAGTCAAAG ACCGCTTGGA AGCAGATGCA	1200
GCAAAGAAGG GAGAAGCTCA TGCCTAA	1227

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...290
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TCGCTAAATA	CGAAATTCTT	TATATCATTC	GTCCAAACAT	TGAAGAAGAA	GCTAAAAACG	60
CTTTGGTAGC	ACGTTTGTAC	TCTATTTTGA	CTGACAACGG	TGCAACTGTT	GTTGAATCAA	120
AAACTTGGGA	AAAACGTCGT	CTTGCATACG	AAATCCAAGA	TTTCCGTGAA	GGACTTTACC	180
ACATCGTTAA	CGTTGAAGCA	AATGACGATG	CAGCTCTTAA	AGAGTTTGAC	CGTCTTTCAA	240
AAATCAACGC	TGACATTCTT	CGTCACATGA	TCGTCAAAAT	TGACGCGTAA		290

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

CAAATAAAAT	ATGCCGAGGG	TTACCCAGGA	CGCCGTTATT	ATGGTGGAAC	TGATGTAGTA	60
GACGTTGTAG	AGACTCTTGC	TATTGAACGC	GCAAAAGAAA	TTTTCGGTGC	TAAATTTGCC	120

AATGTCCAAC	CACATTCAGG	AAGCCAAGCT	AACTGTGCGG	CTTACATGTC	CTTGATTGAG	180
CCAGGTGATA	CGGTTATGGG	AATGGATTTG	GCAGCAGGTG	GACACTTGAC	CCACGGAGCT	240
CCAGTTAGCT	TCTCTGGTCA	AACCTACAAC	TTTCTTTCCCT	ATAGTGTGGA	TCCTGAAACG	300
GAACTTTTGG	ACTTTGATGC	TATCTTGAAA	CAAGCCCAAG	AAGTAAAACC	AAAACGTATT	360
GTAGCTGGTG	CTTCAGCCTA	TTCTCAAATT	ATTGACTTTT	CAAAATTCCG	TGAAATTGCA	420
GATGCTGTTG	GGGCTAAGCT	TATGGTTGAT	ATGGCCCA	TCGCTGGCTT	GGTTGCAGCT	480
GGTCTTCACC	CAAGCCCAGT	GCCATACGCT	CATATCACTA	CAACAACGAC	CCACAAAACC	540
CTTCGTGGTC	CTCGTGGTGG	TTTGATTTTG	ACCAATGATG	AGGATTTAGC	TAAGAAAATC	600
AATTCAGCTA	TTTTCCCTGG	TATTCAGGGT	GGTCCTTTGG	AGCATGTTGT	GGCTGCTAAG	660
GCAGTTTCCT	TCAAAGAAGT	TTTGGATCCA	GCTTTCAAGG	AATATGCTGC	CAATGTAATT	720
AAGAACAGCA	AGGCTATGGC	AGATGTCTTC	TTGCAAGACC	CTGATTTCCG	TATTATTTCA	780
GGTGGAACTG	AAAACCATCT	CTTCCTTGTT	GATGTGACTA	AGGTTGTAGA	AAACGGAAAA	840
GTTGCTCAAA	ACTTGCTGGA	TGAAGTCAAT	ATTACCCTAA	ATAAAAATTC	AATCCCTTAC	900
GAAACCTTGT	CACCATTCAA	GACAAGTGGG	ATTCTGATCG	GAGCAGCAGC	TATTACTGCA	960
CGTGGATTTG	GTGAAGAAGA	AAGTCGCAAA	GTGGCTGAAC	TCATCATTA	AACCCTTAAG	1020
AATTCAGAAA	ATGAGGCTGT	ATTAGAAGAA	GTGAGAAGTG	CAGTCAAAGA	ATTGACAGAT	1080
GCCTTCCCAT	TATACGAGGA	ATAA				1104

(2) INFORMATION FOR SEQ ID NO:599:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

TCAAAAAAAT	ATGCTATTAT	GTTAAAAAAA	TATTTTTTCAA	AATATAAATG	GACGGATTTA	60
TTTTGGATTT	TATTTGTTAT	TTTGACCTGT	CTCTATATTG	GTAACCATGA	TTTGTTTACT	120
CTCAATCATC	AAGAATTCTC	TTTTCTGGGT	AGCGTTTGGG	GTCTGGTACT	GGCCTTATAT	180
CACTTACTAT	TCATTGATAA	GTTTGTTTATA	TCGAATCGAA	AATAA		225

(2) INFORMATION FOR SEQ ID NO:600:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GTTGAAAAAT	ACCTTGTC	CAAC	GTCACCACAC	CGTAATCAAG	ATCTAGATTT	GGCTTACCTG	60
CGTTCAGGAA	TCGCGGATTT	AGGACACCTT	TCTTATCCAG	AACAGCTCAA	GTTTAAAACC		120
AAGCAAGTCA	AGGACAGTCT	CTACAAGATT	GCTGGAATTG	CAGATGTAGA	AGTTGCTGAA		180
ACGCTTG GTA	TGGAACATCC	AGTCAAGTAT	CGCAATAAGG	CGCAGGTGCC	CGTTCGTCGA		240
GTGAATGGTG	TCCTGGAAAC	AGGATTTTTTC	CGTAAGAATT	CGCACGACCT	CATGCCCCCTT		300
GAAGATTTCT	TTATCCAGGA	TCCTGTCATT	GACCAAGTCG	TAGTAGCTCT	TCGAGACCTG		360
CTCCGTCGTT	TTGATTTAAA	ACCTTATGAC	GAAAAGGAAC	AGTCTGGATT	GATTCGGAAT		420
CTTGTTGGTGC	GTCGTGGTCA	CTATTCAGGA	CAAATCATGG	TCGTTTTGGT	GACAACTCGT		480
CCAAAAGTTT	TTCTGTGTTGA	CCAATTGATT	GAACAAGTTA	TCAAGCAGTT	CCCAGAGATT		540
GTGTCTGTCA	TGCAAAATAT	CAACGACCAG	AATACCAATG	CGATTTTTTG	TAAGGAGTGG		600
CGCACTCTTT	ATGGTCAAGA	CTATATTACG	GACCAGATGT	TGGGAAATGA	CTTCCAAATC		660
GCTGGCCAG	CCTTTTACCA	AGTCAATACT	GAAATGGCGG	AGAAACTCTA	TCAAACAGCC		720
ATTGACTTTG	CAGAGTTAAA	AAAAGATGAC	GTGATTATTG	ATGCCTATTCT	TGGTATTGGA		780
ACCATTTGGTT	TATCAGTCGC	CAAGCATGTC	AAAGAAGTCT	ACGGTGTGTA	ACTGATTCCA		840
GAAGCGGTTG	AGAATAGTAA	AAAAAATGCT	CAGCTGAACA	ATATTTCAAA	CGCCCACTAT		900
GTCTGTGACA	CAGCTGAAAA	TGCTATGAAG	AATTGGCTTA	AAGATGGGAT	TCAACCAACC		960
GTTATCTTGG	TTGATCCTCC	ACGCAAGGGC	TTGACAGAAA	GCTTTATCAA	AGCAAGCGCC		1020
CAAACAGGAG	CCGATCGCAT	CGCCTATATC	TCCTGCAATG	TCGCAACCAT	GGCGCGTGAT		1080
ATCAAACCTCT	ACCAAGAATT	GGGATATGAA	TTGAAGAAAG	TCCAGCCGGT	GGATCTATTT		1140
CCTCAAACGC	ATCACGTCGA	GACGGTAGCA	CTTTTGTCCA	AACTCGATGT	CGATAAGCAC		1200
ATAAGTGTTG	AAATTGAGCT	GGATGAGATG	AATTTGACAA	GTGCGGAGAG	CAAAGCAACA		1260
TATGCTCAAA	TCAAAGAATA	TGTTTGGAAAT	AAATTTGAAT	TAAAAGTTTC	GACATTATAT		1320
ATTGCACAGA	TAAAAAAGAA	ATGTGGAATA	GAATTACGAG	AACATTACAA	CAAGTCTAAA		1380
AAGGATAAAC	AAATTATTCC	ACAGTGATCA	CCTGAAAAAG	AAGAAGCCAT	CATGGATGCT		1440
TTGAGACACT	TCAAAATGAT	TTAA					1464

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1242 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GGAGGAAAAT	ACATGTCTTC	TCATCCAATT	CAGGTCTTCT	CAGAAATTGG	GAAACTGAAA	60
AAAGTTATGT	TGCACCGTCC	AGGCAAGGAG	TTAGAAAAC	TGTTGCCGGA	CTATCTTGAA	120
AGGCTTCTTT	TTGATGATAT	TCCTTTCTTG	GAAGATGCTC	AAAAAGAACA	TGATGCATTT	180
GCCCAAGCTC	TTGCGGATGA	AGGAATTGAG	GTTCTCTACC	TAGAACAAC	CGCTGCTGAA	240
TCATTGACCT	CTCCAGAAA	CCGCGATCAA	TTTATCGAGG	AATACTTAGA	CGAAGCCAAC	300
ATCCGTGATC	GTCAAAACCA	GGTTGCTATT	CGTGAATTGC	TTCACGGCAT	CAAGGACAAC	360
CAAGAATTGG	TTGAAAAAAC	AATGGCTGGG	ATTCAAAAAG	TTGAATTGCC	AGAAATTCCT	420
GACGAAGCTA	AAGATCTAAC	TGACTTAGTT	GAATCAGAGT	ATCCATTTGC	AATTGACCCG	480
ATGCCAAACC	TCTATTTTCA	TCGCGACCCA	TTTGCAACAA	TTGGAACGCG	CGTATCGCTT	540
AACCACATGT	TTGCAGATAC	TCGTAACCGT	GAAACACTCT	ACGGTAAGTA	TATCTTCAAA	600
TACCACCCAA	TCTATGGCGG	AAAAGTGGAT	TTGGTCTACA	ACCGTGAAGA	AGATACGCGT	660
ATCGAAGGTG	GAGACGAGCT	AATTCTTTCT	AAAGACGTCC	TTGCAGTAGG	TATCTCTCAA	720
CGTACAGACG	CAGCTTCTAT	CGAAAACTTT	TTGGTCAACA	TCTTCAAGAA	AAATGTTGGC	780
TTCAAGAAAAG	TTTTGGCCTT	TGAATTTGCT	AACAACCGTA	AATTCATGCA	CTTGGATACT	840
GTCTTCACTA	TGGTAGACTA	TGACAAGTTC	ACTATTCAAC	CAGAAATCGA	AGGCGACCTT	900
CACGTTTACT	CAGTTACTTA	CGAAAACGAA	AACTTAAAA	TCGTTGAAGA	GAAAGGTGAC	960
TTAGCTGAAC	TTCTTGCTCA	AAACCTTGGT	GTAGAAAAAG	TTCATTTGAT	TCGTTGCGGT	1020
GGTGGCAATA	TCGTAGCAGC	TGCGCGTGAA	CAATGGAACG	ACGGTTCTAA	CACTTTGACC	1080
ATCGCACCTG	GTGTGGTAGT	TGTTTATGAC	CGCAATACCG	TGACCAATAA	GATTTTGGA	1140
GAATACGGGC	TTGCTTGAT	TAAGATTCGC	GGAAGTGAAT	TGGTTCGGGG	CCGTGGTGGA	1200
CCTCGTTGTA	TGTCTATGCC	ATTTGAACGT	GAAGAAGTGT	AA		1242

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

TGGAGGAAAAT	ATATCATGAT	TTTAATGACA	AAAAATATAA	ATCTAACAAA	TGAAGAATTA	60
GAGCTGATAC	AAGGTGGAGC	AGATCCATAT	GGTAAAAATC	CTAATGGTAG	GTACGATTGG	120
GAAATAGAAC	CAGTATTAA	TCTGCCGGTT	CATGGATTTT	GTCCCAGAGG	CACCTATGAT	180
TTAGGATATA	TTGGAGGAGG	CAATCATCTT	TGCAAGGAA	GTGCTGCGAG	ATTTTAA	237

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

CAGTCAGAAT	ACTACGTTTCG	TTTCCGCGTA	CTCCATGCCC	CGACCAAAAT	TTGGGTTGCT	60
AGCTTGAGGG	GTTTACCGCG	TTCCACTCTC	TCTGTTTCCA	GAAAGACTCC	GTCACTGTGG	120
CACTTTCAAG	CCTACTCTGG	CCTATCCAAG	GACTTAGCCA	TTTCAACTGC	CGTAACGATT	180
CCTCGTCCCT	AG					192

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

ATTATGGAAT	ACAAATTATT	TGAAGAATTT	ATTACCCTCC	AAGCACTACT	CAAAGAACTT	60
GGAATTACAC	ATAGCGGAGG	AGCTATTAAA	TCATTTCTCT	CTGAACATTC	TGTTTACTTT	120
AATAGGGAAT	TAGAGAGTCG	TCGTGGAAAA	AACTTCGTA	TTGGCGATAA	AGTTGACATC	180
CCTGACATGA	ACATTGACAT	CTTGTTGACA	CAACCTACTT	CTGAAGAACA	AGATGAATAC	240
CAAGCTGATA	AAGTTGAAAA	AGAACGGATC	GCTAAACTTG	TCAAAAAGAT	GAATAAGGGA	300
GTTAAAAAAG	ACAAATCGAA	ACCTGCTTCA	TCACCTAAAA	GCCAACAAGC	TCCACGATTC	360
CCTGGTAGAT	AA					372

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1995 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1995
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

CTTTGTCGAT	ACCTACGAAG	AATACACGGT	CGCACCAGTT	ATCCAGACCT	GCACCTATCA	60
CGCAGATGCC	AATCTCTACG	GTGCCCTTGT	CAACTGGCTA	CAGGAGGAAA	AGCAATGGTA	120
AGATTTACAG	GACTTAGTCC	CAAACAAACG	CAAGCTATTG	AGGTTTTAAA	AGGTCATATT	180
TCTCTACCAG	ATGTGGAAGT	GGCTGTCACT	CAGTCTGACC	AAGCCTCTAT	CTCTATCGAG	240
GGTGAGGAAG	GTCACTATCA	ATTGACCTAC	CGCAAACCTC	ACCAACTTTA	TCGTGCCCTTG	300
TCCTTGTTGG	TAACAGTTCT	AGCAGAAGCT	GATAAAGTAG	AGATTGAGGA	ACAAGCAGCT	360
TACGAAGATT	TGGCTTACAT	GGTTGACTGT	TCTCGAAATG	CGGTGCTGAA	TGTGGCTTCT	420
GCCAAGCAGA	TGATTGAGAT	CTTGGCTCTC	ATGGGCTACT	CAACCTTTGA	GCTTTACATG	480
GAAGACACTT	ACCAGATTGA	AGGGCAGCCT	TACTTTGGCT	ATTTCCGTGG	AGCTTATTCA	540
GCAGAGGAGT	TGCAGGAAAT	CGAAGCCTAT	GTTCAACAGT	TTGACATGAC	CTTTGTACCA	600
TGCATCCAGA	CCTTGGCCCA	CTTGTGCGCC	TTTGTCAAAT	GGGGTGTCAA	GGAAAGTCAG	660
GAGCTCCGTG	ATGTAGAGGA	CATTCTTCTC	ATTGGCGAAG	AAAAGGTTTA	TGACCTGATT	720
GATGGTATGT	TTGCCACGTT	GTCTAAACTG	AAGACTCGCA	AGGTCAATAT	CGGGATGGAC	780
GAAGCCCACT	TGGTTGGTTT	GGGACGCTAC	CTGATTTTGA	ACGGTGTTGT	GGATCGTAGT	840
CTCCTCATGT	GCCAACATTT	GGAGCGCGTG	CTGGATATTG	CTGACAAATA	TGGTTTCCAC	900
TGCCAGATGT	GGAGTGATAT	GTTCTTCAAA	CTCATGTCAG	CGGATGGCCA	GTACGACCGT	960
GATGTGGAAA	TTCCAGAGGA	AACTCGTGTC	TACCTAGACC	GTCTCAAAGA	CCGTGTGACT	1020
CTGGTTTACT	GGGATTATTA	TCGGGATAGC	GAGGAAAAAT	ACAACCGTAA	TTTCCGCAAT	1080
CATCACAAGA	TTAGCCATGA	CCTTGCAATT	GCAGGGGGAG	CTTGGAAGTG	GATTGGCTTT	1140
ACACCTCACA	ACCATTTTAG	CCGTCTAGTG	GCTATCGAGG	CTAATAAAGC	CTGCCGTGCC	1200
AATCAGATTA	AAGAAGTCAT	CGTAACGGGT	TGGGGAGACA	ATGGTGGTGA	AACTGCCCAG	1260
TTCTCTATCC	TATCAAGCTT	GCAAATCTGG	GCAGAACTCA	GCTATCGCAA	TGACCTAGAT	1320
AGTTTGTCTG	CGCACTTCAA	GACCAATACT	GGTCTAACGG	TTGAGGATTT	TATGCAGATT	1380
GACCTTGCCA	ACCTCTTACC	AGACCTACCA	GGCAATCTCA	GCGGTATCAA	TCCCAACCGC	1440
TATGTTTTTT	ATCAGGATGT	TCTTTGTCCG	ATACTTGACC	GACACATGAC	ACCTGAACAG	1500
GACAAACCGC	ACTTCGCTCA	GGCTGCTGAG	ACGCTTGCTA	ACATTAAAGA	AAAAGCTGGA	1560
AACTATGCTT	ATCTCTTTGA	AACTCAGGCC	CAGTTGAATG	CTATTTTAAAG	TAGCAAAGTA	1620
GATGTGGGAC	GACGCATTCG	TCAGGCCTAC	CAAGAGGATG	ATAAAGAAAG	TTTACAACAA	1680
ATCGCCAGAC	AAGAATTACC	AGAACTTAGA	AGCCAAATTG	AAGACTTCCA	TGCCCTCTTT	1740
AGTCACCAAT	GGCTGAAAAG	AAACAAGGTC	TTTGGTTTGG	ATACAGTTGA	CATCCGTATG	1800
GGCGGACTCT	TGCAACGCAT	CAAACGAGCA	GAAAGCCGTA	TCGAGGTTTA	TCTGGCTGGC	1860
CAGCTTGACC	GCATCGACGA	GCTGGAAGTT	GAAATCCTAC	CATTTACTGA	CTTCTACGCA	1920
GACAAGGATT	TCGCAGCAAC	TACAGCTAAC	CAGTGGCATA	CCATTGCGAC	AGCTTCGACG	1980
ATTTATACGA	CTTAA					1995

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGTTGTAGAT	ACGACTCACA	TATATACGAC	AAGGCAACGC	TGACGTGGTT	TGAAGAAATT	60
TTTGAAGAGT	ATCATTCTCC	ATCAAAGGCA	TCTTTAATAT	GGTCAAAGAA	GCCTTTTTTC	120
TTTGGATTTA	CTTTCAAGCC	ACCAGCAGCC	GCGAATTCTT	TCAAGGCTAC	TTTTTGGCGG	180
TCGTTCAAGC	CTGTCGGTGT	TACGACATTA	ACAGTAACGT	ATTGGTCACC	AACTGCACCG	240
CCACGAAGGC	TCGGTGCCCC	CTTACTACGT	AGGCGGAATT	TCTTACCAGT	CTGA	294

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

AGAAGGAGAT	ATATAACGAT	GAAGAAAATT	AAACCGCATG	GACCGTTACC	AAGTCAGACT	60
CAGCTAGCTT	ATCTGGGAGA	TGAAGTAGCA	GCTTTTATCC	ACTTCGGTCC	TAATACCTTT	120
TATGACCAAG	AATGGGGGAC	TGGACAGGAG	GATCCTGAGC	GCTTTAACCC	GAGTCAGTTG	180
GATGCGCGTG	AGTGGGTTCG	TGTGCTCAAG	GAAACGGGCT	TCAAAAAGTT	GATTTTGGTG	240
GTCAAGCACC	ACGATGGCTT	TGTCCTTTAT	CCGACAGCTC	ACACAGATTA	TTCGGTTAAG	300

GTCAGTCCTT	GGAGGAGAGG	AAAGGGCGAC	TTGCTCCTTG	AAGTATCCCA	AGCTGCCACA	360
GAGTTTGATA	TGGATATGGG	GGTCTACCTG	TCACCGTGGG	ATGCCCATAG	TCCCCTCTAT	420
CATGTGGACC	GAGAAGCGGA	CTACAATGCC	TATTATCTGG	CTCAGTTGAA	GGAAATCTTA	480
TCAAAATCCTA	ACTATGGGAA	TGCTGGTAAG	TTGCTGAGG	TTTGGATGGA	TGGTGCCAGA	540
GGAGAGGGCG	CGCAAAAGGT	TAATTATGAA	TTTGAAAAAT	GGTTTGAAAC	CATTTCGTGAC	600
CTGCAGGGCG	CTTGCTTGAT	TTTTTCAACA	GAAGGCACCA	GTATCCGCTG	GATTGGCAAT	660
GAACGAGGGT	ATGCAGGTGA	TCCACTGTGG	CAAAAGGTGA	ATCCTGATAA	ACTAGGAACA	720
GAAGCAGAGC	TGAACTATCT	TCAGCACGGG	GATCCCTCGG	GCACGATTTT	TTCAATCGGA	780
GAGGCAGATG	TTTCCATCCG	TCCAGGCTGG	TTCTACCATG	AGGATCAGGA	TCCTAAGTCT	840
CTCGAGGAGT	TGGTCGAAAT	CTACTTTTAC	TCAGTAGGGC	GAGGAACTCC	ACTCTTGCTT	900
AATATTCGCG	CGAATCAAGC	TGGGCTCTTT	GATGCAAAGG	ATATTGAACG	ACTTTATGAA	960
TTTGCGACCT	ATCGCAATGA	GCTCTATAAA	GAAGATTTGG	CTCTGGGAGC	TGAGGTATCT	1020
GGTCCAGCTC	TTTCCGCAGA	CTTTGCTTGT	CGCCATTTGA	CAGACGGCCT	TGAGACCAGC	1080
TCTTGGGCAA	ACGATGCAGC	CTTGCCCATC	CAGTTAGAAC	TCGACTTAGG	TTCTCCTAAA	1140
ACTTTTGATG	TAATTGAGTT	AAGAGAAGAT	TTGAAGCTAG	GGCAACGAAT	CGCTGCTTTT	1200
CATGTGCAAG	TAGAGGTGGA	TGGTGTCTGG	CAGGAGTTTG	GTTCGGGTCA	TACTGTTGGT	1260
TACAAACGTC	TCTTACGAGG	AGCAGTTGTT	GAAGCACAGA	AGATACGTGT	AGTCATTACA	1320
GAATCACAGG	TTTTGCTTTT	GTTGACCAAG	ATTTCACTCT	ATAAACTCC	GAGGTTATCA	1380
CAAACAGTAG	CTGTTACAGG	GCTAGCATTT	GCAGAAAAAA	GCCTAGCTGT	GGCAAAGGGA	1440
GAGACTCTTC	ATTTTAGGAT	TGAACGTAGT	GAAAGTAGCT	CCTCTTTAGA	GGCTAAGATT	1500
TCGATTCAAC	CGGGGACAGG	TGTCCATGGT	GTCGCCTATC	AGGATGAGAT	TCAAGTCCTT	1560
CAATTCCAAG	CAGGGGAAAG	CAAAAAAGAT	TTGCATCTAC	CAACCTGTA	TTTCGCAGGA	1620
GATAAACCT	TGGATTCTA	TCTGAACCTA	ACGGTGGATG	GTGAGCTTGT	GGATCAACTT	1680
CAAGTCCAAG	TTTCATAA					1698

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GGTGTACTC	TAATGGATGA	TATTTTACAA	GCTTTAGCAA	AAATGCTAAA	TATGACTGTT	60
GATGAAGTAA	GTTCTTTGCT	TACAACATTT	AAAGGGAATG	CACCACAGAT	TTATGAAATG	120
TTCGTTAAAG	AAAAGATGTT	TTATGATCTC	TTCAGTCTTT	TTCAAATCAT	GTCAATTGTA	180
ATATTTAGTA	TTTCTGCAGT	AGTTTTAGCA	GTTTTAACTC	TCATATATTT	TACATACGAT	240
GGTGGTTTTG	TTTATTCCTA	TGATATACGT	ACAGGAAAAA	CCGAGGAAGA	AATTAAATTA	300
GAACGCATTG	AACGGAAAAA	AAAGGACTTA	AAAATACCAC	TAAAAATTAG	TTGCATTTCA	360
TCAAGCGCAA	GTTTGATAAC	ATTAGTTATT	GCAATTGTTT	TAAAAGCAAC	TCTTGCACCT	420
AATTATATAT	TCATCGTGAA	TGAGATTTTA	CCAAAATTAA	CGAAGAGATA	G	471

(2) INFORMATION FOR SEQ ID NO:609:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

ATAACTACTC	TATTATTAAA	TAGTTTAGAG	CTGACTGTTG	TATCGATAGT	TGTTTTGCTA	60
GCTTTACGTA	GCGTAATAGC	AGAACTAATT	CTATCTAAAA	AACTGGATGT	TTCGGTTAAG	120
AAAGATATTG	TATTAGAATT	TCTTTTGACG	ATTGTCTTTA	TTTCTTCAAG	TTGGTACTTA	180
CCGATTTGGC	CCGCAGTAAT	AGTTTATTTG	TTAGCGTATA	CTTTATACTT	GTATCTAAAG	240
CGTAAAGATA	TAAAAATGTA	TATAGAATAT	TTTAGAAAAG	AAATATTTGA	ATAA	294

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

ATTAATACTC	TTCGAAAATC	TCTTCAAACC	GTGTCAGTTT	TATCTGCAAC	CTCAAAGCGG	60
TGCTTTGAGC	AACCTGTGGC	TAGCTTCCTA	GTTTGTCTCT	TGATTTTCAT	TGAGTATAAA	120
CTTAGCAAGG	AGACCTCTTT	TTCAGAAAAG	CAGGGTTCTT	TTTGCTGTCT	ATTCCATCCC	180
TGA						183

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

ACTAATACTC	TTCGAAAATC	TCTTCAAACC	ACGTCAGCGT	CGCCTTGCCG	TATATCTGCA	60
ACCTCAAAAC	AGTGTTTTGA	GCTGACTTCG	TCAGTCTTAT	CTACTACCTC	AAAACGGTGT	120
TTTGAGCAAC	CTGTGGCTAG	TTTCCTAGTT	TGCTCTTTGA	TTTTCATTGA	GTATAAAGAG	180
CTTGGCAACA	GGCTCTTTTT	GTATTGCGTT	TATTAA			216

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

TGGATAACTC	TCCAAAATCA	GAAATATCTA	AGGAACTATT	ATATCAAAAT	GGATTTTAGC	60
AGAAAAGGATA	ATCAGTCAAT	GGAATATCGA	AAAATACAAG	AAGCATTAGA	AGCATTGCAG	120
AAGGGACGAC	TTGTTCCTGT	TATAGACGAC	AAGGATAGAG	AAAATGAAGG	AGACTTAATT	180
TGTTCTGCAC	AAGCAGCTAC	AACAGAAAAAT	GTTAATTTTA	TGGCTACTTA	TGCCAAAGGA	240
TTAATTTGTA	TGCCTATGAG	CGAAAGTTTA	GCTAATCAAT	TAATGCTTTC	ACCTATGGTT	300

GAAAAACAATA	CAGATAATCA	TAAGACTGCT	TTTACAGTTT	CAATTGATTA	TAAAGAAACG	360
ACCACAGGTA	TTTCTGCCGA	GGAAAGAGGA	CTGACCGCAC	GTATGTGTGT	AGCTGAAGAT	420
ATAACACCCCT	CTGATTTTCG	CAGGCCAGGA	CACATGTTTC	CTTTAATTGC	AAAAAAAGGT	480
GGTGTCCCTAG	AAAGAAAATGG	ACACACAGAA	GCAACTGTTG	ATTTATTAAA	ATTAGCTGGA	540
CTAAAAGAGT	GTGGCCTATG	TTGTGAAATA	ATGAATCATG	ATGGCAAAAT	GATGAGAACA	600
GATGATTTAA	TTCACTTCTC	GAAGAAACAC	AACATTCCAG	TAATTACCAT	CAAAGAAATTA	660
CAAGAATATA	GAAAAGTATA	TGATCAGCTG	ATAGAACGAG	TTTCAACTGT	CAATATGCCT	720
ACTAGATACG	GTAATTTCAA	AGCAATTAGC	TATATAGATA	AACTAAATGG	GGAACATCAT	780
CTTGCTCTTA	TTATGGGAAA	TATAGAGGAT	GAAGCCAATG	TATTATGTCG	GGTCCACTCC	840
GAATGTTTAA	CAGGAGATGT	TTTAGGCTCT	TTACGTTGCG	ATTGTGGACA	GCAATTCGAT	900
AAAGCTATGA	AAATGATTGT	TGAGAATGGT	TCGGGTGTCT	TACTTTACTT	GCGACAGGAG	960
GGACGAGGAA	TTGGACTTAT	CAATAAATTA	AAAGCCTATC	ATTTACAAGA	TCAAGGCATG	1020
GATACGCTTG	ATGCCAATCT	TGCATTAGGC	TTTGAAGGTG	ATTTAAGAGA	ATATCATATT	1080
GGAGCACAAA	TGCTTAAAGA	TCTGGGACTT	CAGTCACTTC	ATTTACTGAC	AAATAATCCT	1140
GACAAGGTTG	AACAGTTAGA	AAAATATGGA	ATTACCATTT	CCAGTAGAAT	ATCAATCGAA	1200
ATAGAAGCCA	ATCCTTACGA	TAGTTTTTTAT	TTAGAAACAA	AGAAAAATCG	AATGGGGCAC	1260
ATTTTAAATA	TGGAGAAAA	ATAA				1284

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

ATGGCAACTC	TTGATGAATT	GAAAGTCATG	ATTGACGCTG	AGATAGCGCC	TTTCAGGAAG	60
AAGATGAAAG	AAGTCGAGAA	TCAGGTCAAA	GGAACATCTG	ACCAAGTGAA	AAATGCTACT	120
GCCAAAGTTC	GTGAACAGTC	GAGCTCAATC	GGTAGTGCGT	TTGGCAAAGCT	GGCTAAGTTC	180
GCTGGTTTTG	CAATCCTTGG	TAAGAAATTA	CTTGATGTTG	GGATGTATTC	AACGCAGACG	240
GCTCTTGAAG	TATCAGCGTC	TATGAACCAA	ATCAAGCGAC	AGATGGGCGA	GAGTTCGCAA	300
TCTTTCTTAA	AATGGGTTAA	CGATAATGCC	AACGCTATGA	ATATGGGTGT	GGGTGAGGCT	360
ACCAACTACG	GTGCAGTCTA	CTCAAACCTA	TTTTCTGGAT	TTATCAAAGA	TACCAACAAG	420
CTAAGCGCCT	ATACCGCTAA	GATGTTGCAG	ACATCGGCAG	TTGTTGCTGA	AGGTTTCAGGG	480
CGCACGATTA	CAGACGTTAT	GGAGCGGATT	CGCTCAGGTT	TACTAGGGAA	CACCGAAGCG	540
ATTGAGGACC	TAGGAATCAA	CGTCAACGTG	GCTATGATTG	AGTCCACTGA	AGCCTTTAAG	600
AAGTTCGCAA	ACGACAGAG	CTGGCAACAG	TTGGATTACC	AAACCCAGCA	ACAAATCCGC	660
CTTATGGCTA	TTCTGGAACA	GGCTACAGCC	AAGTATGGGG	ATACCTTGTC	TAATTCGTGA	720
AATGGTCGTA	TCAGCCTATT	TAAGTCGCTG	ATGAAGGACG	CAGCATTGAA	CCTTGGTAAC	780
TCTATGTTAC	CGATTATCAA	TGCCATTATG	CCTGTCTTGA	ACTCTTTTGC	TATGGTCTTA	840
AAGAACGTTA	CTGCTAAACT	CGCTGAGTTT	ATCGCTTTGA	TGTTCAACAA	GAAAGCAACA	900
GTGAAAGATG	GTGTTGGTGG	AGCAGTTGGA	GACATGGGTA	ACGCCATGAA	GGATGCTGCA	960

GGCGGAGCAG	GAGACCTTGC	TGACGCAGTA	GACGACGCTG	GAGATTTCAGC	AGGAGGACTT	1020
GCTGACAATC	TTGGGAGACTC	CGCCAAAAAC	GCTAAGAAGG	CCGCTAAAGA	GTTGCTAGGT	1080
CTTTTGGGAT	TTGATGAGAT	TAACATCTTG	CAAAAACCAA	AAGATGACGA	CGCAGGCGGG	1140
TCTGGAGGCG	GTGGCAAAGG	TGGTAAAGGA	AAGGGAGGCG	GTGGCGGACC	TTTCAAAGAC	1200
ATCTTGCCAG	AAGTCGAGTT	GACCGACATG	GACAACAAAT	TCAAGAGCAT	TTTTGATGGT	1260
CTTGGAGATA	AGCTCAAAGG	GTTGTTTGAC	CTCTTCAAGA	AAGGTTTTGA	TGCAGCATTT	1320
AGACCAGAAG	GTATAGAACG	CATTAAGACT	GCCTTAGACC	AAATAGCTAA	GACAATGGGA	1380
GAAATCGCCA	CTGACCCAAG	GGTTGTGAAT	GCCTTTAACC	GAATGGCTGA	GAAAATTGCT	1440
TATGCTTTAG	GGCAAGTGAC	AGGCTCAATA	ACAACATATC	GGCTAGGTAT	CGGTGTTTTTC	1500
CTTGCCGAAA	GTATTGCAAA	TGGCCTTGGA	AGGCAAAAAG	AACGCATTAC	CAGGGCGCTA	1560
GTCGCTTTGT	TTGATAATAT	TGGTAACATT	TCCGAGGCAG	TAGGAAACAT	CGCTCAGGAC	1620
TTTTCTAGTA	CTTTCTACGA	CGTCATTACC	TCAACTGGTG	CGGTTTCGTAT	CGGTAGCGCT	1680
ATTGTGTCAA	CTCTGTTGAG	TTTGACATCT	ACCATTGTTG	AAGTTGGTAG	TAAATTAGCA	1740
GGAAAGTTTGT	TTAAAGGTTT	TGAAAAAGTC	GTTGTGACAA	GCGCTCCTAA	AATTTTCATCA	1800
GTCTTCCAAA	GTTTATTAGA	TACTGTTGCG	CCTGTATTTG	AGAGCATTGA	AAGGTCTGTT	1860
AACAAATTTG	GCGATGGCTT	AAGTCGTGTT	TATGATGAAC	ATGTAGCCCC	TGCTATTAAAC	1920
TCTATTGCTA	ATGCTTTTAA	CGGACTGATT	GATATCATAC	AAATCCTCTG	GGAGAATTCT	1980
TGGCAACCTT	TTGCTGAGTT	TTTATCAGGA	GTATTCGGTG	TTAGTATTGA	AGGAATTTCA	2040
GATTTATTAG	GAGGTGGCCT	TTTAGCCACT	TTGGGACTAT	TGGCGGATGC	TATTAAGTTA	2100
GTGGCAGATG	GTTTCACCGT	TTTTTCTGAC	TGGTGTAAAG	AAAACAAAGA	ACCTATCTTG	2160
GCTTTGATAA	CAACTTGGCA	AACGATTAAT	TTCTTATCAT	GGGCTGAACA	AGCCGGGGGA	2220
CTTGCAAGAG	CATTCAAGTT	GTTAGGTAGT	AAGGTCCTCT	TGATTGTTGG	AGGGATTAAAG	2280
AATCTAGGTC	TTGCTATTAA	AGCATTGACA	TTTGATAAGT	TGGTCAGTTT	TGGTGAAACA	2340
ATCTATTTGA	ACACCTTATA	TGCAAAAAGAT	TTTGTGGTCA	ATTCAAGTTAA	AACAATTGCA	2400
CAGCTAGGAA	AAACTGCTTT	AGAACTTGGT	AAATCAGCTC	TAGCATGGAC	TGCTCATGCA	2460
GCGAAAAATGG	GATTAGCAAC	CGCGGCGGAA	TTTGCACATT	CTGTTGCAGC	AGGAGTCGCT	2520
ACAGCTGCAA	CATGGGCTTT	TAATGCAGCG	TTAGCAGTTT	TGACAAGTCC	AATAACATGG	2580
ATTATTGCAG	CAATCGCAGC	TTTGATTGCT	ATCGGTGTCT	TGCTCTACCA	AAACTGGGAC	2640
ACTGTTGTTG	AGTTTGCTAA	AACTGCATGG	CAAGGACTAT	GTGATTTTAT	TAGTGGTATT	2700
TGTCGAGCTA	TTGGCGAATT	TTTCAGTGGT	CTATGGACAA	AACTACAAGA	AATCTTTGAG	2760
CCGATAGGTC	AATGGTTTGG	CGAGAAGTTC	CAGCAAGCAT	GGGATGCCAT	TGTCAACATC	2820
TTCTCTGGTA	TCGGAGAGTG	GTTCTCTGGT	GTATTCCAAG	GTGCATGGGA	CGCTATCGTT	2880
AATATCTTCA	CTCCAATCGG	CTCATGGTTT	GGACAACGTT	GGGCAGATGT	GACTAGTGCT	2940
TTGGCTAATA	TCGGGGCATG	GTTTACTGAC	ATATTCCAAA	AAGCATGGAC	TGGTCTAACA	3000
AACATCTTTA	GCAAACTAGG	TTTATGGTTT	GGCGAGAGAT	GGGCAGATGT	TACAAGTGTT	3060
CTTGCGAATG	TATCTTCTTG	GTTTGGAAT	ATGTTTACTA	GTGCTTATAA	TGCAGTCAAG	3120
AACGCGTTTA	GTTCAATTGG	TGGCTTCTTC	AGCGGTGTAT	GGTCAACGGT	TCAAAGCATA	3180
TTTGTCAATG	CTGGACAAAA	GGTTGGTAGC	GCTGTAGGTG	GAGCGTTTAA	GAGTGGCGTC	3240
AATGCGGTTT	TTGGAACGAT	TGAAAATGTA	GTCAATGACT	TCATCGGAAT	GATTAATGGA	3300
GTTTTAGGCG	TTGTCAGAAA	CTTACCTGGT	CTAGGATGGG	TTGGTAGTGT	AAGCACAGTT	3360
AGCCTCCCTC	GTCTTGCCCG	TGGTGGTATC	GTGATAGTC	CAACAATCGC	CATGATTGGT	3420
GAAGCTGGTA	AAGAGGCGGT	CGTACCACCT	GAAAAATACAG	GATTTATCCA	AACACTTGGGA	3480
CGAGTAGTCA	GCAAGTGGGT	AGTAAATGCC	ATGGCTGGTA	TTAGTCCACA	AGGTGGTTTTT	3540
TCTAGCGACG	GCGACATCGT	TATTTCAAATC	GCAGGCCATG	AGTTTCGGACG	GGTAGCTATC	3600
CAAGAAATCA	ACAAGGAACA	TGAACGAGCA	GGTCAAACCT	TGCTCAAGAT	TTAG	3654

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

AATATTTTGT	ATGGCGATAA	AGGGTGTGTG	GAAAATTCTC	TAGAAAATCT	TCATGCAATT	60
GGGAATGGAT	TTAAGTTGTC	TTATCTTCAT	GAGATTGATG	CCTGCAAGGT	TCCTGACTGG	120
GTTTCAAATA	CGGTATGGTA	TCAGATATTT	CCTGAAAGAT	TTGCCAATGG	CAATGCTCTA	180
TTAAACCCAG	AAGGGACTTT	AGACTGGGAT	TCATCTGTCA	CACCTAAGAG	CGATGATTTT	240
TTTGGTGGTG	ATTTACAGGG	GATTATTGAT	CATATGGATT	ACTTGCACGA	CTTGGGTATT	300
ACTGGACTAT	ATCTTTGTCC	CATCTTTGAA	TCTACAAGCA	ATCACAAGTA	CAATACGACA	360
GATTACTTTG	AAATTGACCG	TCATTTTGGA	GACAAGGAGA	CCTTTCGGGA	ACTGGTGGAT	420
CAAGCGCATC	ATCGTGGCAT	GAAAGTCATG	CTGGATGCGG	TATTTAATCA	TATTGGTTTCG	480
CAATCTCTTC	AATGGAAAAA	TGTCGTCAAA	AATGGTGAAAC	AGTCTGCTTA	TAAGGATTGG	540
TTCCATATTC	AACAATTCCC	AGTGACAAC	GAAAAGCTAG	TTAATAAGAG	AGACTTACCC	600
TATCATGTTT	TTGGTTTCGA	GGACTATATG	CCTAAGCTAA	ATACAGCCAA	TCCAGAGGTC	660
AAGAAATATC	TTTTAAAGGT	TGCGACTTAT	TGGATTGAAG	AGTTTAAATAT	CGATGCTTGG	720
CGTTTGGATG	TGGCTAATGA	GATTGACCAT	CAGTTCTGGA	AGGATTTTTCG	TAAGGCAGTT	780
TTAGCTAAAA	ATCCTGATCT	TTATATCCTA	GGAGAAGTCT	GGCATACATC	TCAGCCTTGG	840
CTAAATGGAG	ATGAGTTCCA	TGCCGTCTATG	AATTATCCCTT	TATCTGATAG	TATCAAGGAC	900
TATTTCTTAC	GAGGAATTAA	GAAGACAGAC	CAGTTCATCG	ATGAAATCAA	TGGAGAGTCT	960
ATGTATTACA	AGCAGCAGAT	TTCAGAGGTC	ATGTTTAATC	TCTTGGATTC	ACATGATACA	1020
GAGCGAATCC	TGTGGACGGC	CAATGAAGAT	GTTCAACTGG	TTAAATCAGC	CTTAGCCTTT	1080
CTCTTTTTTAC	AAAAAGGAAC	ACCGTGCATT	TATTACGGAA	CCGAGCTAGC	CTTGACTGGA	1140
GGACCAGATC	CAGATTGTCTG	TCGTTGTATG	CCTTGGGAAC	GTGTATCAAG	TGACAATGAT	1200
ATGCTGAACT	TTATGAAGAG	GCTGATTAAG	ATTTCGGAAAT	ACGCGTCAGT	AATCATTTTCG	1260
CATGGCAAGT	ATAGCCTTCA	AGAAATCAAA	TCTGATCTAG	TAGCTCTGGA	ATGGAAATAC	1320
GAAGGACGGA	TCCTCAAAGC	AATATTCAAC	CAATCAACAG	AAGATTATCT	TTTAGAGAAA	1380
GAAGCAGTAG	CACTAGCAAG	CAATTGCCAA	GAATTGGAGA	ATCAGCTTGT	CATCTCTCCA	1440
GATGGATTTG	TGATTTTCTA	A				1461

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

ATAGTATTGT	ATGAAAGTAT	AAGGTTAGTA	TATATGAAAC	GTTCTCTCGA	CTCAAGAGTC	60
GATTACAGTT	TGCTCTTGCC	AGTATTTTTT	CTACTGGTCA	TCGGTGTGGT	GGCTATCTAT	120
ATAGCCGTTA	GTCATGATTA	CCCCAATAAT	ATTCTGCCCA	TTTtagggca	GCAGGTCGCC	180
TGGATTGCCT	TGGGGCTTGT	GATTGGTTTT	GTGGTCATGC	TCTTTAATAC	AGAATTTCTT	240
TGGAAGGTGA	CCCCCTTCT	ATATATTTTA	GGCTTGGGAC	TTATGATCTT	GCCGATTGTA	300
TTTTATAATC	CAAGCTTAGT	TGCATCAACG	GGTGCCAAAA	ACTGGGTATC	AATAAATGGA	360
ATTACCCAT	TCCAACCGTC	AGAATTTATG	AAGATATCCT	ATATCCTCAT	GTTGGGCTCGT	420
GTCATTGTCC	AATTTACAAA	GAAACATAAG	GAATGGAGAC	GCACGGTTCC	GCTGGACTTT	480
TTGTTAATTT	TCTGGATGAT	TCTCTTTACC	ATTCCAGTCC	TAGTTCTTTT	AGCACTTCAA	540
AGTGACTTGG	GGACGGCTTT	GGTTTTTGTA	GCCATTTTCT	CAGGAATCGT	TTTATTATCA	600
GGGGTTTCTT	GGAAAATTAT	TATCCCAGTA	TTTGTGACTG	CTGTAACAGG	AGTTGCTGGT	660
TTCTTAGCTA	TCTTTATTAG	CAAGGACGGA	CGAGCTTTTC	TTCACCAGAT	TGGAATGCCG	720
ACCTACCAA	TCAATCGGAT	TTTGGCTTGG	CTCAATCCCT	TTGAGTTTGC	CCAAACAACG	780
ACTTACCAGC	AGGCTCAAGG	GCAGATTGCC	ATTGGGAGTG	GTGGCTTATT	TGGTCAGGGA	840
TTTAATGCTT	CGAATCTGCT	TATCCCAGTT	CGAGAGTCAG	ATATGATTTT	TACGGTTATT	900
GCAGAAGATT	TTGGCTTTAT	TGGCTCTGTC	CTGGTTATTG	CCCTCTATCT	CATGTTGATT	960
TACCGTATGT	TGAAGATTAC	TCTTAAATCA	AATAACCAGT	TCTACACTTA	TATTTCCACA	1020
GGTTTGATTA	TGATGTTGCT	CTTCCACATC	TTTGAGAATA	TCGGTGCTGT	GACTGGACTA	1080
CTTCCTTTGA	CGGGGATTCC	CTTGCCTTTC	ATTTTCGCAAG	GGGGATCAGC	TATTATCAGT	1140
AATCTGATTG	GTGTTGGTTT	GCTTTTATCG	ATGAGTTACC	AGACTAATCT	AGCTGAAGAA	1200
AAGAGCGGAA	AAGTTCCATT	CAAACGGAAA	AAGGTTGTAT	TAAACAAAAT	TAAATAA	1257

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

AACGCATTGT	ATCAAGTGTT	AGGGGCTGAT	ATCATGCGTT	TTTCTGCTTT	TAAGATTTTTT	60
TCCAACCTCTG	TTTGTAAGCG	CATCATAACA	AAGGGTCTAG	GATTTCAGGGC	TCTCCTCCTA	120
TATACTATTA	GTAAAGTAAA	ACTAAGAGAG	GATATTTTAG	TGTCGCAGTC	TATTGTTCCCT	180
GTAGAGATTG	CACAAATATTG	TCGTTTTTGAT	TCTAAAAAGA	GAAATGGAAT	TCTGTTTAAAC	240
GTTCGTATTG	CCAATCTTAA	ATTTACCTTT	TTTAGATTAG	ACTTCCTGCG	AAATAAAATA	300
TGGTATAGTA	GTTCTATGAA	TGATGAAGCA	AGTAAACAAC	TAAC TGATGC	ACGATTTAAG	360
CGTCTTGTTG	GTGTTTCAGCG	CACGACTTTT	GAAGAGATGT	TAGCTGTATT	AAAAACAGCT	420
TATCAACTTA	AACACGCAAA	AGGTGACGA	AAACCTAAAT	TAAGCCTAGA	AGACCTTCTT	480

ATGGCCACTC TTCAATATGT GCGAGAATAT CGAACTTATG AAGAAATTGC GGCTGTTTTT	540
GGTATCCACG AAAGCAACTT AATCCGTCGG AGCTAA	576

(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

ATGAATATGT ATCGTGTTAT AGAAATGTAC GGAGATTTTG AACCGTGGTG GTTCTTAGAA	60
GGTTGGGAAG AAGATATTGT AGCAAGTAGA AAATTTGACC AGTATTATGA TGCTCTCAAA	120
TACTACAAAA CTTGCTGGTT TAGATTGGAA CAAGAATCGC CTCTTTATAA AAGTAGAAGC	180
GACTTGATGA CCATTTTTTG GGACCCGGA GACCAACGCT GGTGTGATGA ATGTGATGAG	240
TATTTACAAC AATACCATTC TTTGGCTCTT TTGCAGGATG AGCAGGTTAT CCCAGACGAA	300
AAACTACGCT CAGGCTATGA AAAACAAACC AGTCAGGAAA GGAATCGTTC TTGCCGTATG	360
AAATTAAAAAT AG	372

(2) INFORMATION FOR SEQ ID NO:618:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

GAAATGGTGT	ATCAAGTATT	CTCGGTTCTA	TTTTCTTCGG	AGCGAGCATA	CAGTTTCTCA	60
TCTCCCGTCG	CATTGCAAAA	ACTAAGAAAA	ATCAAGATGA	GGATTAGGAG	GAAACTCATG	120
AAAAAAGAAA	AGAAACAGTT	ACGTTATCCT	GGTCTGAAAG	CAGGTTCGAT	TTATGGAACA	180
GTGATATTTT	TTATAATTCC	ACTCATTGAT	ACCCTAACAA	GTGAAAATCC	AAATTTTATC	240
AGTTCTCTTC	TAAATACAAA	ACATATTTTT	AAAACTATGC	TGGGAGCTTT	CTTTTTCGGA	300
GTGATGATAC	ATATTGTCGA	CTCACTTCGT	ATTGCAAGAG	CTAAAAAAGA	CCAGGATTAG	360

(2) INFORMATION FOR SEQ ID NO:619:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...765
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

CAGAACGATT	TATTTTGGAG	TAGGATCATG	GGCTTAACTT	ATCAAATGAA	AATGAAAATT	60
CCTTTTGATA	TGGCTGATAT	GAACGGTCAT	ATCAAACCTC	CAGATGTGAT	TTTGCTGTCA	120
CTGCAAGTTT	CAGGGATGCA	GTCGATTGAA	CTGGGAGTTA	GTGATAAGGC	CATTTTGGAA	180
GAATATAATC	TGGTCTGGAT	TATCGTAGAA	TATGATATTG	AGGTGTTTCG	TTTGCCCTCGT	240
TTTGCGGAAG	AAATTACCAT	CGAAACGGAA	GCCTTGAGCT	ACAATCGACT	TTTTTGCTAC	300
CGTCGCTTTA	CTATTTATAA	TGAAGCGGAG	CAGGAGCTCA	TCCACATGAT	GGCGACCTTT	360
GTTCTCATGG	ACCGCGACAG	TCGAAAAGTC	CATGTTGTTG	AACCTGAGAT	TGTGGCTCCT	420
TACCAGTCTG	ATTTTGATAA	AAAACTTATC	CGTGGACCGA	AGTATGAGTC	CTTGGAAGAA	480
CCGATCAGCA	AGGATTACCA	TGTTCTGTTT	TACGACTTGG	ATATGAATGG	TCATGTCAAT	540
AACAGTAAAT	ACTTGACTG	GATTTTGGAG	GTCATGGGAG	CGGATTTTTT	GACCCACTAT	600
ATTCCAAGA	AAATCAACCT	CAAGTATGTC	AAGGAAGTTC	GACCAGGTGG	GGTGATTACA	660
TCGGCTGTTG	AACGGACTGG	ACTGGAAAGC	AAGCATGAAA	TTACAAGTGA	TGGGGTTATC	720
AATGCCCAAG	CAATCATTAC	TTGGCAAGAA	ATAAAAAAGG	CTTAG		765

(2) INFORMATION FOR SEQ ID NO:620:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GAGAACGATT	TGGTGACTAA	AGTAGAAACG	GCTAGAAGTT	TAGCTCTAGC	AGTGCTAGAG	60
GATGTTTTTG	TGAATCAAGC	ATATTCAAAT	ATTGCCTTAA	ATAAACACCT	CAAGGGGAGT	120
CAGCTCTCTG	CAGCAGACAA	GGGCTTAGTG	ACCGAGCTAG	TCTATGGAAC	GGTAGCCCGT	180
AAACTGACTC	TGGAATGGTA	CTTATCCCAC	TTTATCGAAG	ACAGAGACCA	GTTAGACAGC	240
TGGCTCTATG	TCCTTCTTCT	CATGAGTGCC	TACCAACTCC	GCTATTTGGA	CAAGATTCCA	300
GATCATGCTG	TGGTCAATGA	AGCAGTGGAA	TTGGCCAAAC	TCCGTAAAAA	AGGCAGTGAA	360
AAATTGGTCA	ACGCTGTCCT	TCGCCGTATC	TTGCGTGAAG	GCTGGCCAGA	TATTGCTAGC	420
ATCAAGCGAA	AAAACAAGCG	TGACTCCATT	GCCTATTCTC	TCCCAGTTTG	GCTAGTTACC	480
AAACTCAAGG	AAGAATACGG	AGAGGAGAGA	GCAAAAAGCCA	TCTTTGAAAAG	CCTGTAG	537

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 429 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GACCTATCGT	ACAAAAAGCAG	ACTGCCAGCA	TACGGCTATG	ATTGGTTCCT	CACTAGGAGG	60
CAATATACCC	AGTTTATCGG	TTTGGAATAC	CAAGACCAAA	TTGGTTGCTT	GGGCGTTTTT	120
TCATCTGCAA	ACTGGCTCCA	CCAAGAAGCC	TTTAACCGCT	ATATCGAGTG	CCAGAAACTA	180
TCGCCTGACC	AGCGCATCTT	CATCTATGTA	GGAACAGAAG	AAGCAGATGA	TACAGACAAG	240
ACCTTGATGG	ATGGCAATAT	CAAACAAGCC	TATATCGACT	CGTCGCTTTG	CTATTACCAT	300
GATTTGATAG	CAGGGGGAGT	ACATCTGGAT	AATCTTGTGC	TAAAAGTTCA	GTCTGGTGCC	360
ATCCATAGTG	AAATCCCTTG	GTCAGAAAAT	CTACCAGATT	GTCTGAGATT	TTTTGCAGAA	420
AAATGGTAA						429

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

TTTAGCGATT	TACTATGTG	CCATCTTATC	GCCTCTATCG	GATTAAATAT	GGATTCGACT	60
CCCGTGATTA	TTGGAGCCAT	GTTAATCTCT	CCTTTGATGA	CACCTATTCT	GGGAGTGGGG	120
CTCTCTCTAG	CTATATTTGA	TTTTAAATTG	TTAAGAAAAT	CTTTTAAAAAT	ATTAGCTATT	180
CAAATTCTTG	CCAGTCTAAT	AGCTTCAACA	CTTTATTTT	ATCTTTCTCC	CATTTCGTAT	240
GCTAGTTCGG	AGATTGTTGC	TAGAACCTCT	CCGACTATTT	GGGATGTTCT	CATTGCTTTT	300
GTAGGAGGGA	TAGCAGGTAT	TATTGGTGCT	AGGAAAAAAG	AGACCAATAA	TATTGTTCCCT	360
GGTGTTGCTA	TTGCAACCGC	CTTGATGCCT	CCTCTTTGTA	CAGTAGGTTA	TGCTATTGCT	420
TCTGCTAATC	TAAAAATTTAT	CATAGGCTCC	TCTTACCTAT	TTCTCATCAA	TTGTAGCTTT	480
ATTGTCATTG	CGACTTATAT	AGGTGTTAGG	TTGATGATGG	TTAAGAAAACA	TTATTTTAAA	540
GATAATGAAG	AAGACTCTAA	AATGCGTAGG	ATTTTGCTTC	TAGTTGCTGT	TTTGCTGATG	600
ATTCCGAGTT	TCATCTCTGC	AACGACTTTA	GTGAGAGAAA	CGTTGAAAAA	AGAGTCCCTT	660
AAGAAATTTA	TATCAGAGCA	AGTTTCAGGG	GCATAA			696

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GCGTTCCAGT	ATTTGACAAAT	ATTATACTTC	CTGCGAAACA	AAATATGGTA	TAGTAGTTCT	60
ATGAATGATG	AAGCAAGTAA	ACAACCTAAT	GATGCACGAT	TTAAGCGTCT	TGTTGGTGTT	120

CAGCGTACCA	CTTTTGAAGA	GATGTTAGCT	GTATTAAAAA	CAGCTTATCA	ACTTAAACAC	180
GCAAAAGGTG	GACGAAACC	TAAATTAAGC	CTAGAAGACC	TTCTTATGGC	CACTCTTCAT	240
ATGTGCGAGA	ATATCGAACT	TATGAACAAA	TTGCGGCTGA	TTTGGTATT	CACGAAAGCA	300
ACTTTATCCG	TCGGAGCCAA	TGGGTTGAAG	TAA			333

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

AAAGAAAAGT	ATAAACTAAG	CCCTATAGGG	TGGCTTCGCA	CCACCTTTAG	AAAGAAGAAT	60
AACGTGAAAT	TTAATGAATT	AAACTTGTCT	GCTGATTTGC	TAGCAGAAAT	TGAAAAAGCT	120
GGTTTTGTAG	AAGCTAGTCC	TATCCAAGAA	CAAACTATTC	CTTTGGCCCT	TGAAGGCAAG	180
GATGTTATTG	GTCAAGCTCA	GACTGGTACA	GGAAAACTG	CAGCCTTTGG	CTTGCCCTACC	240
CTTGAAAAAA	TCCGTACAGA	AGAAGCGACT	ATCCAAGCTT	TGGTCATCGC	TCCAACCTCGT	300
GAACTAGCTG	TCCAAAGTCA	AGAAGAAGTC	TTCCGCTTTG	GTCGTAGTAA	GGGAGTCAAA	360
GTCCGTTTCA	TATATGGCGG	ATCAAGCATT	GAAAAACAAA	TTAAGGCTCT	TAAATCTGGT	420
GCCCATATCG	TGGTGGGAAC	TCCAGGTCGC	CTCTTGGACT	TGATTAAACG	CAAGGCCCTTG	480
AAATTACAAG	ACATTGAAAC	CCTTATCCTT	GACGAAGCGG	ATGAAATGCT	TAACATGGGC	540
TTCCTTGAAG	ACATCGAAGC	CATTATTTCC	CGTGTACCTG	AGAACCGTCA	AACTTTGCTT	600
TTCTCAGCAA	CTATGCCAGA	TGCCATCAAA	CGTATCGGTG	TTCAGTTTAT	GAAAGCCCCCT	660
GAACATGTCA	AGATTGCGGC	TAAGGAATTG	ACAACAGAAT	TGGTTGACCA	GTACTATATC	720
CGTGTTAAGG	AACAAGAAAA	ATTTGACACC	ATGACTCGTC	TCATGGATGT	GGCACAACCA	780
GAACTCGCTA	TTGTATTTGG	TCGTACCAAA	CGCCGTGTGG	ATGAATTGAC	TCGTGGTTTG	840
AAAAATTCGTG	GCTTCCGTGC	AGAAGGAATT	CATGGCGACC	TAGACCAAAA	TAAACGTCCT	900
CGTGTCTTTC	GTGACTTTAA	AAATGGCAAT	CTTGATGTTT	TGGTTGCGAC	AGACGTTGCA	960
GCGCGTGGTT	TGGATATTTT	AGGTGTGACC	CATGTCTACA	ACTACGATAT	TCCACAAGAT	1020
CCTGAGAGTT	ATGTTACCCG	TATCGGTCGT	ACAGGTCGTG	CTGGTAAGTC	AGGTCAATCT	1080
ATTACTTTTG	TTGCTCCAAA	CGAAATGGGT	TACCTTCAAA	TCATTGAAAA	CTTGACTAAG	1140
AAACGCATGA	AAGGTCTCAA	ACCTGCAAGT	GTAGAAGAAT	CCTTCCAATC	AAAAAACAG	1200
GTAGCTCTCA	AGAAAAATCGA	ACGTGATTTT	GCAGATGAAA	CCATTCTGTC	CAACTTTGAG	1260
AAATTTGGTA	AGGATGCTCG	CAAATTGGCT	GCTGAGTTTA	CTCCAGAAGA	ATTGGCAATG	1320
TATATCTTGA	GTCTGACAGT	CCAAGACCCA	GATAGCCTTC	CAGAAGTGGA	GATTGCACGT	1380
GAAAAACCAC	TACCGTTTAA	ACCATCAGGT	AATGGTTTCG	GTGGTAAAGC	TAAGGGAGGT	1440
CGTGGAGGCC	GTCGTGGGGA	CGACCGTCGA	GAGCGTGATC	GCCGTGGCAA	TGGTCGCCGT	1500
GATGAGTTCA	AAAAAGGAAG	TCGTGGCAAC	GATCGTTTTC	ATAAGGAAAA	ACGTTACCGT	1560
AAGGATAATA	AAAAACCACG	CAATACTTTA	AGCGAAAAGC	AAACAGGCTT	TGTTATTCGT	1620
AACAAGGGCG	ATAAATAA					1638

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...843
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

TACAGGAAGT	ATGACAGTCG	TAGAATTATA	AATACTTCAT	TTAGAAAGAA	AGTGTATGAA	60
GAAAAGCAGT	ATTTTATTTT	TATTTTATTG	CTATGTATTG	GTTTACAGTA	TGAAACCATC	120
TACTATACGG	ACGGTTCGAG	GTCAGGTGCG	GAATATGGAC	TAATGGGAGT	TTCTATCTTT	180
CTAGCTCTCT	TTTACATGAT	TCCGGCTCTT	TATTTTCTCT	TCCGTATTGG	GAAGAAAATGG	240
GAATTGCCAA	AGAAGGTTTT	GATTCTGTCT	TTATTGGGAG	GGATGTTCCCT	TGCAGGCTGG	300
TTGTCTAGTT	TTGCTAATAC	TTATATCCAT	GATTTACTGG	GGGTTCTTTT	CCCAGATAGT	360
CCATTTTTTAA	ATGCCTTTGA	AAGTGCTATT	GTGGCTCCTT	TGGTAGAAGA	ACCCTTGAAA	420
TTATTGCCAC	TTGTTTTTGT	TTTGGCTTTG	ATTCCCTGTC	GAAAATTAAA	ATTTTTGT	480
TTACTTGGA	TTGCTTCCGG	TTTGGGATTC	CAAATGATTG	AGGATATTGG	TTATATTCGT	540
ACGGATTTGC	CAGAGGGCTT	TGACTTTACT	ATTTTCGCGAA	TTTTAGAGCG	TATCATCTCA	600
GGAATTGCCT	CTCACTGGAC	TTTTTCAGGT	CTAGCTGTAG	TAGGTGTTTA	CTTGCTTTAC	660
AGAGCCTATA	AAGGACAGAA	GGTTGGCAAG	AAACAGGGTC	TTATTTTTCT	AGGTTTAGCC	720
TTGGGAACTC	ACTTCTTGTT	TAACTCTCCC	TTTTGTGGAG	TTGGAAACAG	AGTTGCCTTT	780
AGCGATTCCA	GTGGTTACGG	CTATTGCTCT	CTATGGTTTT	TATCATGCTT	ATTGCTTTGT	840
TGA						843

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 876 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

ATGAAGGAGT	ATGACATGAA	AAAGTGGTGG	AAAGAGCTGA	TAGACAAGCC	TTTATTAAAA	60
GCTTTTTTGC	ATTATTATCA	AGCATCAGAT	AGTGAGTTGA	CCAGTGTCGC	AGTAGCCTAC	120
TATTGGTTGA	TTTCGATTTT	CCCCCTGCTT	TTGGTGGTGG	TCAATATCCT	CCCCATTFTT	180
CAGATTCCTG	TGGGAGAATT	TTTGGGCTTT	ATGAAAGACG	TTCTGCCCCC	AAGCCTCTAT	240
GAAGGTGTGG	AAAAAATAGC	CAGAGAAGTT	TTGACGCAAC	CTTCAACAGG	TTTATTGAGT	300
TTTTCTGTTT	TATCGGCGTT	ATGGAGTTTT	TCAAAATCTA	TGAATTTCTT	GCAAAAAGCT	360
TTTAACAAGG	CTTATGGCGT	CGAAAAGAGT	CGTGGACTTA	TTTCCCATCA	GATGCTAAGT	420
CTCCTAGTCA	GTTTTGGCTT	GCAGATCCTC	TTTGCCTTTG	CCTTGTTTTT	GATCTTATTT	480
GGTCAGATGA	TTTTGGCTTT	ACTTGCTCAT	TATTGGACAA	AAGATGGCAT	TATCTATCAG	540
GCTTTACAAG	GGTTGGCAGG	TCCTCTGATT	TACGCCCTCC	TCTTTGCTAT	CTTGGTCATG	600
CTTTATTATT	TTCTTCCCAA	TCTATCTAAC	AGGAAAATTA	GCTATACCCT	ACCAGGCAGT	660
GCCTTTGTTC	TCTTAGTGAT	TTTAGGTTTA	CTAACTCTGT	TCTCTAGTTA	TCTCAATTAC	720
TATGTCCATC	ATTTGGTGGG	TGTCCGAATT	TTAGGTTCCG	TTCTTCTTGT	TGTTATGATG	780
TTTTGGTTTA	TCTTGATTGC	TAAAATTGTT	ATCCTAGGCG	CGGTTATCAA	TGCCAGTATG	840
CAGAGTTTGA	AAGATCCGGT	CTTTAAAAAA	GACTAA			876

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

AAGAAGGAGT	ATCTACGTAA	TATGAAGAAA	AAAATCTTAG	CGTCACTTTT	ATTAAGTACA	60
GTAATGGTTT	CTCAAGTAGC	TGTTTTAACA	ACTGCGCATG	CAGAAACGAC	TGATGACAAA	120
ATTGCTGCTC	AAGATAATAA	AATTAGTAAC	TTAACAGCAC	AACAACAAGA	AGCCCCAAAA	180
CAAGTTGACC	AAATTCAGGA	GCAAGTATCA	GCTATTCAAG	CTGAGCAGTC	TAACTTGCAA	240
GCTGAAAATG	ATAGATTACA	AGCAGAATCT	AAGAACTCG	AGGGTGAGAT	TACAGAACTT	300
TCTAAAAACA	TTGTTTCTCG	TAACCAATCG	TTGGAAAAAC	AAGCTCGTAG	TGCTCAAACA	360
AATGGAGCCG	TAACTAGCTA	TATCAATACC	ATTGTAAACT	CAAAATCAAT	TACAGAAGCT	420
ATTTACCGTG	TTGCTGCAAT	GAGTGAAATC	GTATCTGCAA	ACAACAAAAT	GTTAGAACAA	480
CAAAAGGCAG	ATAAAAAAGC	TATTTCTGAA	AAACAAGTAG	CAAATAATGA	TGCTATCAAT	540
ACTGTAATTG	CTAATCAACA	AAAATTGGCT	GATGATGCTC	AAGCATTGAC	TACGAAACAG	600
GCAGAACTAA	AAGCTGCTGA	ATTAAGTCTT	GCTGCTGAGA	AAGCGACAGC	TGAAGGGGAA	660
AAAGCAAGTC	TATTAGAGCA	AAAAGCAGCA	GCTGAGGCAG	AGGCTCGTGC	AGCTGCGGTA	720
GCAGAAGCAG	CTTATAAAGA	AAAACGAGCT	AGCCAACAAC	AATCAGTACT	TGCTTCAGCA	780

AACACTAACT	TAACAGCTCA	AGTGCAAGCA	GTATCTGAAT	CTGCAGCAGC	ACCTGTCCGT	840
GCAAAAGTTC	GTCCAACATA	CAGTACAAAC	GCTTCAAGTT	ATCCAATTGG	AGAATGTACA	900
TGGGGAGTAA	AAACATTGGC	ACCTTGGGCT	GGAGACTACT	GGGGTAATGG	AGCACAGTGG	960
GCTACAAGTG	CAGCAGCAGC	AGGTTTCCGT	ACAGGTTCAA	CACCTCAAGT	TGGAGCAATT	1020
GCATGTTGGA	ATGATGGTGG	ATATGGTCAC	GTAGCGGTTG	TTACAGCTGT	TGAATCAACA	1080
ACACGTATCC	AAGTATCAGA	ATCAAATTAT	GCAGGTAATC	GTACAATTGG	AAATCACCGT	1140
GGATGGTTCA	ATCCAACAAC	AACTTCTGAA	GGTTTTGTTA	CATATATTTA	TGCAGATTAA	1200

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

ATAAATTGGT	ATAAGATGAC	GCGCTATGCT	TTGCTGGTGA	GAGGTATCAA	TGTTGGTGGT	60
AAGAATAAGG	TCGTCATGGC	GGAGCTTCGT	CAAGAATTGA	CAAACCTGGG	ACTGGAAAAG	120
GTTGAGAGCT	ACATCAACAG	TGGCAATATT	TTCTTTACTT	CGATAGATTC	CAAAGCCCAA	180
TTGGTTGAAA	AGCTAGAGAC	TTTCTTTGCA	GTCCATTATC	CATTTATTCA	GAGCTTTTCT	240
TTACTGAGTC	TAGAGGACTT	TGAGGCGGAA	CTTGAAAATC	TACCAGCTTG	GTGGAGCAGA	300
GACTTGGCAC	GAAAAGATTT	TCTCTTTTAC	ACTGAGGGTT	TGGATGTGGA	CCAAGTCATC	360
GCGACAGTTG	AAAGTTTAGA	GCTGAAAAGAT	GAAGTGCTTT	ATTTTGGAAA	ACTTGGGATT	420
TTCTGGGGGA	AATTTTCTGA	AGAATCCTAT	TCTAAGACTG	CCTATCAGTA	G	471

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GA	ACTATGGT	ATAATAAGAG	AATGAACTAT	CCAAAAATTG	ATTTAAAAAC	AATTCGTCAG	60
GAG	TCAAAAC	ATTTTCAGGC	TGACACCCCC	CGTCTCTTTC	TCCTCTATAT	CCTTCCCAGT	120
ATG	CTGGTCA	TCTTATCTGG	TTTTCCTTAAT	CCCTTATCTC	GGATCCACGG	GACTGTTTTA	180
GA	ACAGCCAT	TTTTCAGCAT	ACTTGGCCAA	ATACCTTCAA	CCTACCTCTT	TCCTCTACTA	240
GT	CTCCTTTA	TCGGGACTAT	TCTTTTGACC	AGTTCCGTCT	ATGCAACACT	GACACTCATG	300
AA	GATTCTA	AAACGGAGCC	ATCTGTAAAA	AACAGCCTAG	CTCTCTTTGA	TGAGGAGCGC	360
TT	TTCTCAAA	CCTTTTGGAC	CCTACTTCTC	AAACGTTTCT	ATCTCTTTTT	ATGGAGTATC	420
CCT	AATTTAC	TTGGGATTTA	CCTCCTCTTT	TATAGTAGCT	TTTtagccaa	AAAATTCGTC	480
ACC	CTACATC	CTGAGTTTCC	AAATCTAGAT	CTCTCATCAG	TTGAAACCGA	GCGTTTCCTC	540
AT	GGTCTTTG	GACTCTACTT	TCTTGCAAGT	CTCATCTTGA	TCATTGTAGG	AAATATCCTC	600
TAT	ATTTCCAC	AGTATTATGC	CTATTCACAG	GTGGAATTTC	TTCTCTGTTA	TAGTCTAGAC	660
CT	AGGACAGG	TCCCACCAAG	ACGAATCCTA	AAAAC TAGCC	GTTCCCTTAT	GAAGGGCTAC	720
AAG	TCCAGC	ACTTTGTCTT	AGATTTACAG	CTTCTTCCCT	GGTACTTCCT	CAATTGGATT	780
AC	CTTTGGCA	TTGCTAGTTT	TTCAC TCCTA	CCTTATATCC	AATGCACTAA	AATTATGTTT	840
TAC	CGAGCAG	TATTGGCCCG	AAAACGTCCA	AAAGCTTGA			879

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

AT	GTTAGATT	TGATTCAGAC	TAGACGAGAT	TTACACCAGA	TACCAGAGAT	TGGCTTGGAG	60
GAG	TTCAAGA	CTCAGGCTTA	TTTGCTGGAT	GTGATTGAGA	AATTGACTAC	GGGCAAGGAT	120
TT	TGTTCAA	TTCGTACTTG	GCGGACAGGG	ATTTTGGTCT	ACCTGCAGGG	AAGTCAGCCG	180
GAG	CGAACCA	TTGGTTGGCG	GACAGATATT	GATGGCCTGC	CTATCGTCGA	ACAAACAGGT	240
CT	ACCTTTTG	CTTCTCAACA	CCAAGGTCGC	ATGCATGCCT	GTGGTCATGA	TTTTCATATG	300
ACC	ATTGCCT	TAGGCTGTCT	TGAGCGCGCC	CTTGAGGAGC	AACCAAGAA	TAATCTGCTC	360
TT	TCTATTT	AGCCTGCTGA	AGAAAATGAA	GCTGGTGGTA	TGCTCATGTA	TGAGGACGGT	420
GCT	TTTGGAG	ATTGGTTGCC	AAACCAATTC	TATGGTCTCC	ATGTTCTGTC	AGATTTGAAA	480
GT	CGGCCAGA	TTGCGACTAA	TACTCATACA	CTCTTTGCAG	GAACCTTGCGA	GGTGAAGATC	540
CG	TTTCAAAG	GCAAAGGTGG	CCACGCAGCT	TTTCCTCATG	AAGCCAATGA	CGCCTTGGTG	600
GCG	GCTAGTT	ACTTTGTGAC	CCAAGTGACG	TCAGTTGTTA	GCCGCAATGT	CAACCAATC	660
GAG	GGGAGCAG	TGGTGACCTT	CGGCGTTTTT	CAAGCTGGAA	CCACCAACAA	TGTCATCACA	720

GACACAGCTT	TTTTACATGG	AACTATTCGT	GCCTTGACAC	AGGACATGAG	TCTCTTGGTG	780
CAAAAGAGGG	TAAAAACAGT	TGCAGAAGGG	GTTGCAGCTG	CCTTTGATAT	GGAAGTCGAA	840
GTGGAACCTCA	AACAAGGTGG	ATACCTACCT	GTTGAGAACA	ATCCAGCCTT	GGCGCGTGAA	900
CTGATGGACT	TCTTTGACGA	GAAAGACGGA	ATCGAGTTGA	TTGATATCGA	ACCTGCTATG	960
ACAGGCGAGG	ACTTTGGTTA	TCTCCTTTCA	AAGGTTGATG	GCGTGATGTT	TTGGCTAGGT	1020
ATCGATAGTC	CCTACGCTCT	TCATCACCTT	CAAATGAGTC	CTAAGGAAGA	AGTCTTAGCT	1080
ATTGGGGTGG	CTGCGGTGTC	TAGTTTCCTG	AAAAAGAAGG	CAGCAGAATA	G	1131

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...642
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

CTTGCGTGGT	ATGACGACAG	AAGAGCTGGC	GGTAGCAACG	ACTGCAAATG	CAGAACGAAT	60
TTTTGGATTG	GACAGCAAGT	AATGAAAGAG	AAAAATTTCTC	AAGTTATCGT	GGTTGAAGGT	120
CGCGATGATA	CGGTCAATCT	CAAGCGTTAT	TTCGATGTGG	AGACCTATGA	GACACGAGGT	180
TCTGCCATCA	ATGATCAGGA	TATAGAGCGA	ATTCAGCGTC	TACACCAACG	TCATGGAGTC	240
ATTGTCTTTA	CAGACCCAGA	TTTTAATGGG	GAGCGGATTC	GGCGCATGAT	CATGACGGCC	300
ATTCCAACAG	TTCAGCATGC	CTTTCTCAAG	CGAGATGAAG	CTGTTCCCAA	GTCCAAGACC	360
AAGGGGCGTT	CTCTGGGAAT	TGAGCATGCC	AGCTATGAAG	ACCTGAAAAC	GGCTCTAGCT	420
CAGGTGACAG	AACAATTTGA	ACATGAGAGT	CAGTTTGACA	TTAGTCGTAG	CGATTTGATT	480
CGCCTTGGTT	TTCTAGCAGG	GGCAGACAGC	CGTAAGCGTA	GAGAATATCT	CGGAGAGACT	540
CTCCGAATCG	GCTATTCTAA	CGGCAAGCAA	CTCCTCAAAC	GCCTAGAGTT	GTTTGGGGTT	600
ACTTTGGCAG	AAGTGGAAGA	AGCTATGAAA	TCTTATGAGT	AG		642

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GAAAAGAGGT	ATCTTATGAC	AACATTTACT	ATCCATACAG	TAGAGTCAGC	ACCAGCAGAA	60
GTGAAAGAAA	TTCTTGAAAC	AGTAGAAAAA	GACAACAATG	GCTATATTCC	CAACCTAATC	120
GGTCTCTTGG	CCAATGCCCC	GACTGTTTTA	GAAGCCTACC	AAATTGTCTC	ATCTATCCAC	180
CGTCGCAACA	GCCTGACACC	CGTTGAGCGT	GAAGTGGTGC	AAATCACGGC	AGCCGTGACC	240
AATGGTTGTG	CCTTCTGTGT	CGCAGGTCAC	ACAGCCTTTT	CCATCAAACA	AATCCAGATG	300
AATGATGACT	TGATTCAAGC	TCTTCGCAAT	CGTACTCCAA	TTGAAACAGA	TCCTAAATTG	360
GATACCCTAG	CTAAGTTTAC	CTTGGCAGTT	ATCAATACCA	AGGGTCGTGT	AGGAGATGAA	420
GCCTTGCTCG	AGTTTTTAGA	AGCTGGCTAC	ACTCAACAAA	ATGCCTTGGA	TGTGGTTTTT	480
GGTGTCAGCC	TAGCAATCCT	CTGTAACTAT	GCCAACAAC	TAGCTAATAC	ACCAATTAAT	540
CCAGAATTGC	AACCTTATGC	CTAA				564

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

ATTTGGAGGT	ATTGTATGAG	CAAGGAATTA	CACATTAACA	CAATTTTGGC	CCAGGCGGGT	60
ATTAAGTCAG	ATGAAGCGAC	AGGTGCATTG	GTGACACCGC	TTCATTTTTC	AACGACCTAT	120
CAGCATCCAG	AGTTTGGTCG	ATCTACTGGG	TTTGACTATA	CGCGCACTAA	AAATCCAAC	180
CGTAGTAAGG	CTGAGGAAGT	CTTGCGGACT	ATTGAGTCAG	CAGACTATGC	CTTAGCGACT	240
AGCTCAGGGA	TGTCAGCTAT	TGTACTGGCC	TTTAGCGGCT	TTCCAGTAGG	AAGTAAGGTC	300
TTGGCAGTGC	GTGATCTTTA	CGGCGGTTCT	TTTCGCTGGT	TTAACCAAGT	GGAGCAGGAA	360
GGTCGTTTCC	ATTTTACCTA	TGCCAATACA	GAAGAAGAGT	TGATTGCCGA	GTTAGAAAAG	420
GATGTGGATG	TTCTCTATAT	CGAAACCCCA	ACCAATCCCT	TGATGTTGGA	ATTTGATATC	480
GAAAACTAG	CAAAATTGGC	TCATGCTAAG	GGTGCCAAAG	TGGTGGTGGA	CAATACCTTC	540
TATAGCCCTA	TCTACCAACG	TCCGATTGAA	GATGGAGCAG	ATATCGTTCT	CCATTTCAGCA	600
ACCAAGTATC	TAGCAGGCCA	CAATGATGTC	TTGGCTGGAG	TGGTTGTGAC	CAATAGTTTA	660
GAACTATACG	AGAAGCTTTT	TTACAATCTC	AATACAACAG	GGGCAGTCTT	GTCTCCATTT	720
GACAGCTACC	AGTTGCTTCG	TGGTCTCAAG	ACCTTGCTCT	TTCGTATGGA	GCGCTCAACA	780

GCTAACGCCC	AAGAAGTGGT	TGCCTTTTTG	AAGGATTCTC	CAGCAGTTAA	GGAAGTTCTC	840
TACACTGGTC	GTGGAGGCAT	GATTTCCCTT	AAAGTAGCCG	ATGAAACACG	CATTCCTCAT	900
ATTTTGAACA	GTCTCAAGGT	CTTCTCTTTT	GCGGAAAGTT	TGGGCGGAGT	GGAAAGTCTT	960
ATTACTTATC	CAACGACTCA	AACTCATGCT	GATATTCCAG	CAGAAGTACG	CCATTCTTAT	1020
GGTTTGACAG	ATGACCTCTT	GCGTTTGTCT	ATTGGGATTG	AGGATGCTAG	AGATTTGATT	1080
GCAGATTTGC	GCCAAGCCTT	AGAAGGATAA				1110

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...606
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GCAGCAGATT	TAGCTATTGG	TGATTTTGAA	GGAACCATT	ATAAGGATCA	TTATTTAGCG	60
GGTTATCTTC	TCTTTAATGC	TCCTGTTGAA	GTTATGGATG	CTATTAAGGA	GGCAGGTTAT	120
CATGTGCTGG	ATTTAGCTCA	TAATCATATT	TTGGATTTCG	AAATTGAGGG	AGTTATTTCA	180
ACGGCCGATA	TTATTGAGAA	AGCTGGAATC	ACTCCAATCG	GAGTTTATAC	GCACGAACCA	240
CGTGATCAGG	CTCCGCTGGT	CATTAAGGAA	GTGAATGCTA	TCAAGGTTGC	ATTGTTAGCC	300
TATTCCTATG	GTTTCAATGG	AATTGAGCAG	TATATTTTTC	AGGAAGACTA	TAATCGTTAT	360
CTTTCAGATT	TAAACGAAGA	TAAGATAAAG	GCTGAAGTTG	AACGGGCAGA	GAAGGAAGCA	420
GATATCACCA	TTATCATGCC	TCAGATGGGT	GTTGAGTATC	GATTGGAACC	AACTGAAGAA	480
CAAAAAGCTC	TTTATCACAA	GATGATCGAT	TGGGGAGCGG	ATATTATCTT	TGGAGGGCAT	540
CCTCACGTTG	TTGAACCATC	TGAAACGGTT	GAAAAAGATG	GAGATAAGAA	ACTCATTATC	600
TATTAA						606

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GCCATTATNT	ATGATATGAA	TTTAAACATG	TCTATTATNT	CTATGGTTTT	AGTAGTCGTT	60
GTAGCCGTCT	TTGCAGGTCT	TGAAGGCATC	CTCGACCAGT	TCCAATTTCA	CCAACCACTT	120
GTAGCCTGTA	CCCTTATTTG	GCTTGTAACA	GGTCACCTGG	AAGCAGGGAT	TATCCTCGGT	180
GGATCGCTTC	AAATGATTGC	CCTTGGTTGG	TCAAATATCG	GTGCTGCTAT	CGCTCCTGAT	240
GCTGCACTTG	CTTCTGTGCG	TGCTGCCATT	ATCATGGTTC	TTGGTGGTGA	CTTTACCAAG	300
ACTGGTATCG	GTGTGCCCCA	AGCGTTTGCT	ATCCCTCTTG	CCGTAGCTGG	ACTTTTCTTG	360
ACAATGATTG	TTCGTACAAT	TTCAGTTGGT	TTGGTTCATA	CTGCAGATGC	TGCCGCTAAA	420
AAAGGTGACT	TCGGCGCTGT	GGAGCGTGCG	CATTTTCATTG	CGCTACTCTT	CCAAGGACTT	480
CGTATCGCGC	TTCTTGCAGC	TCTTCTCCTT	ATGGTACCAA	CTGAAACTGT	ACAAAGTATC	540
CTTAGTGCCA	TGCCAGACTG	GCTCAAAGAT	GGTATGGCTA	TCGGTGGTGG	TATGGTCGTT	600
GCCGTTGGTT	ACGCCATGGT	TATCAACATG	ATGGCAACTC	GTGAAGTATG	GCCATTCTTC	660
GCTCTTGGTT	TCGTTCTCGC	TGCTGTGTCA	GATATTACTC	TAATCGGATT	CGGTGCTATC	720
GGTGTGCTA	TCGCTCTTAT	CTACCTTCAC	CTTTCTAAAA	CTGGTGGAAA	TGGTGGCGGA	780
GGAGCCGCAA	CTTCTAACGA	CCCAATCGGC	GATATCCTAG	AAGACTACTA	A	831

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

AATCAATATC	TATTGATGGA	GAAAGTGATG	TCCAAACACC	CTCATTATGA	ATTGTTAAAT	60
TTAATTGGCT	ACGGTCTTGC	CAAGTTTGAC	AAGCTTTTTA	TAAAAGAATT	TCAATGCTCT	120
AGCAAGTCGG	AGTTTTATCG	CTATGTGGTT	TCTCTGGGAA	TTGCTGAAAC	AACTGGAGTT	180
GTAAAAAATA	GAATGGATTT	ATTTTGATCCT	TATTTTGACA	ATAATCGAAA	AGGTTGGTGG	240
CAGAAAGCTG	AAGTTTATCG	TTTTCGTAAA	GATTTAATTG	ATATGATGTT	TGGAAATGAA	300
GATGTTTCATA	GTTATGCTGA	AATAGTTAAA	ATGTTACTTG	CCAGTGAAGG	GAAGAAAACA	360
GGCATAACCA	TCGTTGAAAA	ACCAATAGTT	CGAACTAAAT	TCAAACGTCT	ACAGGAAACG	420
GGAATGGAGG	CTGAGAATTA	TTTTATCCTT	CATTTTGATA	AAGAAGAAAA	ATTCCAAGGT	480
GGACAGTTAA	CCGATGCCCG	TCTTTATGGT	GATGGATATG	ACTTTCAGGT	AGATGTCCAA	540
GAGTATTCTT	ACCTTGCCGA	AGTAAAAGGT	ATCCGAAAAT	CTAAGGGGCG	TGTGCGTTTA	600
ACTGCAAAAG	AATTTGAAAA	AGTCAAGGAG	TTTCAATCGG	ATTTTATTTT	ATCCTTGGTC	660

ACAAATCTAG ATGATATTCC AAAGTTAGTG TTAATCGATA ATCCTTTAAA ACATTTTGAG	720
TTTAAAAAGA ATATTATCAA AAATGAAATC ATTGAATATA GAAGCGTAGA GGATTTGTAT	780
TAG	783

(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GAAATGTATC TCGTTATAGG AATTGTATTA GCCTTTATAG TGTCATTTTG GAAGGATAAT	60
AGAAGTTTGT GGAATCCAGT ATTATTTTTA TTATCCCTCA TTTCAAGTTA TTTTATCTA	120
TCCTACCTTT TTTATAAAAA TGGATACGAG AATGTTTCAGT TAGCTTTTTA TGTATTTGCC	180
TTTGTCTTAC TTCCTTTTTT GCTTTTTTCTA AGTGGCATCT TTTTAATCTA TAATGGGGTC	240
ATTTTGTGTA AGCGAGAGGG ACGTTCCAAG CCCCATATC TCTCAATGCT ATTTGATTTT	300
TATTGA	306

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 873 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...873
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

CAAATGGATT	TCACATGGGC	ACTGAAGTAT	GCCACTGAAT	TTTTGGGAAC	TGCCATTTTG	60
ATCATTCTTG	GGAATGGTGC	AGTTGCCAAC	GTTGAACTTA	AAGGTACGAA	AGGTCACCAA	120
AGTGGCTGGA	TCGTCATCGC	TGTTGGTTAT	GGTATGGGGG	TTATGATCCC	TGCCTTGATG	180
TTTGGTAACG	TATCTGGGAA	TCACATCAAC	CCTGCTTTCA	CTCTAGGGCT	TGCAGTTAGC	240
GGTCTTTTCC	CTTGGGCACA	AGTGGTACCT	TATATTATCG	CGCAAGTCTT	GGGGGCTATC	300
TTTGGCCAAG	CCTTAGTTGT	GGCAACATAC	CGTCCATTCT	ACTTGAAAAC	TGAAAACCCA	360
AATAACATCT	TGGGAACTTT	CTCAACTATT	TCAAGTATTG	ACCATGGTAC	AAAAGAAAGT	420
CGCTATGCAG	CAACTGTCAA	TGGTTTGATT	AATGAGTTTG	TTGGTTCATT	TGTTTTGTTC	480
TTTGCAGCTC	TTGGTTTGAC	TAAAAAATTTC	TTTGGTGCTG	AAGTGCTTCA	ATTCATGAAA	540
CAAAAAGGCAA	TAGAAGCAGG	ACAAAACAGTT	GATTTTTTCTG	ACTTGGCTAT	TAAAGCACAG	600
GTGGCTCCAC	ACACTGCTTC	AGGACTTTTCT	GTGGCTCACT	TGGCACTTGG	ATTCCTCGTT	660
ATGGCTTTGG	TAACATCACT	TGGAGGACCT	ACAGGACCTG	CCTTGAACCC	AGCCCGTGAC	720
TTGGGACCAC	GTCTCCTTCA	TGCTTTCCTT	CCAAAATCAG	TTCTTGGTGA	GCATAAAGGC	780
GATTCAAAAT	GGTGGTATTC	TTGGGTACCA	GTAGTAGCAC	CTATCGCAGC	AGCAATTGCG	840
GCAGTAGCTG	TATTCAAATT	CCTTTATCTC	TAA			873

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

AAGCACCATC	TTCTTGCCA	AGTCATAAAT	CTTGACTGGT	TTGCCCATAT	CAAGGATAAA	60
GACTTCCCCA	TCTTTGGCAT	AAGCACCAGC	ATGGATAACC	AGACGACTAG	CTTCTGGAAT	120
GGTCATAAAG	TAACGGGTCA	TGCGGAAGTC	TGTCACCGTT	ACAGGCCAC	CTTCAGCAAT	180
CTGACGTTCA	AAGACTGGAA	TGACACTACC	ACGGCTACCA	AGAACATTCC	CAAAACGAAC	240
TGCACAGTAG	GTTGA					255

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

TTTAAGGATT	TTCTTAAGGG	CGTGGAAGAT	TTCAGCACCG	TAACGAAGGG	CTTCTTTAAA	60
TGTTGGCGCA	CCAACTGGCA	AGATCATGAA	CTCTTGGA	GCGATTGGAG	CGTCAGAGTG	120
AGAACCACCG	TTGATGATGT	TCATCATTGG	AGTTGGAAGA	ACTTTAGTGT	TGAATCCACC	180
AAGGTAGCTG	TAAAGTGGGA	TTTCAAGGTA	GTCAGCAGCA	GCACGAGCTA	CAGCGATAGA	240
CACACCGAGG	ATTGCATTTC	CACCCCATTT	ACCTTTGTTA	GGAGTACCGT	CAAGTGCGAT	300
CATAGCACGG	TCAATAGCTT	GTTGATCACG	TACATCGTAG	CCAATGATAG	CTTCAGCAAT	360
GATGTTGTTT	ACGTTGTCAA	CAGCTTTTTG	TGTACCAAGA	CCACCGTAAC	GAGATTTGTC	420
ACCGTCGCGA	AGTTCAACTG	CTTCGTGTTT	ACCAGTAGAA	AGCTCCTTGA	TGGAACCATA	480
CCACGTCCGA	AAGCACCTGA	TTCAGTGTA				510

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 792 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GCAAACAATC	TTGAAAGGAG	CCAAGTTAAG	CAAATGACAG	CAATTGTAGA	ATTAAAAAAT	60
GCAACCAAAA	TCGTTAAAAA	TGGCTTTGAT	GAAGAAAAGA	TTATTTTAAA	TGATGTTTCC	120
TTAGAAATTT	TTGAACGGGA	CTTTATCACG	ATTTTGGGCG	GAAATGGTGC	TGGAAAATCA	180
ACCCTCTTTA	ACACTATAGC	AGGGACCTTA	TCACTAACTA	GTGGAACAT	CCGTATTTTA	240
GGTGAAGAAC	TCACTAAGTT	TTCACCCGAG	AAGCGTGCCA	AGTACCTGTC	TCGTGTCTTC	300
CAAGATCCAA	AGATGGGGAC	AGTCCCCCGT	ATGACGGTGC	CTGAAAATCT	TTTAATCGCC	360
AAGTTTCGTG	GTGAAAAGCG	TGGATTGTTA	CCACGACGCT	TGACTAGCTA	TAAGGATGAA	420
TTTCAGGCAA	CCATTGAAAA	AGTAGGAAAT	GGTCTTGAGA	AACACTTGAA	TACACCGATT	480
GAGTTCCTAT	CAGGTGGACA	AAGACAGGCT	TTGAGTCTCT	TGATGGCAAC	CTTGAAGCGA	540
CCTGAATTAC	TCTTGTTAGA	CGAGCATACT	GCTGCCCTGG	ATCCAAAGAC	TAGTGTGCT	600
TTGATGGGAT	TGACAGATGA	ATTTGTTAAG	AAAGATCAAT	TGACAGCCCT	TATGATTACC	660
CATCATATGG	AAGATGCTCT	CAAATATGGC	AATCGCTTGA	TTGTCATGAA	AGAAGGACGG	720
GTTATCCAAG	ATTTGAAACA	AGAAGAAAAA	GCAAAAATGA	AAATCTCTGA	TTATTATCAA	780

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GAGGTAAATC	TAATGGCTAA	AAAATCAATG	GTAGCTAGAG	AGGCTAAACG	CCAAAAAATT	60
GTTGACCGTT	ATGCTGAAAA	ACGTGCTGCA	TTAAAGGCGG	CAGGGGACTA	CGAAGGTTTA	120
TCTAAATTAC	CTCGCAACGC	TTCACCGACT	CGTTTACATA	ATCGTTGTAG	AGTTACGGGG	180
CGCCACATT	CAGTTTACCG	CAAATTTGGT	CTGAGTCGTA	TCGCTTTTCG	CGAACTTGCG	240
CATAAAGGTC	AAATTCCTGG	TGTAACAAAA	GCATCTTGGT	AA		282

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

TTTTTTTTTC	ACTTCCCCC	ACACCCACCC	CCATTCNCNT	TTCTTCCTTT	CTTCCCCCCT	60
CCCAACCTCC	CCCCNNCCCC	NCCTTTTCCT	TCCCCCTTTT	TCCCCANACC	TCCCNCAACA	120
CCCTTTTTTT	CCTTCTTTTC	CCCCCCCCNN	CCNTCACCCC	NCCTTCTTCC	TCCTTTCCCT	180

CCCTCCCCNT	TTTCTCCCC	CCCTTCNNNT	TTCCCTCTTT	TTTTTNNTTT	CCCTTTTNNN	240
NNNNNTNNNT	TTTTTTTTTT	TTNNNNNNNN	NTNNNNNTA	TTNNNTTNCC	CCCANNNNNN	300
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNTATTCAAT	GA		342

(2) INFORMATION FOR SEQ ID NO:644:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1305
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GTTTCTTTTC	ATCAGGAGGA	GAGATTGTTT	AAGAAAAATA	AAGACATTCT	TAATATTGCA	60
TTGCCAGCTA	TGGGTGAAAA	CTTTTTCAG	ATGCTAATGG	GAATGGTGGA	CAGTTATTTG	120
GTTGCTCATT	TAGGATTGAT	AGCTATTTCA	GGGGTTTCAG	TAGCTGGTAA	TATTATCACC	180
ATTTATCAGG	CGATTTTCAT	CGCTCTGGGA	GCTGCTATTT	CCAGTGTTAT	TTCAAAAAGC	240
ATAGGGCAGA	AAGACCAGTC	GAAGTTGGCC	TATCATGTGA	CTGAGGCGTT	GAAGATTACC	300
TTACTATTAA	GTTTCCTTTT	AGGATTTTTG	TCCATCTTCG	CTGGGAAAGA	GATGATAGGA	360
CTTTTGGGGA	CGGAGAGGGA	TGTAGCTGAG	AGTGGTGGAC	TGTATCTATC	TTTGGTAGGC	420
GGATCGATTG	TTCTCTTAGG	TTAATGACT	AGTCTAGGAG	CCTTGATTCT	TGCAACGCAT	480
AATCCACGTC	TGCCCTCTTA	TGTTAGTTTT	TTATCCAATG	CCTTGAATAT	TCTTTTTTCA	540
AGTCTAGCTA	TTTTTGTTCT	GGATATGGGG	ATAGCTGGTG	TTGCTTGGGG	GACAATTGTG	600
TCTCGTTTGG	TTGGTCTTGT	GATTTTGTGG	TCACAATTAA	AACTGCCTTA	TGGGAAGCCA	660
ACTTTTGGTT	TAGATAAGGA	ACTGTTGACC	TTGGCTTTAC	CAGCAGCTGG	AGAGCGACTT	720
ATGATGAGGG	CTGGAGATGT	AGTGATCATT	GCCTTGGTCG	TTTCTTTTGG	GACGGAGGCA	780
GTTGCTGGGA	ATGCAATCGG	AGAAGTCTTG	ACCCAGTTTA	ACTATATGCC	TGCCTTTGGC	840
GTCCGTACCG	CAACCGTCAT	GCTGTTGGCC	CGAGCAGTTG	GAGAGGATGA	TTGGAAAAGA	900
GTTGCTAGTT	TGAGTAAACA	AACCTTTTGG	CTTTCTCTGT	TCCTCATGTT	GCCCCTGTCC	960
TTTAGTATAT	ATGTCTTGGG	TGTACCATTA	ACTCATCTCT	ATACGACTGA	TTCTCTAGCG	1020
GTGGAGGCTA	GTGTTCTAGT	GACACTGTTT	TCACTACTTG	GGACCCCTAT	GACGACAGGA	1080
ACAGTCATCT	ATACGGCAGT	CTGGCAGGGA	TTAGGAAATG	CACGCCTCCC	TTTTTATGCG	1140
ACAAGTATAG	GAATGTGGTG	TATCCGCATT	GGGACAGGAT	ATCTGATGGG	GATTGTGCTT	1200
GGTTGGGGCT	TGCCTGGTAT	TTGGGCAGGG	TCTCTCTTGG	ATAATGGTTT	TCGCTGGTTA	1260
TTTCTACGCT	ATCGTTACCA	GCGCTATATG	AGCTTGAAAG	GATAG		1305

(2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 915 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

ATGGAAAATC	TTGTGAAAAG	CACAAGTGAT	ACATATATAC	TGGAGGAAAT	CATGTCCTTTT	60
TCTGATTTAA	AGCTGTTTGC	CCTTTCTTCT	AATAAAGAAT	TGGCAGAACG	TGTGGCGCAG	120
GAGATTGGGA	TAGAGTTGGG	GAAATCAAGT	GTTCGCCAAT	TTTCAGATGG	AGAGATTCAG	180
GTCAACATTG	AAGAATCAAT	CCGTGGGAAA	CACGTCCTTTA	TCCTACAATC	AACTAGTTTCG	240
CCTGTAAATG	ACAACTGCT	TGAAATTTTG	ATTATGGTAG	ATGCTTTGAA	GCGTGCGAGT	300
GCAGAATCTG	TCAATGTTGT	CATGCCCTTAC	TATGGGTATG	CACGTCAGGA	TAGAAAGGCG	360
AGAGCGCGTG	AGCCAATCAC	TTCAAAACTT	GTGCGAAATA	TGCTTGAAGT	AGCTGGAGTG	420
GATCGTTTAT	TGACCATCGA	CTTGCATGCT	GCGCAAATTC	AAGGATTCCT	TGATATTCCT	480
GTGGATCATT	TGATGGGTGC	TCCTCTGATT	GCAGATTATT	TTGAGCGTCG	TGGTATGGTT	540
GGTTCTGACT	ATGTGGTTGT	CAGCCCAGAC	CATGGAGGGG	TGACTCGTGC	TCGTAAGTTG	600
GCAGAATTTT	TGAAAACATC	TATCGCTATT	ATTGATAAAC	GTCGTAGCGT	TGATAAGATG	660
AATACTAGTG	AAGTTATGAA	CATCATCGGT	AAGGTTGAAG	GCAAGACTTG	TATCTTGATT	720
GATGATATGA	TTGATAACGC	TGGAACGATT	TGTCATGCGG	CAGATGCTCT	TGCGGAAGCT	780
GGTGCTGTTG	AAGTCTATGC	AAGCTGTACG	CACCCAGTTC	TTTCTGGTCC	TGCTACGGAC	840
AATATCCAAA	AATCAGCTAT	TAAGAAAGTG	GTTGTTTTTG	ATACCATCTA	TCTGCCAGAA	900
GAGCGCTCTG	ATTGA					915

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GGTCTCTTTC	AATCCAAACC	CTTTAAACTA	TACGTCATTT	CGGTCCTGCT	AAGTCTTGTG	60
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GTAATTTTAG	GTTTGATTTT	ACTTTTCTTT	TCACAAGAGC	CTCTGCACGC	TTCTTATTTG	120
ATGGTCGTC	TCCCTGTTTT	CCTACTTTTA	TTGGTAACCA	ATATTAAGAG	TCAACAGAGG	180
GGGCGTAGTG	CTAGAAGAAA	CCGAAGAGAA	ACGCCAGTTA	GCCTATGGAG	TCGTTTCTTC	240
AAAGGAAATC	TATATCTGCT	AGTTTTTGAG	TTTGTCTATC	TTTTGTCTGT	TCCTTTTTTG	300
ATGAAGTTTG	TCCTTTATCC	AGTACCTTAT	CAAGAACGTA	ATCGTCTTGC	TGATTTGGTA	360
AAAGAGGAGA	CAAATACGGA	AGATGCTATC	TATGCATGGG	ATGATACTGC	GACTCTTTAT	420
CGTAAGAGTG	AGCGCTTGTC	GCCATCGGCG	ATTTTGTC	CGTTGCACTA	TACAGCAACT	480
GAGGAAAATC	GTAATAAGTT	ACTTAATGAC	TTGAAAAGAAA	AACAACCTAA	GGTGATTGTG	540
GTAAATGATA	AGGTGGTAGT	CTGGTCTGAA	GTGGAAACAC	TCTTAAAAGA	AAATTACCAA	600
CAAGTAAAGA	CTGATTACTC	AGAGTTTAAA	GTCTATAAAA	TTAAATAA		648

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

AATCGCTTTC	AAACAAGAAC	AAAATGTTAT	ATAAGGAGAT	TTTTGCAAAT	GAACAATCAG	60
GAAATTGCAA	AAAAAGTCAT	CGATGCCCTG	GGCGGACGTG	AAAAATGTCAA	TAGTGTTGCC	120
CACTGTGCGA	CTCGTCTACG	TGTCATGGTC	AAAGATGAAG	AGAAAATCAA	TAAAGAAGTG	180
ATTGAGAACT	TGGAAAAAGT	TCAAGGTGCT	TTCTTTAACT	CAGGGCAATA	CCAAATTATC	240
TTTGGTACAG	GTACAGTTAA	CAAAATGTAC	GATGAAGTTG	TTGTACTTGG	CTTACCAACA	300
TCATCTAAGG	ATGACATGAA	AGCAGAAAGT	GCTAAACAAG	GGAAGTGGTT	CCAACGTGCT	360
ATCCGTACTT	TCGGTGATGT	TTTCGTTCCA	ATCATCCCAG	TTATCGTAGC	GACAGGTCTC	420
TTCATGGGTG	TGCGTGCTCT	TTTCAACGCT	CTTGAAATGC	CACCTCCAGG	TGACTTTGCA	480
ACTTACACAC	AAATCTTGAC	AGATACAGCC	TTCATCATCT	TGCCAGGTTT	GGTTGTGTGG	540
TCAACCTTCC	GTGTATTTGG	TGGAAATCCT	GCCGTTGGTA	TCGTTCTTGG	TATGATGCTT	600
GTCTCTGGCT	CACCTCCAAA	CGCTTGCGCA	GTTGCTCAAG	GTGGTGAAGT	AACAGCGATG	660
AACTTCTTTG	GTTTCATCCC	TGTTGTTGGT	TTGCAAGGTT	CCGTTCTTCC	AGCCTTCATC	720
ATCGGGGTTG	TCGGAGCTAA	ATTTGAAAAA	GCTGTCCGCA	AGGTTGTTCC	AGATGTCATT	780
GACCTCTTGG	TAACACCAT	CGTGACACTT	TTGGTCATGT	CTATCCTTGG	ACTCTTTGTC	840
ATTGGACCAG	TTTTCCACGT	TGTTGAAAAC	TACATCCTTA	TTGCTACAAA	AGCGATTCTT	900
AGCATTCAT	TTGGTCTTGG	TGGTTTCTTG	ATTGGTGGGG	TTACCCAATT	GATCGTCGTG	960
TCAGGTGTGC	ACCACATCTT	CAACTTGCTT	GAAAGTGAAT	TACTTGCTGC	TGACCATGCT	1020
AACCCATTCA	ACGCTATCAT	CACAGCTGCT	ATGACAGCTC	AAGGTGCTGC	TACTGTTGCG	1080
GTTGGTGTTA	AAACAAAAAA	TCCAAAACTG	AAAACACTTG	CTTTCCCGGC	TGCTCTTTCT	1140
GCCTTCCTAG	GTATTACAGA	GCCTGCTATC	TTCCGGGTGA	ACTTGCGCTT	CCGTAAACCA	1200
TTCTTCCTTT	CATTGATTGC	TGGTGCAATC	GGTGGTGGAT	TGGCTTCTAT	CCTTGACTT	1260
GCTGGTACTG	GTAATGGTAT	CACCATCATC	CCTGGTACAA	TGCTTTATGT	TGTAACGGA	1320

CAACTTCCAC	AATACCTTCT	TATGGTAGCT	GTATCATTTG	CCCTTGGTTT	TGCTCTTACT	1380
TACATGTTTG	GTTACGAAGA	TGAAGTAGAC	GCAACTGCAG	CTGCAAAACA	AGCTGAAGTG	1440
GCTGAAGAAA	AAGAAGAAGT	TGCGCCAGCA	GCTCTTCAAA	ATGAAACACT	TGTAACCTCT	1500
ATCGTCGGTG	ATGTTGTCGC	TCTTGCTGAT	GTCAATGACC	CAGTCTTCTC	AAGTGGAGCT	1560
ATGGGACAAG	GTATCGCTGT	GAAACCAAGC	CAAGGCGTGG	TCTATGCACC	AGCTGATGCT	1620
GAAGTTTCAA	TTGCCTTTCC	AACAGGGCAC	GCTTTTGGTT	TGAAAACAAG	AAATGGTGCT	1680
GAAGTTTGA	TTACAGTTGG	TATTGACACT	GTATCTATGA	ACGGTGACGG	TTTTGAAGCA	1740
AAAGTTGCTC	AAGGTAATAA	GGTGAAAGCT	GGCGATGTTC	TTGGAACATT	TGACTCAAAC	1800
AAAATCGCTG	CAGCTGGACT	TGATGATACA	ACAATGGTTA	TCGTTACAAA	TACAGCTGAC	1860
TACGCTTCAG	TAGCTCCAGT	CGCAACAGGT	TCAGTTGCGA	AGGGGGATGC	TGTGATCGAA	1920
GTGAAAATCT	AA					1932

(2) INFORMATION FOR SEQ ID NO:648:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5919 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...5919
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

ATTTTATTTT	AAGGAGGAAT	AATGGAAAAG	TATTTTGGTG	AAAAACAAGA	GCGTTTTTCA	60
TTTAGAAAAA	TATCAGTAGG	ACTTGTATCT	GCAACGATTT	CAAGTTTATT	TTTTATGTCT	120
GTATTAGCTA	GTTTATCTGT	GGATGCTCAA	GAAACTGCGG	GAGTTCATA	TAAATATGTG	180
GCAGATTGAG	AGCTATCATC	AGAAGAAAAG	AAGCAGCTTG	TCTATGATAT	TCCGACATAC	240
GTGGAGAATG	ATGATGAAAC	TTATTATCTT	GTTTATAAGT	TAAATTCTCA	AAATCAACTG	300
GCGGAATTAC	CAAATACTGG	AAGCAAGAA	GAGAGGCAAG	CCCTAGTTGC	TGGTGCTAGC	360
TTAGCTGCTC	TGGGAATTTT	AATTTTGTCT	GTTTCCAAGA	AAAAGGTTAA	GAATAAAACG	420
GTATTACATT	TAGTATTGGT	TGCGGGAATA	GGAAATGGTG	TCTTAGTTTC	AGTCCATGCT	480
TTAGAAAATC	ATCTTTTGCT	AAATTACAAT	ACGGACTATG	AATTGACCTC	TGGAGAAAAA	540
TTACCTCTTC	CTAAAGAGAT	TTCAGGTTAC	ACTTATATTG	GATATATCAA	AGAGGGAAAA	600
ACGACTTCTG	ATTTTGAAAGT	AAGTAATCAA	GAAAAATCAG	CAGCCACTCC	TACAAAACAA	660
CAAAAGGTGG	ATTATAATGT	TACACCAAAT	TTTGTAGACC	ATCCATCAAC	AGTACAAGCT	720
ATTCAGGAAC	AAACACCTGT	TTCTTCAACT	AAGCCGACAG	AAGTTCAAGT	AGTTGAAAAA	780
CCTTTCTCTA	CTGAATTAAT	CAATCCAAGA	AAAGAAGAGA	AACAATCTTC	AGATTCTCAA	840
GAACAATTAG	CCGAACATAA	GAATCTAGAA	ACGAAGAAAG	AGGAGAAGAT	TTCTCCAAAA	900
GAAAAGACTG	GGGTAAATAC	ATTAAATCCA	CAGGATGAAG	TTTTATCAGG	TCAATTGAAC	960
AAACCTGAAC	TCTTATATCG	TGAGGAAACT	ATAGAGATAA	AAATAGATTT	TCAAGAAGAA	1020
ATTCAGAAAA	ATCCTGATTT	AGTTGAAGGA	ATTGTAAGAG	TAAAACAAGA	AGGTAAATTA	1080
GGTAAGAAAAG	TTGAAATCGT	CAGAAATATC	TCTGTAAACA	AGGAAGAAGT	TTGCGGAGAA	1140
ATTGTTTCAA	CTTCAACGAC	TGCGCCTATT	CCAAGAATAG	TCGAAAAAGG	TACTAAAAAA	1200
ACTCAAGTTA	TAAAGGAACA	ACCTGAGACT	GGTGTAGAAC	ATAAGGACGT	ACAGTCTGGA	1260
GCTATTGTTG	AACCCGCAAT	TCAGCCTGAG	TTGCCCCAAG	CTGTAGTAAG	TGACAAAGGC	1320

GTACCAGAAAG	TTCAACCAGC	GTTGTCCAAA	GCAGTTATAA	CCGACAAAGG	TGAGACTGAG	1380
GTTCAACCAG	AGTCGCCAGA	TACTGTGGTA	AGTGATAAAG	GTGAACCTGA	ACAGGTAGCA	1440
CCGCTTCCAG	AATATAAGGG	TAATATTGAG	CAAGTAAAAC	CTGAAACTCC	GGTTGAGAAG	1500
ACCAAAGAAC	AAGGTCCAGA	AAAACTGAA	GAA GTTCCAG	TAAAACCAAC	AGAAGAAACA	1560
CCAGTAAATC	CAAATGAAGG	TACTACAGAA	GGAACCTCAA	TTCAAGAAGC	AGAAAAATCCA	1620
GTTCAACCTG	CAGAAGAATC	AACAACGAAT	TCAGAGAAAG	TATCACCAGA	TACATCTAGC	1680
GAAAATACTG	GGGAAGAGTC	CAGTAATCCT	AGTGATTTCGA	CAACCTCAGT	TGGAGAATCA	1740
AATAAAACCAG	AACATAATGA	CTCTAAAAAT	GAAAATTCAG	AAAAAACTGT	AGAAGAAGTT	1800
CCAGTAAATC	CAAATGAAGG	CACAGTAGAA	GGTACCTCAA	ATCAAGAAAC	AGAAAAACCA	1860
GTTCAACCTG	CAGAAGAAAC	ACAAACAAAC	TCTGGGAAAA	TAGCTAACGA	AAATACTGGA	1920
GAAGTATCCA	ATAAACCTAG	TGATTCAAAA	CCACCAGTTG	AAGAATCAAA	TCAACCAGAA	1980
AAAAACGGAA	CTGCAACAAA	ACCAGAAAAAT	TCAGGTAATA	CAACATCAGA	GAATGGACAA	2040
ACAGAACCAG	AGAAAAAACT	CGAATTAAGA	AATGTTTCTG	ATATTGAGTT	GTATAGTCAG	2100
ACGAATGGAA	CCTACAGACA	ACATGTTTCA	TTGGATGGAA	TTCCAGAGAA	TACGGATACT	2160
TACTTTGTCA	AGGTAAAAATC	TTCAGCATTT	AAAGATGTCT	ATATACCAGT	AGCTTCAATA	2220
ACTGAAGAGA	AAAGAAATGG	GCAGTCAGTT	TATAAAATCA	CAGCCAAAGC	TGAGAAACTC	2280
CAGCAAGAAC	TAGAAAAATA	ATATGTCTGAC	AATTTACACCT	TCTACCTCGA	TAAGAAGGCT	2340
AAAGAGGAAA	ATACAAACTT	TACTTCCTTT	AGCAACCTGG	TCAAAGCTAT	AAACCAAAAT	2400
CCCTCTGGAA	CCTATCATTT	AGCGGCCAGC	CTGAATGCTA	ACGAAGTGGA	GCTTAGTACT	2460
GATGATAAAT	CCTATATCAA	GGGAACCTTT	ACTGGTCAGT	TGATTGGTGA	AAAAGATGGT	2520
AAGCATTATG	CTATTTACAA	CTTGAAAAAG	CCTCTTTTTG	AAAACCTGAG	TGGTGCTACA	2580
GTAGAAAAAC	TGAGTCTAAA	AAATGTTGCT	ATTTTCAGGGA	AAAATGATAT	TGGTTCCTG	2640
GCAAAATGAAG	CTACGAATGG	CACAAAGATT	AAACAAGTTC	ATGTTGATGG	TGTTCTGGCT	2700
GGAGAACGTG	GTGTCGGTGG	TTTGTGGGCT	AAGGCAGACC	AATCAAGCAT	CGCAGAGAGC	2760
AGTTTCAAGG	GAAGAATTGT	CAATACCTAT	GAAACGACTG	ATTCTTACAA	TATTGGCGGT	2820
CTGGTCGGTC	ATTTAACAGG	AAAAAATGCG	TCTATTGCTA	AATCCAAAGC	GACAGTAACC	2880
ATTTTCGTCAA	ACACCAATAG	GTCAGATCAG	ACTGTCCGGT	GTCTTGCCAGG	TCTAGTAGAC	2940
CGAGACGCAC	AGATCCAAGA	TAGCTATGCT	GAAGGTGATA	TCAACAATGT	CAAGCACTTT	3000
GGTAGAGTCG	CTGGAGTGGC	AGGCAATTTG	TGGGATCGAA	CTTCTGGTGA	TGTTAGGCAT	3060
GCTGGAAGTT	TGACCAATGT	TCTCAGCGAT	GTTAATGTAA	CAAACGGAAA	TGCCATCACT	3120
GGATACCACT	ATACAGGAAT	GAAGGTAGCT	AATACATTTA	GTAAGTAAGG	TAATAGAGTT	3180
TTCAATGTCA	CTTTAGAGAA	GGATGAGGTC	GTCAGCAAGG	AATCCTTTGA	AGAAAGAGGA	3240
ACAATGCTAG	ATGCTTCTCA	AATTGTAAGC	AAAAAAGCAG	AAATAAGTCC	TCTCACTCTA	3300
CCAACGGTGG	AACCCCTCTC	AACAAGTGGC	AAGAAAGACA	GTGATTTTTT	TAAGATAGCC	3360
CATTATCAAG	CTAACCGTGC	TTTGGTTTAT	AAGAACATTG	AAAAATTGTT	ACCTTTTTTAT	3420
AATAAGTCAA	CCATCGTGAA	ATACGGAAAC	CTGGTTAAGG	AGAACAGTCT	CTTATACCAA	3480
AAAGAACTCT	TATCTGCAGT	TATGATGAAG	GATGACCAAG	TAATCACAGA	TATTGTTTTCC	3540
AACAAACAGA	CTGCAAAACAA	ACTATTACTT	CACTATAATG	ACCATTTCATC	TGAGAAATTT	3600
GATCTCAAGT	ACCAGACTGA	TTTTGCCAAT	CTAGCAGAAT	ATAATCTAGG	TAATACGGGA	3660
CTTCTCTACA	CTCCTAACCA	ATTCTTATAT	GATCGAGACT	CTATTGTTAA	GGAAGTCTTG	3720
CCTGAGTTGC	AGAAGCTTGA	TTACCAGTCA	GATGCTATCA	GAAAGACACT	TGGTATTTCT	3780
CCAGCAGTTA	AGTTAAACCGA	GCTCTATTTA	GAAAGCAGT	TCTCCAAAAC	AAAACAAAAT	3840
CTGGGAGGCA	GCTTGAAAAA	ACTTTTGTC	GCAGATGCCG	GTCTAGCTAG	CGATAACTCA	3900
GTCACCAGAG	GCTATCTTGT	AGATAAAATC	AAGAATAATA	AGGAAGCCTT	GCTACTCGGT	3960
TTAACTTATT	TAGAACGTTG	GTATAACTTT	AACATATGGT	AAGTGAATGT	CAAAGACCTA	4020
GTTATGTATC	ATCCAGACTT	CTTTGGTAAA	GGAAATACTT	CCCCACTAGA	TACTCTGATT	4080
GAGTTAGGTA	AATCTGGCTT	TAACAATCTT	CTTGCCAAGA	ACAATGTCTGA	TACTTATGGT	4140
ATCAGTCTAG	CCAGCCATCA	TGGAACGACA	GATTTGTTTA	GCGCACTTGA	AACTTACCGA	4200
AAAGTCTTTT	TACCAAACAC	TAGCAACAAT	GACTGGTTTA	AAAAACAGAC	CAAAGCTTTC	4260
ATTGTGGAAG	AAAAATCCAC	TATTGCAGAG	GTCAAAGCCA	AGCAAAAGCA	AGCAGGAAC	4320
AAGTACTCTA	TCGGTGTTTA	TGACCGAATT	ACTAGTAATA	CTTGGAAGTA	CCGGAATATG	4380
GTCTTGCCCTC	TCCTTACCTT	GCCAGAAAGA	TCTGTATTTG	TCATCTCAAC	CTTGTCTAGT	4440
CTAGGATTTG	GTGCTTACGA	TCGCTACCGT	AATAGTGAAC	ATAAAGCAGG	CAAGGACCTC	4500
AATAATTTTCG	TTGAAGAAAA	TGCGAGTGAA	ACTGCCAAAC	GTCAGCGAGA	TCACTACGAT	4560
TATTGGTATC	GCATTTTAGA	TAATGAGGGA	CGTGAAAAAC	TATATCGTAC	GATTCTCCTT	4620
TATGATGCCT	ATAAGTTTGG	TGATGACACA	ACATCTGGAA	AAGCTACAGT	GGAGGCTAAG	4680
TTTGATAGCT	CCAATCCAGC	CATGAAGAA	TTCTTTGGTC	CAGTTGGTAA	TAAGGTTGTT	4740

CATAATCATC	ACGGTGCCTA	CGCAACAGGA	GATGGTGTCT	ACTATATGTC	TTACCGCATG	4800
CTCGACAAGG	ATGGAGCCAT	TACCTATACC	CATGAGATGA	CCCATGATTC	GGATCAAGAT	4860
ATTTACCTTG	GCGGCTATGG	TCGAAGAAGT	GGTCTTGGTC	CTGAGTTCTT	TGCTAAAGGT	4920
TTATTACAAG	CGCCAGACCA	TCCATATGAT	GCGACCATTA	CCATTACCAT	TAACCTCTATC	4980
TTGAAACATT	CAAAATCAGA	TAGCTTAGAA	GGATCGCGTC	TGCAAGTCTT	GGATCCGACA	5040
GAAAGATTCC	AAAACCTCAG	AGATCTTCAA	AACTATGTTC	ACAACATGTT	TGACCTCATC	5100
TATATGTTGG	AATATCTAGA	AGGGCAATCG	ATTGTTAAGA	AACTGAATGT	TTCTCAGAAA	5160
ATGGAAGCTC	TCAGAAAAAT	CGAGAATCAA	TATCTAACAG	ATCCTGCTGA	TGGAAATGAG	5220
GTTTACGCTA	CTAACGTAGT	CAAAGAATTG	ACAGAAGAAG	AGGCCCGAAA	CCTGAATAGT	5280
TTTGATAGTT	TGATTGACAA	TAATATTCTT	TCAGCTCGTG	AGTATAAGGC	TGGTACATAT	5340
GAGAGAAATG	GCTACTTTAC	TATAAACTC	TTTGCACCAA	TCTTTTCAGC	ATTGAGCAGT	5400
GAGAAAGGTA	CTCCTGGAGA	TCTTATGGGA	CGAAGGATAG	CTTATGAACT	CTTAGCTGCT	5460
AAAGGATTTA	AAGATGGTAT	GGTACCATAT	ATTTCCAACC	AATATGAAGG	AATTGCTAAA	5520
CAAAATGGTC	AGACAATCAA	CCTTTACGGT	AAAAAGCAAG	GATTAGTGAC	AGATAAGCTT	5580
GTTTTTGAAA	AGATATTCTC	TGGCAAGTAT	CCATCTTGGA	CAGCCTTTAA	AAAAGCTATG	5640
TATCAAGAGC	GTATTGCTCA	GTTTGATCAT	TTGACTAAAG	TTATTTTTTAA	AGATCCGACA	5700
AAACCATGGC	CAAGCTATGG	CACAAAGACT	ATCAATAATG	TGGATGAATT	GCAAGCCCTC	5760
ATGGACCAAG	CTGTTCTCAA	GGATGCTGAA	GGTCCACGTT	GGAGTAATTA	TAATCCAGAA	5820
ATCGACAGTG	CCGTTCATAA	GTTGAAGAGA	GCAATCTTTA	AAGCCTATCT	TGACCAAACA	5880
AATGATTTTA	GAAGTTCAAT	TTTTGAGAAT	AAAAAATAG			5919

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

AGCCATCTTC	ATATGAACCC	AGACCCTGAA	GCCTTGGGAT	TTCAGGTGGG	ATTGAAAGCC	60
TTGCTGGAAC	ATCAGGTCCC	ACAAAAAACC	ATCAAAGCCG	TCGGTTTTGA	TGAACCAACT	120
CTTACTTGGA	TGGCTGAGAT	GGATCTTGTT	GAAGATAGGG	CCTACCAAGG	CGCACTTGTC	180
ATCGTCTGTG	ATACAGCTAA	TACTGCTCGT	ATCGATGATA	AACGCTATAG	TCAAGGTGAT	240
TTTCTCATTA	AGATTGACCA	CCATCCAAAT	GATGATGTAT	ACGGTGACCT	GTCTTGGGTC	300
GATACTAGTT	CAAGTAGCGC	TAGCGAGATG	ATTACCCTAT	TTGCCCAAAC	AACCCAACATA	360
GCCTTGGCAG	ATCGCGATGC	TGAGTTGCTC	TTTGCAGGAA	TTGTGCGTGA	TACAGGTCGC	420
TTCTCTACC	CTTCTACCAC	TGCACGGACT	CTTCGCCCTGG	CTGCTTATTT	GAGAGAACAT	480
AACTTTGACT	TTGCAGCTCT	CACTCGCAAA	ATGGACACTA	TGAGCTACAA	AATTGCTAAA	540
CTGCAAGGCT	ACATCTACGA	CCATCTGGAA	GTGGATGAAA	ATGGTGCTGC	TCGCGTTATC	600
CTGAGTCAGA	AAATCTTGAA	ACAATACAAT	GTAACCGATG	CTGAAACTGC	GACCATTTGTA	660
GGTGACCTTG	GACGCATTGA	CAGAGTGAGT	CTCTGGGGAA	TTTTTGTCTGA	ACAGGCTGAT	720
GGCCACTACC	GAGTTCGCTT	ACGCAGTAAA	GTCCATCCTA	TCAATGAAAT	TGCCAAGGAG	780

CATGATGGTG GAGGCCACCC TCTAGCAAGT GGTGCTAATT CCTATAGCCT AAAAGAAAAC	840
GAAATCATCT ACCAAAAGTT AAAAAACTTG CTAAAAAACT GA	882

(2) INFORMATION FOR SEQ ID NO:650:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

TATTTTATTC AGAGAAAGAA AAAAGACTGAA AGGTGGGAAA TGATTATGAA TACACATATA	60
AATGGTATTA GTAAAAAAGG CAAAGTTCTT ATATATGGTT ATATGCTCCT TACCATTTTA	120
ATTTCTATTT TCCCTATTGC GTGGATTTTT TTATCATCAT TAAAAGCAGA TCCTATGAAA	180
AATCCAGGTA TTAGTTTACC GACTGACTTT ACTCTTGAAG GTTATATAAA TGTTTTTTACA	240
AAACTTCATG TTTTCACTTA CTTTTGGAAT AGCTTTAAAG TAGTGTCTAT ATCAGTTATT	300
ATTAGCATTG TTATGATCTC CATGTCTTCA TATGTTATTG CTAGGATGGA ATTTAGAGGG	360
AAGAAGTTGG TGACTTCTAT GCTGTATTCT ACTCTATTTA TTCCAGCAAC AGCTATGACT	420
TTTCCAGTTT ATAGATTAGT AAATGAGTTG GGGATTTATA ATACCCCAGT TGCTCTAATT	480
CTGGTCTACT CTGTAGTGG AATTGCTATG AGTTTCTTTA TTATAAAGAA CTATTTTGAA	540
ATTATTCCAA AAGAATTGGA GGAGGCAGCA GAGATTGATG GTGCGACATA TGCTCAAAC	600
TTTTGGAAAAG TGATGTTACC AATTGCTAGA CCAGGAATTT TAACAGCAGC AGTACTTGCC	660
TTTATTAATA ACTGGAATGA ATATTATTGG GCATCTATGT TGGTGATTGA TAAAAATGAA	720
TTAACAGTAC CAGCATTACT AGGTCAATTT ACTACAAGTT TTAATACTAA TTATAATGGT	780
CTATTTTCAG CTATTGTTGT AATCGTATTA CCACCAATCA TTCTATTCGC ATTTACAAGT	840
AAATACTTCA TTGAAGCTTT AGGAGGAGGA GCAGTAAAAG GATGA	885

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

TTGAAGAATC	TAAGGATAGC	CCTTATCTCG	AAGGATTGGA	TTTGGAAGT	TAGAAAGAGG	60
AATAAAGAAA	TGACAAAAAG	AATACCTAAT	TTACAAGTTG	CATTAGACCA	TTCAGACTTG	120
CAAGGAGCGA	TAAAGCAGC	TGTTTCTGTT	GGTCAGGAAG	TAGATATTAT	CGAAGCTGGA	180
ACTGTTTGCT	TGCTTCAAGT	TGGAAGTGAA	CTGGCTGAAG	TCTTGCGTAG	CCTTTTCCCA	240
GATAAGATTA	TTGTGGCAGA	CACAAAATGT	GCTGATGCTG	GTGGAACAGT	TGCTAAAAAT	300
AATGCGGTTT	GTGGAGCAGA	CTGGATGACT	TGTATCTGTT	GTGCAACCAT	CCCTACTATG	360
GAAGCAGCTC	TAAAGGCTAT	CAAGACTGAA	CGAGGAGAAC	GAGGCGAAAT	CCAGATCGAG	420
CTTTATGGCG	ATTGGACTTT	TGAACAAGCT	CAGCTTTGGC	TAGATGCAGG	TATCTCACAA	480
GCTATTTTATC	ACCAATCTCG	TGATGCTCTT	CTTGCTGGTG	AAACTTGGGG	TGAAAAAGAC	540
CTTAATAAGG	TTAAAAAACT	CATTGACATG	GGCTTCCGTG	TATCTGTAAC	AGGTGGTCTA	600
GATGTAGATA	CTCTCAAACT	CTTTGAAGGT	GTTGATATCT	TTACCTTTAT	CGCAGGTCGT	660
GGAATTACAG	AGGCTGCGGA	TCCAGCAGGA	GCAGCGCGTG	CCTTCAAGGA	TGAAATCAAA	720
CGAATTTGGG	GGTAA					735

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GGCTGTATTC	AATTGCCCTT	CCTAGTTTTG	AACCTGCTAA	AACTGACTGA	CGGCGGCACC	60
AAGCAAAGAA	GTCTTCTATT	AGGGGTTGGA	GCTCTTCTTG	ACGTTTCTGT	AGTCGTTTCAT	120
CAGCTGGCAA	AGCCTCCCAG	TCTCTTTCCA	AGGAAAATAA	CTGATCACAA	TAGGCTAATC	180
CTTTAG						186

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GGCTGTATTC AATTGCCCTT CCTAGTTTTG AACCTGCTAA AACTGACTGA CGCCGGCACT	60
AAGCAAAGAA GTCTTCCATT AAGGGCTGGA GATGTTCTTG ACGTTTCTGT AGTCGTTTAT	120
CAGCTGGCAA AGCCTCCCAG TCTCTTTCCA GGGAAAATAA CTGATCACAA TAAGCTAAAC	180
CTTTAG	186

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1011
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

AAAAGAGTTC AATTCGAACT CTTTTTTTGC TATAATGAGG GGAGAAAAAT CAGACAGGAG	60
ATCGACATGT CAGAACCATT ATTTTACAA TCAGTTATGC AAGAAAAAAT CTGGGGTGGA	120
GCCAAGCTAC GTGATGAGTT TGGCTACGAT ATCCCAAGTG AAAAAATCGG AGAATATTGG	180
GCCATCTCAG CCCATCCAAA TGGAGTCTCT AAAGTTGCCA ATGGTCGTTA CGAGGGAACA	240
GATCTTGCTA CTTTGTATGC GGAACACCGT GAATTATTTG GCAATCGTCC AGAACCTGTA	300
TTTCCACTTT TGACCAAGAT CCTCGATGCC AACGACTGGC TCAGTGTCCA AGTTCACCCA	360
GACGATGCTT ATGGACTCGA GCATGAAGGC GAACTCGGAA AAACAGAATG CTGGTACATT	420
ATCGCAGCGG ATGAAGGTTC AGAGATTATC TACGGTCACA ATGCCAAGTC AAAAGAAGAA	480
CTCCGCCAGC AAATCGAGGA TAAGAACTGG GATGCGCTGT TGACAAAAAGT GCCAGTTAAA	540
GCAGGAGATT TCTTCTATGT ACCAAGCGGT ACCATGCACG CTATCGGGGC GGGTATCTTG	600
ATTCTTGAAA CCCAGCAGTC TAGCGATACC ACTTACCGTG TCTATGACTT TGACCGTAAG	660
GATGACAAGG GCAATTTACG TGAACCTCAC CTTGAAAAAT CTATCGATGT CTTGAACATT	720
GGTGAACCTG CAAATAGCCG TCCAGTGACA ATCAAAGCAG ATGATCTACG TTCCACTCTC	780

CTTGTATCCA	ATGATTTCTT	CGCAGTTTAC	AAATGGGAAA	TTACTGGAAA	AGTTAACTTT	840
GAAAAGACAG	CTGACTACAG	CTTGGTTGAGT	GTCTTGGCTG	GTCAAGGTCA	ACTAACTGTT	900
GACGGGAAAA	ACTATCCAAT	CCAAAAAGGG	AGACACTTTA	TCCTACCAAG	TGATGTTGAA	960
TCTTGGACTC	TAGAAGGGCA	AGATTTAGAA	TTAATTGTTA	GTCATCCATA	A	1011

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

CTTTTGTTTC	AAAGTAGAGA	AAGGAATATC	ATGGCAAATC	ATTTCGTAC	GGATCGTGTG	60
GGCATGGAAA	TCAAGCGTGA	AGTCAATGAG	ATTTTGCAAA	AGAAAGTCCG	TGATCCACGT	120
GTCCAAGGTG	TGACCATCAC	AGATGTTTCAG	ATGCTGGGTG	ACTTGTCTGT	TGCCAAGGTT	180
TATTACACCA	TTTTGAGTAA	CCTTGCTTCG	GATAACCAAA	AAGCCCAAAT	CGGGCTTGAA	240
AAAGCAACTG	GTACCATCAA	ACGTGAACTT	GGTCGCAATT	TGAAATTGTA	CAAAATCCCA	300
GATTTGACCT	TCGTCAAAGA	CGAGTCCATC	GAGTATGGAA	ACAAGATTGA	CGAGATGCTA	360
CGCAATCTGG	ATAAGAACTA	A				381

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1953 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

AAGATGTCTC	ATATTATTGA	ATTGCCAGAG	ATGCTGGCAA	ACCAAATCGC	AGCTGGAGAG	60
GTCATTGAAC	GTCTTGCCAG	TGTGGTCAAA	GAGTTGGTAG	AAAATGCCAT	TGACGCGGGC	120
TCTAGTCAGA	TTATCATTGA	GATTGAGGAA	GCTGGTCTCA	AGAAGGTTCA	AATCACGGAT	180
AACGGTCATG	GAATTGCCCA	CGATGAGGTG	GAGTTGGCCC	TGCGTCGCCA	TGCGACCAAGT	240
AAGATAAAAA	ATCAAGCAGA	TCTCTTTCCG	ATTCCGACGC	TTGGTTTTTCG	TGGTGAAGCC	300
TTGCCTTCTA	TTGCGTCTGT	TAGTGTCTTG	ACTCTGTATA	CGGCGGTGGA	TGGTGCTAGT	360
CATGGAACCA	AGTTAGTCGC	GCGTGGGGGT	GAAGTTGAGG	AAGTCATCCC	AGCGACTAGT	420
CCTGTGGGAA	CCAAGGTTTG	TGTGGAGGAT	CTCTTTTTTCA	ACACGCCTGC	CCGTCTCAAG	480
TATATGAAGA	GCCAGCAAGC	GGAGTTGTCT	CATATCATTG	ATATTGTCAA	CCGTCTGGGC	540
TTGGCCCATC	CTGAGATTTC	TTTTAGCTTG	ATTAGTGATG	GCAAGGAAAT	GACGCGGACA	600
GCAGGGACTG	GTCAATTGCG	CCAAGCAATC	GCAGGGATTT	ACGGTTTGGT	CAGTGCCAAG	660
AAGATGATTG	AAATTGAGAA	CTCTGACCTA	GATTTTCGAAA	TTTCAGGTTT	TGTGTCCTTG	720
CCTGAGTTGA	CTCGGGCTAA	CCGCAATTAT	ATCAGCCTCT	TCATCAATGG	TCGTTATATC	780
AAGAACTTCC	TGCTCAATCG	TGCTATTTTG	GATGGTTTTCG	GAAGCAAGCT	TATGGTTGGA	840
CGTTTTCCAC	TGGCTGTCT	TCACATCCAT	ATCGACCCCT	ATCTAGCGGA	TGTCAATGTG	900
CATCCAACTA	AGCAAGAGGT	GCGGATTTCC	AAGGAAAAAG	AACTGATGAC	TCTGGTTTTCA	960
GAAGCTATTG	CAAAATAGTCT	CAAGGAACAA	ACCTTGATTG	CAGATGCCTT	GGAAAACTTT	1020
GCCAAATCGA	CCGTGCGCAA	TCGTGAGAA	GTGGAGCAAA	CTATTCTCCC	ACTCAAAGAA	1080
AATACGCTCT	ACTATGAGAA	AACTGAGCCG	TCAAGACCTA	GTCAAAGTGA	AGTAGCTGAT	1140
TATCAGGTAG	AATTGACTGA	TGAAGGGCAG	GATTTGACCC	TGTTTGCCAA	GGAAACCTTG	1200
GACCGATTGA	CCAAGCCAGC	AAAAGTGCAT	TTTGACAGAGA	GAAAGCCTGC	TAACTACGAC	1260
CAGCTAGACC	ATCCAGAGTT	AGATCTTGCT	AGCATCGATA	AGGCTTATGA	CAAACCTGGAG	1320
CGAGAAGAA	CATCCAGCTT	CCCAGAGTTG	GAGTTTTTTCG	GACAAATGCA	CGGGACTTAT	1380
CTCTTTGCCC	AAGGGCGAGA	TGGACTTTAC	ATCATAGATC	AGCACGCTGC	TCAGGAACGG	1440
GTCAAGTACG	AGGAGTACCG	TGAAAGCATT	GGCAATGTTG	ACCAGAGCCA	GCAGCAACTC	1500
CTAGTGCCCT	ATATCTTTGA	ATTTCCCTGCG	GATGATGCCC	TGCGTCTCAA	GGAAAGAATG	1560
CCTCTCTTAG	AGGAAGTGGG	CGTCTTTCTA	GCAGAGTACG	GAGAAAATCA	ATTTATTCTA	1620
CGTGAACATC	CTATTTGGAT	GGCAGAAGAA	GAGATTGAAT	CAGGCATCTA	TGAGATGTGC	1680
GACATGCTCC	TTTTGACCAA	GGAAGTTTCT	ATCAAGAAAT	ACCGAGCAGA	GCTGGCTATC	1740
ATGATGTCTT	GCAAGCGATC	TATCAAGGCC	AATCATCGTA	TTGATGATCA	TTCAGCTAGA	1800
CAACTCCTCT	ATCAGCTTTC	TCAATGTGAC	AATCCCTATA	ACTGTCCTCA	CGGACGTCCT	1860
GTTTTGGTGC	ATTTTACCAA	GTCGGATATG	GAAAAGATGT	TCCGACGTAT	TCAGGAAAAAT	1920
CACACCAGTC	TCCGTGAGTT	GGGAAATAT	TAA			1953

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GATGTCCCTC	AGGCACCAAA	ACAAGAAAGG	AATACGCACA	TGTCAAAATT	GCTAGATAAG	60
ATATTATCAC	GCGAAAATAT	GCTGGAAGCC	TACAATCAAG	TAAAATCCAA	TAAAGGCTCA	120
GCTGGGATTG	ATGGAATGAC	TATCGAAGAG	ATGGATAATT	ATCTCAGACA	AAACTGGCGC	180
TTGACTAAGG	AACTGATAAA	ACAGAGAAAA	TATAAGCCTC	AACCAGTTCT	TAGAGTTGAG	240
ATACCTAAAC	CAGACGGAGG	TATCCGTCAA	CTAGGAATTC	CAACAGTTAT	GGATAGAATG	300
ATTCAACAGG	CCATTGTCTA	A				321

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

AATTCACCTC	ACGATATTAT	ACCAAAATTC	GCTAATTTTG	TCAGTTTTTA	CAAATTTTAC	60
TGCTTTTGTG	GTACAATAGA	AACTATGGCA	AGTATCACAC	TCACACCAAG	CGAAAAGGAT	120
ATTCAGGCTT	TTCTTGAACA	CTATCAAACC	AGTCTGGCTC	CTAGCAAGAA	TCCCTATATC	180
CGCTACTTTT	TGAAACTACC	TCAAGCAACG	GTTTCTATCT	ATACTTCTGG	AAAAATCTTG	240
CTTCAGGGTG	AAGGGGCTGA	AAAATACGCC	AGTTTCTTTG	GCTATCAAGC	TGTAGAGCAA	300
ACCAGCGGAC	AAAATCTTCC	TTTAATTGGG	ACAGATGAGG	TGGGAAATGG	TTCTACTTTT	360
GGTGGGCTTG	CAGTTGTGGC	TGCCTTTGTC	ACACCTGACC	AGCACGACTT	TTTACGAAAA	420
CTCGGTGTGG	GGGATTCTAA	GACTCTGACC	GACCAAAAGA	TCCGTCAGAT	TGCTCCTATT	480
CTCAAGGAAA	AAATTCAGCA	CCAGGCACTC	CTTCTCTCAC	CCAGCAAGTA	CAACGAGGTC	540
ATCGGAGACC	GCTACAATGC	TGTTTCGGTT	AAGGTTGCCC	TCCATAATCA	GGCTATCTAT	600
CTCCTCCTTC	AAAAAGGTGT	TCAGCCTGAG	AAAATTGTGA	TTGATGCCTT	TACCAAGTGCT	660
AAAAATTATG	ACAAGTACTT	GGCACAAGAG	GCCAATCGTT	TCAGCAATCC	TATCAGCTTA	720
GAAGAAAAGG	CTGAGGGCAA	ATACTTGTCT	GTCGCAGTTT	CTTCTGTCAT	TGCGCGTGAT	780
CTCTTTCTGG	AAAATCTTGA	AAATCTGGGA	CGAGAACTGG	GTTATCAGCT	TCCAAGTGGA	840
GCTGGAACGG	CTTCTGACAA	GGTGGCTAGC	CAGATTTTGC	AAGCCTATGG	TATGCAGGGA	900
CTCAACTTCT	GCGCCAAATT	GCACTTTAAA	AACACTGAAA	AAGCGAAAAA	ACGCTTAGAA	960
AGGTAA						966

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

AAAGGAACTC	ACATGTCAAT	TATTGAAATG	AGAGATGTCG	TTAAAAAATA	CGACAACGGA	60
ACGACTGCTC	TACGCGGTGT	TTCGGTCAGC	GTTCAACCGG	GGGAATTTGC	TTACATCGTA	120
GGACCTTCAG	GAGCAGGGAA	GTCAACTTTT	ATTCTGTTCTC	TGTATCGTGA	AGTAAAAATC	180
GATAAAGGAA	GCCATACAGT	TGCTGGTTTT	AATCTGGTTA	AGATCAAAAA	GAAAGATATC	240
CCGCTTCTAC	GTCGTAGTGT	TGGGGTTGTC	TTCCAGGATT	ATAAATTGTT	ACCAAAGAAA	300
ACTGTCTATG	AAAAATATGC	TTACGCTATG	GAAGTAATCG	GGGAAAATCG	CCGTAATATC	360
AAAAGACGAG	TGATGGAAGT	TTTGGACCTG	GTTGGATTGA	AGCATAAGGT	TCGTTCTTTC	420
CCAAATGAAC	TCTCAGGTGG	GGAGCAACAG	CGGATTGCGA	TTGCGCGTGC	AAATTGTAAAT	480
AATCCCAAAG	TATTGATAGC	TGATGAGCCA	ACAGGAAATC	TGGATCCGGA	TAATTCATGG	540
GAAATTATGA	ATCTCTTGGA	ACGGATTAAC	CTACAAGGAA	CAACTATTTT	GATGGCGACT	600
CATAATAGCC	AGATTGTAAA	TACCTTGCGC	CACCGTGTCA	TTGCCATTGA	AAATGGCCGT	660
GTCGTTCGTG	ACGAATCAAA	AGGAGAGTAT	GGATACGATG	ATTAG		705

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

AATCTTGCTC	ATGTAGGTTA	CTACAGCAAG	CTTAGCTTTT	TCTTTTTTCCT	GATTAATGTC	60
TGGTACGCTT	GGTTTCTTGC	CTTCTGGTTG	AGGGCTTGGT	TTGGTATCCG	GAGATGGAGT	120
TGTTGGTTTT	TGATGCTCTG	GATTTTCCGG	CTGCGGAGTT	TCTGGTTTAT	TGGAGGATCC	180
TGA						183

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

AACCCAGCTC	ACACCGACTT	GCTACGGTGC	TTCTATTTCGT	TTGAAGCAAA	AGCAAGGCAA	60
AGCCTCTCCC	TCTATCTTCA	CGCAACAGAT	GAAC TGACAG	TAGAGCAAGT	AGATAAGCGA	120
ACTCTTGCCC	TGCGACAAGA	AGGTAAAACT	GAAACCAACA	AAAATTTCGCT	AACGATGTTC	180
ACTGCCCTAC	AAATGAACAC	GGATATTCTT	GCTATCAGCC	AAGAAGCTGG	AGACTGGCGA	240
ATTGACTTAG	TAAGTAGTCA	AACCGAGATG	CAACTAGCCA	CTTCTTTTCAT	CTCTCCTTCT	300
CAAGCTCTAA	TCAATCTACC	TCAAGAAGAT	TTTGATAGCT	GTAAAGCAAG	TGCCCCAAGCG	360
GATTGGGAAA	ATCTCCTCCA	TCGTTTTTGAT	GTTATAGAGA	CAGGAGAGGC	TAACCGAACC	420
TTCTTTTGACC	ACTGTCTCTA	CAGACTCTTC	CTCTTCCCAC	AGACTTTTTTA	TGAGGTTGAT	480
GAGTCAGGGC	AAGCCATCCA	CATGGATCTG	GCTACTGGTA	CTGTCAAGCC	TGGTGTCCCTC	540
TTTAGCAACA	ATGGTTTCTG	GGATACCTTC	CGCACCACCT	TCCCCCTCTT	TGCCCTTATC	600
ATACCGGAGC	ACTATCAACG	CTTTTTTAGAA	GGTTTCCTCA	ATAGCTACCG	CGATACTGGT	660
TTCTTTCCAA	AATGGCTGGC	TCCAGATGAA	CGGGGTATGA	TGCCAGGTAC	ACTTTTAGAC	720
GGTATTATCG	CAGATAGCGC	CTGCAAGGAC	ATGGCCCCTG	ACCTAGAAGG	AGAACTCTTC	780
CAAGCCATGC	TCGAAACAGC	CAGCAAAGCC	GACCCTCTCG	GCATCAATGG	CCGCCACGGA	840
CTAGCCCAAT	ACCAAGAACT	AGGTTACCTC	TCTACCGACC	ACCACGAAAG	TGTTAGCCAT	900
ACTCTAGACT	ATGCCTATAG	TGACTTTTGT	ATCGCTAGCT	GTGCCAAAAA	ACTAGAGAAC	960
ATAGAAATCG	CTGAAACCTA	CAAGGCTGCT	TCACAAAATT	ACCGCCAGCT	ATTTGACGCT	1020
GAGACAGGTT	ACATGCGAGC	ACGAGACAAT	CAAGGAAACT	TTCACCCTGA	CTTCTCTCCT	1080
TATAGTTGGG	GGCGAGACTA	CGCTGAATGC	TCTGCCATTC	AAGCTACTTT	AGGCGTTCTC	1140
CACGACATCC	CTGGCTTAAT	CCAAC TGATG	GGTGGAAAAG	AAACCTTTAG	CAACTATCTT	1200
TTGAAAGCTT	GTCAAGATGC	TCCCCCTCTT	GAAACAACAG	GCTATGGTTA	CGAAATTCAC	1260
GAAATGAGCG	AGATGGCTAC	TGCTCCTTTT	GGACAAATAG	CCATTTCCAA	CCAGCCTAGT	1320
TTCCACATTC	CTTATCTCTT	CCGCTACAGC	GATTACCCTG	ACTACACTGC	CCTTCTTATC	1380
AAGACGCTCC	GTCAGAAAGC	TTTTTCACCA	AGTTGGGAAG	CCTATCCTGG	AGATGAAGAC	1440
AATGGTAGTC	TCTCTGCTTG	GTACATCTGG	TCAGCTCTCG	GATTTTATCC	AACCTGTCCA	1500
GGAAAACCAA	GCTATGACCT	CGGAATCCCT	CTCTTTGACC	ATCTACGAGT	CTACCTCGCT	1560
AAAGAAGATA	AATGGCTGGA	TATCCATACT	AAACAAAACC	ACAACCATTT	TAAC TTTGTC	1620
AAAGAATGCC	GACTGGACAA	AACACTCGTA	TCAACTATTC	AACACCAAGA	CCTCTTAAAA	1680
GCTGAACAAAC	TAAC TTTTAC	CCTCAGCTGG	TTACCAAGTC	ACTAA		1725

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

ATCGGAGCTC	ACTTCCTTAC	TAAGCAAGCT	GGTGGCTCTG	GTGTTCTACC	TGGTGGTGTA	60
CCAGGTGTTT	CAAAAGGAAA	AGTAACTATC	ATCGGTGATG	GTGTCGTCGG	TACACATGCT	120
GCCCCGATCG	CCCTTGGTCT	TGGTGCTCAA	GTGACTATTT	TAGATATTAG	TGCCAAGCGT	180
CTCTCAGTTC	TAAAAGAAGT	CTTTGGAAGT	CAAATTTAA			219

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

TGTTTGGCTC	AGATTTCAT	CCTTCATTTT	GATTTCTTAT	CTATTGACAA	GCATAGTCAC	60
ACTGTCTTTA	ATACTCTTCG	AAAATCTCTT	CAAACCACGT	TAGCTCTATC	TGCAACCTCA	120
AAACAGTGTT	TTGAGCAACT	TGCGGCTAGC	TTCCTAGTTT	GCTCTTTGAT	TTTCATTGAG	180
TATAAGGTAT	GA					192

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

CCTATGGCTC	AGTTAACTGT	CCAGATCGTG	ACACCAGATG	GTCTCGTCTA	TGATCACCAT	60
GCCAGCTATG	TATCGGTTTC	AACTCTGGAT	GGTGAGATGG	GGATCTTGCC	ACGACATGAA	120
AATATGATTG	CGGTTTTAGC	AGTTGATGAA	GTAAAGGTAA	AACGTATCGA	TGATAAAGAT	180
CACGTGAACT	GGATTGCAGT	AAACGGTGGC	GTTATTGAAA	TTGCCAATGA	TATGATCACA	240
ATCGTCGCTG	ACTCTGCAGA	ACGTGCTCGT	GATATCGATA	TCAGTCGTGC	AGAACGTGCC	300
AAACTTCGTG	CAGAACGTGC	AATTGAAGAA	GCACAAGACA	AACATTTGAT	TGACCAAGAA	360
CGTCGTGCTA	AGATTGCTTT	GCAACGTGCC	ATTAACCGTA	TTAATGTCGG	AAATAGACTA	420
TAA						423

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

CAGATTTATC	ATCTTGGACA	GCCTATTTTC	AGGAGTTTTG	GACAATTTTTT	CAATGGTGTC	60
CTCTTTACTC	TGGCCCTAGC	GATTGGATCC	TTTATCCTCG	CCATGGTCTT	AGGAATCTTC	120
TTTGGTGCCA	GGTCAACCAG	TAAACGTCCA	ATTTTACGCA	TTTTAGCTCG	CATCTTCGTG	180
GAATTTTACC	AAAACACTCC	CCTCTTGGTG	CAGTTTGTTA	TTGTTTTTTA	TGGCCTACCT	240
CTTATCAGTG	ACCACATCAT	CATGATTCCA	ATTTATTGGA	CAGCCGTTCT	CTGCGTGGA	300

CTCTATCACG	GCGCTTATAT	CGCTGAGGTT	ATTCGTTTCAG	GGATTCAGTC	TATTCCTAGT	360
GGTCAGATGG	AGGCCGCCTT	GTCGCAAGGT	TTTACCTATA	TCAGTGCCAT	GCGCTTGATT	420
ATCTTGCCTC	AGGCCTTCCG	CATCATTTCTC	CCTCCATTGA	CCAACCAAAT	TGTTAACCTC	480
ATCAAGAACA	CATCTACTGT	AGCTATCATC	TCTGGAGTAG	ACTTGATGTT	TGTGACTAAG	540
TCTTGGTCGG	CTCTCAACGG	AACTATATC	CCAGCCTTTT	TAGGTGCTGC	TCTTCTCTAC	600
TTTGCCCTAT	GCTTCCCTGT	TGCCCAGTTT	GGTCGCAAGA	TGGAGCAAGC	CAATAAAAAA	660
GCCTATTCAC	TTTAG					675

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

AAAGCTTATC	AAGGTAGAAA	AATTGGGAGC	CAATTGCTTG	CTACTTTAGA	GAGTGAGCTC	60
GCTAAAAAAG	TTGGTTATCT	GCAGGTCAAA	ACAGTGGCAG	AAGGTTCTAA	TAAAGATTAT	120
GATCGAACAA	ATGACTTTTA	TCGAGGTCTT	GGCTTTAAAA	AGTTAGAGAT	TTGTCTTCAA	180
CTATGA						186

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

AAAGAAGATC	TTATGAAAAT	CGCATTAATC	AATGAAAATA	GTCAAGCTAG	CAAGAATCAC	60
ATTATTTACG	ATAGTCTAAA	AGAAGCGACA	GATAAAAAAG	GCTACCAATT	ATTTAACTAT	120
GGTATGCGTG	GAGAAGAAGG	AGAAAGTCAA	TTAACTTATG	TGCAGAACGG	ACTAATGGCT	180
GCCATCCTTT	TAAATACAAA	GGCAGTTGAC	TTTGTTGTTA	CCGGCTGTGG	TACGGGTGTA	240
GGGGCTATGC	TTGCTTTAAA	CAGCTTCCCT	GGTGTGTCT	GTGGTCTAGC	AGTGGACCCA	300
ACTGACGCTT	ACCTTTATTTC	TCAAATCAAT	GGTGGTAACG	CCTTGTCTAT	CCCTTATGCC	360
AAAGGATTTG	GCTGGGGGGC	AGAACTGACC	CTCAAATTGA	TGTTTGAACG	CTTATTTGCT	420
GAAGAAATGG	GCGGTGGCTA	CCCAAGAGAA	CGTGTAATCC	CTGAACAACG	CAACGCTCGT	480
ATCTTAAACG	AGGTGAAACA	AATCACCAC	AATGATTTGA	TGACCATCCT	TAAAATAATC	540
GACCAAGACT	TCCTCAAAGA	CACCATCTCT	GGCAAATACT	TCCAAGAATA	CTTCTTTGAA	600
AACTGCCAAG	ATGATGAAGT	TGCTGCTTAT	TTGAAAGAAG	TATTAGCCAA	GTAA	654

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

TATAATTATC	AAAAGACAAA	AGGAGTTCAC	CTCATGGTAG	AATTGAATCT	TAAAAATATT	60
TACAAAAAAT	ATCCAAACAG	CGAACACTAT	TCAGTTGAAG	ATTTCAACTT	GAACATCAAA	120
GATAAAGAAT	TTATCGTTTT	CGTAGGACCT	TCAGGATGTG	GTAAATCAAC	TACACTCCGT	180
ATGATTGCTG	GTCTTGAAGA	CATCACAGAA	GGTACTGCAT	CTATCGATGG	CGTGGTTGTC	240
AACGACGTAG	CTCCAAAAGA	CCAGTGA				267

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

AATAACTATC	AAAAAACAAG	GAAGAAAATT	ATGTCATTAA	CATCAAAACA	ACGTGCCTTC	60
CTCAACAGCC	AGGCACACAC	CCTCAAACCT	ATCATCCAAA	TCGGGAAAAA	TGGACTCAAC	120
GACCAAATCA	AAACCAGCGT	CCGTCAAGCT	CTTGATGCGC	GTGAATTAAT	CAAGGTTACT	180
CTCTTACAAA	ACACAGATGA	AAACATCCAC	GAAGTAGCTG	AAATTTTGGA	AGAAGAAATC	240
GGTGTGGATA	CAGTCCAAAA	AATAGGACGC	ATCTTGATTT	TGTTTAAACA	ATCTAGCAAG	300
AAAGAAAATC	GCAAGATTTC	TAAGAAAGTC	AAAGAAATCT	AA		342

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1422 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

TCATTGTATC	ACAAAAGGGG	AGATTGGGAT	AGGATGGAAG	TCAAAGCTGT	TTTTTTTGAT	60
ATCGATGGAA	CCTTGGTCAA	CAATCGCAAG	AGTGTTTTGA	AATCCACTAA	GGATGCGATT	120
AAGATTGTCA	AAGAACAAGG	GGTACTAGTT	GGCGTAGCGA	CAGGGCGAGG	ACCTTTTTTTT	180
GTTAAGGAAT	TGATGGACGA	TTTGATCTG	GATTTTGCGG	TAACTATAA	TGGCCAGTAT	240
ATCTTTAGTA	AAGACAGAGT	CTTGTTACAG	AGCCCTATTT	CCAAGTTACA	TTTGCGCCAT	300
CTAATTAGCT	ATGCTAAAAA	AGAGGGCACG	GAGATTGCCC	TAGGGACCAA	GGATGCCATG	360
TTGGGTTCTA	AAATCATGTC	CTTTGGTCTG	GGTTCTTTTT	CCCAACGAAT	TAGTCGCTTC	420
GTTCCCTCTG	TTTTAACTCG	GACGGTGAGT	CAGTCTTTTA	ATCGCATGGT	CAGCAAGGTT	480
GTTCCCCAAA	AGGAAGAGGA	CCTGCTTCAC	CTGATGAATC	AGCCTATCTA	CCAAGTTTTG	540
ATGCTGATGA	CACCAGAAGA	ATCTGAGAAG	GCGGCAGCTG	ATTTTGAAGA	CTTGAAATTG	600
ACACGTAGCA	ATCCTTTTGC	ATCGGATGTC	ATCAATCAGG	GAAATTCTAA	ATTAGAAGGC	660
ATTCGCCGAG	TTGGGAAAGA	ATATGGCTTT	GACCTCAATC	AAGTCATGGC	TTTTGGTGAC	720
TCAGATAATG	ACCTTGAAAT	GCTGGCTGGC	GTCTGGTATG	CGGTCGCTAT	GGGAAATGGT	780
AGTAGCAGTG	TCAAGGAAGC	TGCCAAGCAC	ATTACCACTA	GCAATCAACA	AGATGGGATC	840
CACAAGGCCCT	TGGAACATTT	TGGTGTTTTG	TCTTCAGAAA	AAGTCTTTGT	CAGCCGTGAC	900
TATCATTTCA	ATAAGGTCAA	GACCTTCCAC	CACATGATGG	ATGAACGAAC	CCAAGAAGAA	960
CCTCGAGCTT	GGGATTTAGA	GGGTGCAACC	CATAGGGCTG	GTTTTAAAAT	AGAAGAATTG	1020
GTGGAGTTTG	TTGAGCAGC	CAGTCCTTCT	GAAGAAGATT	TTGGTCAAGG	TGTATGGCAA	1080

TTTCATCAGG	CCCTTGATAA	GGCAGCAGAT	AAAGTAGCCA	AGAAGACACC	TGCTCAGCAA	1140
GATTTGATAG	GGCAAGTGGA	TGCCTTGATT	GACACGCTTT	ACTTCACGTA	CGGCAGTTTT	1200
GTCTTGATGG	GGGTGGACCC	AGAACGTATT	TTTGATATTG	TCCATCAGGC	CAATATGGGG	1260
AAAATTTTTC	CAGATGGCAA	GGCTCATTTT	GATCCAGTGA	CCCATAAAAT	CTTAAAACCA	1320
GATAATTGGG	AAGAAAAATA	TGCTCCAGAA	CCTGCTATTA	AAAAGGAACT	GCAGCGCCAG	1380
CTCAAGGCTT	ACGAACGCCA	TAAAGAGAGA	AATAAATCGT	AA		1422

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

AGGGTGGATC	TGATGGCTTA	TATTGAGATG	AAACACTGTT	ACAAGCGTTA	TCAGGTTGGG	60
GACACGGAGA	TTGTGGCTAA	TCGTGATGTG	AATTTTGAGA	TTGAAAAGGG	GGAGCTGGTT	120
ATTATCCTTG	GTGCTTCAGG	TGCAGGCAAG	TCAACAGTTC	TCAACCTTCT	TGGGGGAATG	180
GATACCAATG	ATGAAGGGGA	AATCTGGATT	GATGGTGTTA	ATATTGCGGA	TTATAGTTCC	240
CACCAGCGCA	CCAATTACCG	TAGAAATGAT	GTGGGGTTTG	TTTTTCAGTT	TTATAATCTA	300
GTTTCTAATC	TGACAGCTAA	GGAAAATGTG	GAACTGGCTT	CTGAAATTGT	GACAGATGCC	360
TTGAATCCTG	ATCAGGTCTT	GACAGATGTA	GGTCTGGCTC	ATCGTCTAAA	TAACTTTCCA	420
GGCCAGCTTT	CTGGAGGGGA	GCAACAGCGA	GTCTCCATTG	CACGCGCGGT	AGCCAAAAAT	480
CCTAAAATTC	TTCTTTGTGA	TGAACCTACT	GGAGCCTTGG	ATTATCAGAC	GGGCAAGCAG	540
GTTTTGAAAA	TTCTCCAAGA	TATGTCTCGT	CAAAAGGGAG	CGACGGTGAT	CATCGTGACT	600
CATAATGGAG	CTTTGGCGCC	CATTGCTGAT	CGCGTGATTG	ATATGCACGA	TGCCAGTGTC	660
AAGGATGTGG	TGCTCAACCA	GCATCCTCAG	GATATTGACA	GTTTGGAGTA	CTAG	714

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

AACGTCAATC	AGCCTTGGTC	GTCTTTAGTG	GTGGTCAAGA	TTCAACAACC	TGCCTTTTCT	60
CGGGCCCACG	GCAGTATGAA	ACAGTCGAAG	CTGTCACCTT	TGGCCTACGG	CAACATCATC	120
ACCTCGAAAT	TCAAATTGCT	AGAGAAATCG	CCAAGGAACA	GGGGCATTCG	TCACCCATAT	180
CCTCGATATG	TCTCTGCTGG	GACAAATCAC	TGCTCAACCA	CGACTTTGCG	ACGATTTCAT	240
ATTTCTTACA	TTTCTGACAA	GCTCTGTGTC	GAGTCAAAAT	CTCTCAAAC	ATATCTATTT	300
AGTACCGAA	ATCACGGAGA	TTCCACGAA	AACTGTATCA	ACACCATCGG	GAAAGACTTG	360
GTCAACTTGG	TAGACCTTCG	CTATTTAGAA	ATCGGGGGAA	ATTTATTCCG	CGCGGTGGCA	420
TGTCAATCGA	CCCCTATTAC	AATTACGGTA	AGCAAGGAAA	TAAGTATGAG	GNCTTGGCAG	480
AACAACGCGT	TTTCCAACAC	GACGTTTATC	CAGAGAAAAAT	TGACAACCGC	TAAAGTCATA	540
CTCAATGAAA	ATCAAAGAGC	AAACTAG				567

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...831
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

AAGGAAAATC	ATCTTATGAG	TAAATACCTG	CTAAAACTTC	TCGTTTATTG	TTTTTCAGCT	60
TTAACCTTTG	GCTCTCTCTT	TTTAATCATT	GGTTTTATCC	TCATCAAAGG	CTTACCTCAT	120
CTAAGTCTAT	CCCTCTTTTC	TTGGACTTAT	ACTTCTGAGA	ACATTTCCTT	TATGCCAGCG	180
ATTATTTCCA	CCGTTATTCT	GGTTTTTGGT	GCTCTTCTTT	TAGCCTTGCC	CATAGGGATT	240
TTTGCTGGTT	TTTATCTTGT	GGAATATACA	AAAAAAGATT	CCCTTTGTGT	TAAAATCATG	300
CGATTGGCCT	CAGATACCTT	GTCTGGGATT	CCTTCCATTG	TTTTTGGTCT	GTTTGGCATG	360
CTCTTCTTTG	TAGTCTTCTT	AGGTTTTCAA	TACTCTCTGT	TATCAGGAAT	CTTAACCTCA	420
GTTATCATGG	TGTTGCCAGT	CATTATTCGC	TCAACAGAAG	AAGCCCTTTT	ATCTGTTAGT	480
GATAGCATGC	GTCAAGCAAG	TTATGGACTT	GGGGCAGGTA	AGTTACGGAC	TGTTTTTAGA	540
ATTGTTCTAC	CAGTTGCCAT	GCCAGGTATT	TTAGCTGGAG	TGATACTAGC	TATTGGCCGT	600
ATCGTTGGTG	AAACAGCTGC	CCTCATGTAT	ACATTAGGTA	CCTCTACCAA	TACGCCAAGT	660
AGTCTCATGT	CTTCAGGTCG	TTCTCTAGCC	CTGCATATGT	ATATGCTGTC	AAGTGAGGGG	720

CTACATGTCA ATGAAGCCTA TGCTACCGGT GTGATTTTGA TTATTACTGT TTTAATGATA	780
AATACTCTAT CAAGCTTATT ATCTCGGAAA CTTGTGAAAG GAGCTTCCTA G	831

(2) INFORMATION FOR SEQ ID NO:674:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

AGGTTGCGTC AAAACTTCTC TGGCTATTTT TTCCACACCT TCATAGAGGC TTGGGGGCAG	60
AACGTCTTTC ATAAAGCCCA AAAATTCTCC CACAGGAATC TGAAAATAGG GGAGGATATT	120
GACCACCACC AAAAGCAGGG GGAAAATCGA AATCAACCAA TAGTAGGCTA CTGCGACACT	180
GGTCAACTCA CTATCTGA	198

(2) INFORMATION FOR SEQ ID NO:675:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

TGCCGGCGTC AGTCAGTTTT AGCAGGTTCA AAAC TAGGAA GGGCAATTGA ATACAGCCTC	60
AAGTATGAAG AAACCTTTAA GACTATTTTG AAAGACGGAC ATCTGGTCCT TTCCAATAAT	120
CTAGCTGAAC GCGCCATTAA ATCATTGGTT ATGGGACGGA GTAAAAGAAT TCAGTGGACT	180

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

CCACTTTGTC	TTGTTCTGTC	TTGTCCTGTT	GGGCTTTCTA	GCTACCAGTA	CAGTCAACTC	60
TTACAACATT	TTCTGAAAA	TCATTGGCCT	ATCCTTTTGT	TTGTAGGAAT	TACGTCTGTT	120
TTACTTTTAC	TTTGGGGAGG	AATTGCCACC	TATATGGAGG	CTCCAGACAA	GCTCTTTCTC	180
TTAGTTGGAG	AAGAGGAAAT	CAAGCTCCAT	CTCAAGCGTC	AAACTGGCAT	TTCCCTAGTC	240
TTTTGGCTCT	TTGTACAGAC	CCTTTTCTTG	CTGTTATTTG	CGCCCTTGTT	TTTAGCAATG	300
GGTTATGGCT	TGCCAGTTTT	TCTGCTCTAT	GTGCTTTTAT	TGGGGGTAGG	AAAATATTTT	360
CACTTTCGTC	AAAAGGCCAG	CAAATTTTTT	ACTGAAACTG	GACTGGACTG	GGACTATCTT	420
ATTTCTCAAG	AAAGCAAGCG	TAAGCAAGTC	TTGCTTCGTT	TCTTTGCCCT	CTTTACGCAG	480
GTCAAGGGAA	TTTCAAACAG	TGTCAAGCGT	CGTGCCTATC	TGGACTTTAT	CTTAAAGGCT	540
GTTCAGAAGG	TGCTGGGAA	GATTTGGCAA	AATCTCTATC	TGCGTTCTTA	TCTGCGAAAT	600
GGCGACCTCT	TTGCTCTCAG	TCTTCGTCTT	CTCTTACTTT	CCGTACTGGC	GCAGGTTTTT	660
ATCGAGCAAG	CTTGGATTGC	GACAGCAGTG	GTAGTTCTCT	TTAACTACCT	CTTGCTCTTC	720
CAGTTGCTGG	CCCTCTATCA	TGCCTTTGAC	TACCAGTATT	TGACCCAAC	CTTTCCGCTG	780
GACAAGGGGC	AAAAGGAAAA	AGGCTTACAG	GAGGTAGTTC	GAGGATTGAC	CAGTTTTGTT	840
TTACTTGTGG	AAGTAGTTGT	TGGGTTGATT	ACCTTCCAAG	AAAAACTAGC	CCTTCTAGCC	900
TTACTAGGAG	CTGGTTTGGT	TTTACTAGTC	TTGTATTTGC	CTTATCAGGT	AAAACGTCAG	960
ATGCAGGACT	AA					972

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

CAAGAATTCC AGTTTATCTG GAGTTTCCAA CATCATTTCT TCCCAAGTGT AGCCGGTCCA	60
GGACCAGATG TCCTTGTCTG GCAATTCCTT CCGAATCCGC TTAACAAGTG GCAAGAGAAT	120
CCCAGTATTA AGAAAAGGCT CCCCTCCCAA CAAAGTCAAA CCTTGAACAT AGGGCTGAGC	180
AAGATCTGCC ATGATCTGCT CTTCTAA	207

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

ACAAAAATCC AGAAGAAGCT AAAGCATTCG TTGAAGCAGT TGCATCAAAA CTTCCTTCAT	60
CAGATCTTGT TGAAGCAGGT ATCGCTGCTC ACAGCTCTTG ATTTGACAAC TGTTCTTGCT	120
GTTGCAAAAG GCTCAAACCT TAAAGTTGCT GCTCAAAACT GCTACTTTGA AAATGCAGGT	180
GCTTTCACAG GTGAAACTAG CCCACAAGTT TTGAAAGAAA TCGGTACTGA CTACGTTGTT	240
ATCGGTCACT CAGAACGCCG TGACTACTTC CATGAAACTG ACGAAGATAT CAACAAAAAA	300
GCAAAAGCAA TCTTTGCGAA CGGTATGCTT CCAATCATCT GTTGTGGTGA ATCACTTGAA	360
ACTTACGAAG CTGGTAAAGC TGCTGAATTC GTAGGTGCTC AAGTATCTGC TGCAATGGCT	420
GGATTGACTG CTGAACAAGT TGCTGCCTCA GTTATCGCTT ATGAGCCAAT CTGGGCTATC	480
GGTACTGGTA AATCAGCTTC ACAAGACGAT GCACAAAAAA TGTGTAAAGT TGTTTCGTGAC	540
GTTGTAGCTG CTGACTTTGG TCAAGAAGTC GCAGACAAAG TTCGTGTTCA ATACGGTGGT	600
TCTGTTAAAC CTGAAAATGT TGCTTCATAC ATGGCTTGCC CAGACGTTGA CGGTGCCCTT	660
GTAGGTGGTG CGTCACTTGA AGCTGAAAGC TTCTTGGCTT TGCTTGACTT TGTAATAATA	720

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

AGGAGAATCC ATCTAATGGT AAAATTGGTT TTTGCTCGCC ACGGTGAGTC TGAATGGAAC	60
AAAGCTAACC TTTTCACTGG TTGGGCTGAT GTTGATTTGT CTGAAAAAGG TACACAACAA	120
GCGATTGACG CTGGTAAATT GATCAAAGAA GCTGGTATCG AATTTGACCA AGCTTACACT	180
TCAGTATTGA AACGTGCTAT CAAAACAACT AACTTGGCTC TTGAAGCTTC TGACCAATTA	240
TGGGTTCAG TTGAAAAATC ATGGCGCTTG AACGAACGTC ACTACGGTGG TTTGACTGGT	300
AAAAACAAAG CTGAAGCTGC TGAACAATTT GGTGATGAGC AAGTTCACAT CTGGCGTCGT	360
TCATACGATG TATTGCCTCC AAATATGGAC CGTGATGATG AGCACTCAGC TCACACAGAC	420
CGTCGTTATG CTTCACTTGA CGACTCAGTA ATCCCAGATG CTGAAAACCTT GAAAGTGACT	480
TTGGAACGTG CTTTTCCATT CTGGGAAGAT AAAATCGCTC CAGCTTTTAA AGATGGTAAA	540
AACGTATTCTG TAGGAGCTCA CGGTAACCTCA ATCCGTGCCC TTGTAAAACA CATCAAAGGT	600
TTGTCAGATG ATGAGATCAT GGACGTGGAA ATCCCTAACT TCCCACCATT GGTATTTCGAA	660
TTCGATGAAA AATTGAACGT TGTCTCTGAA TACTACCTTG GAAAATAA	708

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

AGAATGATCC AAATCGGCAA GATTTTTGCC GGACGCTATC GGATTGTCAA ACAGATTGGT	60
CGAGGAGGCA TGGCGGATGT CTACCTAGCC AAAGACTTAA TCTTAGATGG GGAAGAAGTG	120
GCACTGAAGG TTCTGAGGAC CAACTACCAG ACGGACCCGA TAGCTGTAGC TCGTTTTTCAG	180
CGTGAAGCGA GAGCTATGGC AGATCTAGAC CATCCTCATA TCGTTCGGAT AACAGATATT	240
GGCGAGGAAG ACGGTCAACA GTATCTTGCA ATGGAGTATG TTGCTGGACT AGACCTCAAA	300

CGCTATATCA	AGGAACATTA	TCCTCTTTCT	AATGAAGAAG	CAGTCCGTAT	CATGGGACAA	360
ATTCTCTTGG	CTATGCGCTT	GGCCCATACT	CGAGGAATTG	TTCACAGGGA	CTTGAAACCT	420
CAAAATATCC	TTTTGACACC	AGATGGGACG	GCCAAGGTCA	CAGACTTTGG	GATTGCTGTA	480
GCCTTTGCAG	AGACAAGTCT	GACCCAGACT	AACTCGATGT	TGGGCTCAGT	TCATTACTTG	540
TCACCAGAGC	AGGCGCGTGG	TTCGAAGGCG	ACTGTGCAGA	GTGATATCTA	TGCCATGGGG	600
ATTATTTTCT	ATGAGATGTT	GACAGGCCAT	ATCCCTTATG	ACGGGGATAG	CGCGGTGACC	660
ATTGCCCTCC	AGCATTTCCA	GAAACCCCTG	CCGTCCGTTA	TTGCAGAAAA	TCCATCTGTA	720
CCTCAGGCTT	TAGAAAAATGT	TATTATCAAG	GCAACTGCTA	AAAAGTTGAC	CAATCGCTAC	780
CGCTCGGTTT	CAGAGATGTA	TGTGGACTTG	TCTAGTAGCT	TGTCCTACAA	TCGTAGAAAT	840
GAAAGTAAGT	TAATCTTTTG	A				861

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GCGTTTTCCC	ATGTAAACAT	TAATACCAAA	TCTCTTGTTG	AATTGCTGCA	CATCATAGAA	60
TGTTTTCATA	AGACTCATTT	TACCAAAATT	TCGTGTTTTT	TTCAAGAAGA	GACTCACACA	120
ATGCTCCTTA	TTTTCTTATC	TTCTTTAGCG	ATTCTAAGGC	AAGTATGGTA	CAATAAAAAC	180
ATGAGAAATC	AACAATTACA	TTATATTATC	AAAATCGTCG	AAACTGGCTC	CATGAATGAG	240
GCAGCCAAGC	AACTCTTTAT	CACTCAGCCA	AGTCTCTCCA	ATGCAGTGCG	AGATTTGGAA	300
AATGAAATGG	GCATTGAGAT	CTTTATCCGC	AATCCCAAGG	GAATCACCTT	GACCCGTGAT	360
GGGATGGAGT	TTCTCTCTTA	TGCCCCTCAG	GTTGTCGAGC	AGACCCAGCT	TCTGGAGGAA	420
CGCTATAAAA	ATCCTGTCGC	CCACCGCGAA	CTCTTTAGCG	TTTCGTCTCA	ACACTATGCC	480
TTTGTGGTCA	ATGCCTTTGT	CTCTTTGCTC	AAGAAAAAGC	ATATGGAGAA	ATACGAACTC	540
TTCTTTCGTG	AAACTCGGAC	TTGGGAGATT	ATCGACGACG	TCAAGAACTT	CCGCAGTGAG	600
GTCGGGGTCC	TCTTCTTAAA	CAGTTACAAC	CGTGATGTTT	TAACCAAGAT	GCTGGATGAC	660
AATCACCTGC	TAGCCCACCA	TCTCTTCACA	GCGCAACCGC	ATATCTTTGT	CAGCAAGACC	720
AACCTCTGG	CAAAGAAAGA	CAAGGTGAAA	CTGTCTGATT	TGGAGAATTT	CCCTTACCTC	780
AGCTATGACC	AAGGGACGCA	CAACTCCTTC	TACTTTTCAG	AAGAGATTCT	TTCTCAAGAA	840
CACCACAAGA	AATCCATTGT	GGTCAGTGAC	CGTGCCACCC	TCTTTAATCT	CTTGATTGGT	900
TTGGATGGTT	ATACCATTGC	GACAGGGATT	TTGAACAGCA	ACCTAAACGG	AGACAATATC	960
GTTTCTATCC	CACTGGATAT	TGATGACCCG	ATTGAGCTGG	TCTATATCCA	GCATGAGAAA	1020
ACCAGCCTAT	CTAAGATGGG	CGAACGCTTT	ATCGACTATC	TACTAGAAGA	AGTTCAGTTT	1080
GATAGTTGA						1089

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

CTCTATTCCC AGATTAGACC GAGATTCTGG CGTTTTGCTT TACAAATTCT CCTATGGGAT	60
AGCCTGATGA TTCTCTCCTT GGTGTCTTTA AGTGATATTC CACTTTTCCT TCAGGGAACT	120
CTCCTCATCC TAGGACATCT CATCCCTTCC TATCGCATCT GCCAAAGCCT GAAAAGAGAC	180
TTCCCCCAAG CATATCAAGA ACCGATTTCT TTTTGAGTA TTTTATGA	228

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GAACGTTCCC AGCTAAGACT TTTGAAGAGC TATTTTCAGGG AGTTTTCGCT TTGGATTGGG	60
AAAATTATTT ACCACTTGGA GCTCGGTTCC CGATTTCAAA AGCTAAATGT GTTAAGTCCA	120
AACTTCACAA TGAGCCAGT GTTCAGGCTA TTTCTAAGAA AGCTGTTGTC AAGAAATTGC	180
AGAAACACTA TGCTCGCCCA GAAGGGGTTT CTCTGA	216

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GTCAGCTCCC AGTTTGCCAT CATAGCTGTA TGTCTCATCT TTCAGGCGCC AGCTTGTTTT	60
GGTAGTGAAT TGGTCGGAAT TGTAAGCTAAC AGTATAAGGA TGTTTTGTGT CAGAGAAATC	120
TCCGCTGTAG GTCACCTTCT TACCAGCTTC ATCGATTGCA ACATCGGTAA TAGTTACCTT	180
GTTTCCTAG	189

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 759 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

CTATTGTGTC TTCTGACTAT TTTTGGTAT AATAGTAGAG AAAAAGGTGA ACATATGAAA	60
AAAATACTAA TTGTAGATGA TGAGAAACCA ATCTCGGATA TTATCAAGTT TAATATGACC	120
AAGGAAGGTT ATGAAGTTGT AACTGCTTTT AATGGTCGTG AAGCGCTAGA GCAATTTGAA	180
GCAGAGCAAC CAGATATTAT TATTCTGGAT TTGATGCTTC CAGAAAATTGA TGGTTTAGAA	240
GTTGCTAAGA CCATTCGTAA GACAAAGCAGT GTGCCCATTTC TTATGCTTTC AGCCAAAGAT	300
AGTGAATTTG ATAAGGTTAT CGGTTTGGAA CTTGGGGCAG ATGACTATGT AACGAAACCC	360
TTCTCCAATC GTGAGTTGCA GGCGCGTGTT AAAGCTCTTC TGCGTCGTTC TCAACCTATG	420
CCAGTAGATG GTCAGGAAGC AGATAGTAAA CCTCAACCTA TCCAAATTGG GGATTTAGAA	480
ATTGTTCCAG ACGCCTACGT GGCTAAAAAA TATGGCGAAG AACTAGACTT AACCCATCGT	540

GAATTTGAGC	TTTTGTATCA	TTTAGCATCG	CATACAGGTC	AAGTCATCAC	GCGCGAACAC	600
TTGCTTGAGA	CTGTCTGGGG	TTATGACTAT	TTTGGTGATG	TCCGCACAGT	TGATGTGACT	660
GTACGACGTC	TGCGTGAGAA	GATTGAAGAT	ACGCCCAGCC	GACCAGAGTA	TATCTTGACG	720
CGCCGTGGTG	TAGGGTATTA	CATGAGAAAT	AATGCTTGA			759

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

AACGTCGCCC	AGGTGATATC	GCTGCCTGCT	ACTCAGACCC	AGCAAAAGCT	AAAGCAGAAC	60
TCGGTTGGGA	AGCAGAACTC	GACATCACCC	AAATGTGTGA	AGACGCATGG	CGTTGGCAAA	120
GCAAGCATCC	AAATGGATTT	GAAGACTAAG	ATGATGATTT	CAATCATCGT	CCCTTGTTTA	180
AACGAAGAGG	AAGTACTTCC	TCTTTTTTAT	CAGGCTCTGG	AAGCTTTACT	TCCAGATTTG	240
GAAACAGAAA	TCGAGTATGT	CTTTGTCTGAT	GATGGATCAA	GTGATGGGAC	CTTGGAAGTC	300
TTAAAGGCCCT	ATCGGGAGCA	AAATCCGGCA	GTCCATTATA	TTTCTTTCTC	TCGAAATTTT	360
GGCAAAGAAG	CAGCCCTTTA	TGCAGGCTTG	CAATATGCGA	CAGGAGATTT	GGTGGTGGTG	420
ATGGATGCAG	ACCTCCAAGA	TCCTCCTAGT	ATGTTGTTTG	AGATGAAAAA	TGTA TAGAC	480
AAAAATGTAG	ACTTGGAAGT	CGTTGGGACA	CGGAGAACTA	GTCGGGAGGG	AGAACCCTTC	540
TTTCGCAGTT	TCTGTGCTGT	TCTCTTTTAT	CGCCTCATGC	AAAAAATCAG	CCCAGTAGCT	600
CTGCCGTCGG	GTGTCCGTGA	CTTTCGTATG	ATGAGAAGGT	CTGTGGTCGA	TGCCATTTTA	660
AGCTTGACTG	AGTCCAATCG	TTTTTCTAAG	GGACTCTTTG	CCTGGGTCGG	CTTTAAAACC	720
CACTATCTGG	ACTATCCAAA	TGTCGAAAGG	CAGGCTGGCA	AGACCAGTTG	GAGTTT TAGG	780
CAACTCTTTT	TTTACTCCAT	TGAAGGGATT	GTTAATTTTT	CAGATTTCCC	TTTGACTATA	840
GCCTTTGTAG	CTGGTCTCCT	ATCTTGTTTT	CTTCTCTGTC	TGATGACCTT	TTTTGTGTGT	900
GTTCGGACCC	TCATTTTGGG	CAATCCGACA	TCTGGTTGGA	CCTCTCTGAT	GGCTGTTATT	960
CTCTTTCTTG	GAGGCATTCA	ACTCTTGACC	ATTGGGATTC	TCGGTAAAGTA	TATCAGTAAG	1020
ATTTATTTTAG	AGACTAAAAA	AAGACCACTT	TATCTTATCA	AAGAAAAAAG	TGATGATAGG	1080
CTAAAAAAGA	TAGAATTTAT	CTGA				1104

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

CGTGTTTACC	AATCCAAAAG	ATCAGCGCAC	AGAAGACTAT	ATTTTCAGGAC	GGTTCGGATA	60
AGGAAGGAAA	AACCTATGAG	AAATCAATTT	GACTTAGAAT	TGCATGAATT	AGAACAATCC	120
TTTTTAGGAC	TAGGGCAACT	TGTCCTTGAA	ACAGCTTCAA	AAGCCTTACT	GGCCTTAGCC	180
TCCAAAGACA	AGGAGATGGC	AGAGCTAATT	ATCAATAAGG	ATCATGCTAT	CAACCAAGGT	240
CAAAGCGCTA	TCGAATTGGC	CTGTGCCCGT	TTGTTAGCCT	TGCAGCAGCC	ACAAGTGTCT	300
GACCTTCGAT	TTGTAATTAG	CATCATGTCT	TCTTGTTCAG	ACCTTGAACG	TATGGGAGAC	360
CATATGGCAG	GCATTGCCAA	AGCTGTTTTG	CAACTAAAAG	AAAATCAACT	AGCCCCTGAC	420
GAAGAACAGT	TACACCAAAT	GGGTAAATTA	TCCCTCAGCA	TGCTAGCCGA	TTTATTGGTT	480
GCCTTTCCTT	TGCACCAAGC	CTCAAAAGCT	ATTAGTATTG	CTCAAAAAGA	TGAACAGATT	540
GACCAATATT	ATTATGCCCT	ATCAAAGGAA	ATCATTGGAC	TTATGAAAGA	CCAAGAAACC	600
TCAATTCCCA	ATGGAACCTA	ATACCTTTAT	ATCATAGGGC	ATCTGGAACG	CTTCGCTGAT	660
TACATTGCTA	ACATTTGTGA	ACGCCTAGTC	TACCTAGAAA	CAGGAGAACT	GGTGGATTGT	720
AATTAA						726

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAATCTTACC	ATGGTTCTAG	AGTTACCATG	TACTTTCCAA	CATCCTCTGC	CTTGATTGAA	60
TTTCTCATCT	TGGCTGTACT	GGAGCAGGGT	GATTCTTATG	GTTATGAGAT	TAGCCAAACC	120
ATTAAGCTGA	TCGCTAATAT	CAAAGAATCC	ACACTCTATC	CCATCTCTCA	AAAATTGGAA	180
GGCAATAGCT	TTCTGACAAC	CTATTCTAGA	GAGTTCCAAG	GTCGCATGCG	CAAATACTAC	240
TCCTTGACAA	ACGGTGGTAT	AGAGCAGCTC	TTGACCCTAA	AAGATGAATG	GACACTCTAT	300
ACAGACACCA	TCAATGGCAT	CATAGAAGGG	AGTATCCGCC	ATGACAAGAA	CTGA	354

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

ATGTCTTACC	AAGAAAATTA	CCAGAAATGG	GTTGATTTTG	TGGAGCTTCC	TGACTACCTT	60
CGTCAAGATT	TGGAAAATAT	GGACGAAAAA	ACTAAGGAAG	ATGCCTTCTA	TACAAATCTT	120
GAATTTGGTA	CTGCAGGTAT	GCGTGGCTTG	GTTGGTGCTG	GTACAAACCG	TATCAACATC	180
TACGTTGTTC	GCCAAGCTAC	TGAAGGATTG	GCTCGTTTGA	TTGAGTCAAA	AGGTGGAAAC	240
GAGAAAGAAC	GCGGTGTAGC	AATTGCCTAC	GATAGCCGTC	ACTTCTCACC	TGAGTTTGCC	300
TTTGAATCTG	CGGCAGTTCT	TGCTAAACAC	GGCATCAAAT	CTTACGTATT	TGAAAGCCTT	360
CGTCCGACTC	CAGAACTATC	ATTTGCAGTT	CGTCATCTCA	ACTGTTTCGC	AGGTATCATG	420
GTCACAGCCA	GCCACAACCC	TGCTCCATTT	AACGGTTACA	AGGTTTACGG	TGAAGACGGT	480
GGACAAATGC	CTCCACACGA	TGCGGACGCT	TTGACTACTT	ATATCCGTGC	AATCGAAAAC	540
CCATTTGCAG	TTGAAGTTGC	TGATGTGGAA	ACTGAAAAAG	CTTCTGGCTT	GATTGAAGTT	600
ATCGGCGAAG	CTGTTGACGT	AAAATACCTT	AAAGAGGTTA	AGGACGTAAA	CATCAACCCA	660
GCCTTGATTG	AAGAATTTGG	TAAAGACATG	AAGATTGTCT	ACACACCACT	TCATGGTACT	720
GGTGAAAATG	TGGCTCGTCG	TGCTCTTGCC	CAAGCAGGAT	TTGACTCTGT	TCAAGTTGTT	780
GAAGCGCAAG	CAACTGCTGA	CCCAGACTTC	TCAACTGTAA	CATCTCCAAA	CCCAGAAAAGC	840
CAAGCAGCCT	TTGCCCTTGC	TGAAGAACTT	GGTCGTCAAG	TTGGTGCAGA	TGTTCTTGTC	900
GCAACTGACC	CAGACGCTGA	CCGTGTTGGT	GTTGAAGTTC	TTCAAAAAGA	TGGTAGCTAC	960
CTCAACCTTT	CAGGTAACCA	AATCGGTGCT	ATCATGGCTA	AATACATCTT	GGAAGCTCAC	1020
AAAAACGCTG	GAATCTTTCC	TGAAAATGCC	GCTCTCTGCA	AATCTATCGT	TTCAACTGAC	1080
TTGGTAACGA	AAATTGCTGA	AAGCTACGGC	GCAACTATGT	TCAACGTCTT	GACAGGTTTC	1140
AAATTTATCG	CTGAAAAAAT	CCAAGAATTC	GAAGAAAAAC	ACAACCACAC	TTACATGATG	1200
GGATTTGAAG	AAAGCTTCGG	TTACTTGATT	AAACCATTTG	TACGTGATAA	AGATGCCATC	1260
CAAGCCGTTT	TTGTCGTTGC	TGAACCTGCT	GCCTACTACC	GTTCTCGTGG	TTTGACACTT	1320
GCTGACGGTA	TCGAAGAAAT	CTATAAAGAA	TATGGCTACT	ACGCAGAAAA	AACAATCTCT	1380
GTTACTCTTT	CAGGTGTCGA	TGGTGCTGAA	CAAAATCAAAG	CGATTATGGC	TAAATTCCGC	1440
AACAATGCTC	CAAAAGAATG	GAACGCAACA	GCTATCACTG	TCGTAGAAGA	CTTCAAGGCA	1500
CAAACTGCTA	CTGTTGCTGA	CGGTACTGTT	ACAAACTTGA	CAACTCCTCC	AAGTGATGTG	1560
TTGAAATACA	CACCTGCTGA	CGGTTTCATG	ATTGCCGTTT	GCCCTTCAGG	TACAGAACCA	1620
AAAATCAAGT	TCTACATTGC	AGTTGTAGGG	GAAACCAACG	AAGAATCACA	AGCTAAGATT	1680
GCTAACATCG	AAGCAGAAAT	CAATGCATTT	GTAAAAATA			1719

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

CAACGTTACC	AAAATATCAT	GGTCGCAATC	GATGGTTCTA	AGGAAGCGGA	CTTGGCTTTT	60
GTCAAGGGAG	TTCATTCTGC	TCTACGAAAC	GACGCTAAAC	TCACCATCGC	ACATGTCATT	120
GACACACGCG	CTCTCCAAAG	CGTATCCACC	TTTGATGCTG	AAGTTTACGA	AGAACTCCAA	180
GTCGACGCTG	AAAGTCTGAT	GAAAGAGTAC	GAAAAACGTG	CTAAAGATGC	TGGGGTAGCA	240
GATGTTTCATA	TCGTCATTGA	AATGGGAAAT	CCAAAGACCC	TGCTAGCACG	TACTATTCCA	300
GATGCCGAGG	AAGTGGACCT	CATCCTCGTT	GGCGCAACTG	GTCTCAACGC	CTTTGAACGC	360
CTCTTGGTGCG	GCTCTTCATC	TGAATACATA	CTCCGCCATG	CTAAGGTCGA	TTTGCTGGTT	420
GTGAGAGAAC	AAGAAAAAAC	CTTATAA				447

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

CGCCTCCACC	AGCAGACAAG	CAGGTACCGC	ATCATGATGT	TGTCATCGCT	GATATGGATA	60
AGTCTTATAC	AGAATACAAG	GGAGAATATG	GTGGCTAAAA	AAAAAATCTT	ATTTTTTATG	120
TGGTCTTTTC	CTCTTGAGG	TGGTGCAGAG	AAGATTCTAT	CAACCATTGT	TTCAAATCTG	180
GATCCAGAAA	AGTATGATAT	TGATATTCTT	GAAATGGAGC	ACTTTGACAA	GGGATATGAA	240

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

CCCTACCACC	AGAAGAAAAA	CGCTTCTACA	GTCATGAATT	TCACGCTTAT	AAATTGGAGG	60
ATTAGGATGC	AATATTTAGA	AAAAAAGAA	ATTAAAGAAA	TTCAACTAGC	CCTGCTGGAC	120
TATATTGATG	AGACTTGTA	GAAATATGAT	ATTCTTATT	TTCTCAGTTA	TGGAACCATG	180
CTTGGAGCCA	TCCGCCACAA	AGGTATGATT	CCTTGGGATG	ATGATATTGA	TATTTCCCTT	240
TATCGTGAGG	ATTATGAGCG	TTTACTGAAG	ATTATTGAAG	AAGAAAATCA	CCCTCGCTAC	300
AAGGTTCTTT	CCTACGATAC	ATCTTCTTGG	TACTTCCATA	ATTTCGCATC	GATTTTGGAC	360
ACTTCTACTG	TTATAGAAGA	CCATGTTAAG	TACAAGCGTC	ATGATACCAG	CCTTTTCATC	420
GATGTCTTCC	CAATTGATCG	ATTACAGAC	TTGAGCATTG	TCGACAAGAG	CTATAAGTAT	480
GTGGCCCTTC	GTCAACTAGC	TTACATCAAA	AAATCACGAG	CAGTTCACGG	TGATAGCAAA	540
CTAAAAGATT	TTCTTAGATT	ATGTAGCTGG	TACGCTCTCC	GATTTGTCAA	TCCTCGCTAC	600
TTTACAAGA	AAATTGATCA	ACTAGTCAAA	AATGCTGTAA	CCAACACTCC	TCAATATGAA	660
GGAGGAGTTG	GGATCGGTAA	GGAAGGGATG	AAAGAAATCT	TCCCAGTTGA	TACCTTTAAA	720
GAACTCATCT	TAAGTGAGTT	TGAGGGCCGT	ATGTTGCCTG	TTCCCCAAAA	ATATGACCAA	780
TTTTTAACCC	AGATGTATGG	CGATTATATG	ACACCACCAT	CAAAAGAAAT	GCAAGAATGG	840
TATAGTCATA	GTATTAAAGC	TTATCGTAAA	AGCTGA			876

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```
ACTATTAAACC AGTTAAGTAA TAGAGAGGAG TTTCTGCAAT TTAGAAATGA ATTGCAACTA      60
GAAATATCAA ATAGAAAGAG AGTTTCGATG AAAATTAATA AGAAATACCT TGTGTTCT      120
GCGGCAGCTT TGATTTTAAG TGTTTGTCT TACGAGTTGG GACTGTATCA AGCTAGAACG      180
GTTAAGGAAA ATAATCGTGT TTCCTATATA GATGGAAAAC AAGCGACGCA AAAAACGGAG      240
AATTTGACTC CTGATGAGGT TAGCAAGCGT GAAGGAATCA ATGCTGAGCA AATCGTCATC      300
AAGATAACAG ACCAAGGCTA TGTCACCTCA CATGGCGACC ACTATCATTA TTACAATGGT      360
AAGGTTCCCTT ATGATGCGAT TTCAGTGAA GAATTACTCA TGAAAGATCC AAATAATAAG      420
CTAAAAGATG AGGATATTGT TAATGAGGTC AAGGGTGGAT ATGTTATCAA GGTAGATGGA      480
AAATACTATG TTTACCTTAA GGATGCTGCC CACGCGGATA ACGTCCGTAC AAAAGAAGAA      540
ATCAATCGAC AAAAACAAGA ACATAGTCCA CATCGTGAAA AGTTGGACTC CAAAAAAACC      600
AAGTTTCCGT TGCCCTGGGG CCCTTTCGCA AGGGACGCTA TACTACAGAT GATGGTTATA      660
TCTTTAATGC TTCTGATATC ATATAGGATA CTGGTGATGC TTATATCGTT CCTCATGGAG      720
ATCATTACCA TTACATTCCT AAGAATGAGT TATCAGCTAG CGAGTTGGCT GCTGCAGAAG      780
CCTTCCTATC TGGTCGGGGA AATCTGTCAA ATTCAAGAAC CTATCGCCGA CAAAATAGCG      840
ATAACACTTC AAGAACAAAC TGGGTACCTT CTGTAA      876
```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

```
TACAAAAACC AAGCTGAAGA AGACAAACCG CTATCTGATA AATATATTTT CGAAAAAATA      60
TTAGGAAAAA CATATGCAGC CTTCAAAAAA GATCAAATTA ATGAGCGTGT CGAGAAATTA      120
GGTAAGTTAA AACCTATTAC AATAAATTAC AACGGAAAAA CAGAAGTAAT TGATAGTAAA      180
GAAAAATTAC AAGAGCTTAT GAATAAAGCC GTTAAAGACG AAGTGGCTCA AATATAG      237
```

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

TGCTATTGCC	AAATCCCTAA	TAGTGGTATA	CTAGGTCAGT	ATTTTATAAA	TATGAAGGAA	60
ATTTTATATG	CTAAAAAAGG	TACCCTAACA	GGTTTGCTCC	TGTTTGGAAT	ATTTTGTGGT	120
GCGGGGAAC	TGATTTTCC	GCCTTCTCTA	GGTGCTCTAT	CTGGAGAACA	TTTTCTTCCT	180
GCCATCGCAG	GTTTTGTCTT	TTCAGGCGTT	GGTATCGCCG	TCTTGACCCT	TATTATTGGA	240
ACGCTAAATC	CTAAAGGATA	TATCTACGAG	ATTTTCAGCGA	AGATAGCGCC	TTGGTTTGCG	300
ACTCTTTACC	TCTCAGTTCT	TTACTTGTC	ATCGGTCCAT	TCTTTGCTAC	CCCACGTACT	360
GCTACAACAG	CTTACGAAGT	AGGGATTAGC	CCCCTTTTGT	CGGATGCAAA	TAAAGGACTT	420
GGCTTGATTG	TATTTACGGT	TCTGTATTTT	GCGGCAGCCT	ATTTGATTTT	GCTTAATCCA	480
TCAAAAATCT	TAGACCGCAT	TGGACGTATT	TTAACGCCAG	TCTTTGCAAT	TTTGATTGTT	540
ATCTTGGTCT	TTCTGGGAGC	TATCAAATAT	GGTGGAACAA	GTCCTCAAAC	TGCTTCATCT	600
GCTTATCAAG	CTTCTGCCTT	TGGTACAGGT	TTCCCTAGAA	GTTACAATAC	CTTGGACGCC	660
CTTGCCTCAG	TGGCCTTTAT	CGTAATCGCA	GTTCAAACCT	TGAAACAAC	TGGATTTTCA	720
AGTAAGAAAA	AATACATTTT	AACTATTTGG	GTTGTTGGTA	TCGTTGTTGC	CCTTGCCTTC	780
AGCGCTCTAT	ACATCGGTTT	AGGTTTTCTT	GGAAATCATT	TCCCAGTACC	AGCTGAAGCG	840
ATGAAGGGTG	GAACACCAGG	TGTTTACATC	TTGTCACAAG	CCACTCAAGA	AATCTTTGGC	900
TCAACAGCTC	AACTCTTCCT	TGCAGCTATG	GTTACCGTAA	CCTGCTTCAC	AACGACTGTT	960
GGTTTGATTG	TGTCACAGC	TGAGTTCTTT	AATGAGCGCT	TCGCACAAAT	CAGCTACAAG	1020
GTTTATGCGA	CAGCCTTTAC	CTTGATTGGA	TTTGCTATTG	GCANATCTNN	NNAAAAACANT	1080
NNNNNNNNTN	NNTTTNTTAA	AAATATTAAT	TCCCTTGTA	AAAATGTTCA	TTNCCCTAAA	1140
ATTTACAATT	TTCCACCTTT	ACCTCCTTTC	CTGT			1174

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

CTGGCCTGCC	AATCGCACCG	ACACATGTGG	TTTCTAGCAT	TGCGGAGTGG	GATTTTGATG	60
AAACTAAAT	TGATCTTTTG	GGGCTCTATG	CTCTTTCTCC	TCTCCCTCTC	CATCCTTCTG	120
ACCATTTATC	TGGCTTGAT	TTTCTATCCT	ATGGAGATTC	AGTGGCTAAA	CTTAACGAAT	180
CGAGTCTATC	TAAAACCAGA	AACCATTCAA	TACAATTTTC	ATATCTTGAT	GAATTATCTG	240
ACCAATCCTT	TTAGTCAGGT	CTTACAGATG	CCTGATTTTC	GTTCGTCAGC	AGCTGGTCTG	300
CACCATTTTCG	CAGTGGTCAA	GAATCTCTTT	CATTTGGTTC	AGCTAGTAGC	TCTAGTGACA	360
CTGCCAAGTT	TCTATGTCTT	TGTCAATAGG	ATTGTGAAAA	AGGACTTTTTT	GTCTCTTTTAT	420
CGAAAAAGTC	TCCTGGCTCT	AGTAGTTTTA	CCTGTAATGA	TTGGACTTGG	GGGAGTTTTG	480
ATTGGTTTTG	ACCAATTCTT	TACTCTTTTC	CATCAAATTC	TCTTTGTGGG	AGATGATACC	540
TGGCTTTTTG	ATCCAGCCAA	GGATCCTGTT	ATTATGATTT	TGCCAGAGAC	CTTCTTTCTT	600
CATGCCTTCC	TCCTCTTTTT	TGCCCTCTAT	GAAAAC'TTCT	TTGGCTATCT	GTGTGTGAAA	660
AGTCGTAGGA	AGTGA					675

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GGCTCAAGCC	AGTCTGTAGG	GGATACCTAT	ATCCAACATT	CGACAGGTGT	TCCTGACGGG	60
AAAGAAGGAT	TTGCAGCCTT	CTTTGCAGAT	TTCTTTGAGC	GTCATCCAGA	GCGTCAGATT	120
AAGATTGTCC	GCACCATTGA	GGATGGCAAT	CTGGTCTTTG	TTCATGTTCA	TCAATATCTG	180
AATGGTGGAG	AAGCTCAATG	GGTGACGACG	GATACTTTCC	GTGAGGATGA	GAATGGTTGT	240
ATTGTTGAGC	ATTGGGATGT	CATTGACTAC	TATCGAACAC	CTGAAAATGA	CCAAC'TAGAT	300
CAAATTTTTG	GAGATTTTGA	AATCAAGGAT	TTGGATAAGA	AAGCAGAAAA	TAAAAAGCTG	360
GTTCGCCGTT	TCTTGACAGA	AATTTTCCAA	AATGGGGAGC	TAGAGCAGTG	GAGTGATTAT	420
GTGGCAGACG	ATTTGATTCA	GCATAATCAT	GAGATTGGAC	AAGGAAGTGC	TGCTTATAAA	480
AACTATGTGG	CTGAATATAG	TGTCACTTTT	GACTTTGTTT	TCCAAC'TCTT	AGGACAAGGA	540
AACTATGTGG	TTAGCTATGG	TCAGACTCAG	ATTGATGGCG	TTGCTTATGC	CCAGTACGAT	600
ATCTTCCGTT	TAGAGAACGG	GAAAATTGTG	GAGCAT'TGGG	ATAATAAGGA	AGTCATGCCT	660
AAGGTAGAA	ACTTGACTAA	TCGAGGGAAG	T'TTTAA			696

(2) INFORMATION FOR SEQ ID NO:698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

TTTTCTAGTC	TAATAAAAGA	GGCAGAGAAT	GAACTCCAAA	GGAGCATAAG	ATGTACGATT	60
ATCTTATCGT	TGGTGCTGAT	CTCTTTGGCG	CATAGCTTTG	GCTCAGTTTC	TATTATCGCT	120
CACACCATCC	ATCAGAAAGT	TAATTTGAAG	GTACCCAATT	ATCGCCAAGA	AGAAGATTGG	180
GCTAGGATGG	GTTTACCAAT	CACACGTAAG	GAAATCTCTA	ATTGGCATAT	CAAGGCAAGT	240
CAATACTATT	TAGAGTCCCT	TTATAACCTT	TTACGAGAAA	AGTTGTTAGA	ACAACCTCTT	300
CTTCATGCGG	ATGAAACCTC	TTATCGGGTG	CTAGAGAGTG	ATAGCCATCT	GACCTACTAT	360
TGGACCTTTT	TGCTGGGAA	AGCTGAGAAT	CAAGCAATCA	CGCTGTACCA	TCATGATCAG	420
CGTCGGAGTG	GTTTAGTAGT	ACAAGAATTC	CTAGGAGATT	ATTCTGGCTA	TGTGCATTGT	480
GATATGTTGC	GGCAGTAA					498

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

ACATATAGTC	TAATTTGTTT	ACAAGGAGGA	AATATGCAAG	AAAGTAACAA	ACGCTTAAAA	60
ACAAAGCGAA	CTATTGAAAA	TGCTATGGTA	CAATTACTGA	TGGAACAGCC	ATTTGATAAA	120
ATTTCTACTG	TCAAATTAGT	AGAAAAAGCC	GGAATTAGTC	GTTCCAGCTT	CTATACTCAC	180

TATAAGGATA	AGTATGATAT	GATTGAGCAC	TATCAAAGCA	AGCTATTCCA	TACATTTGAA	240
TATATTTTTTC	AAAAACATGC	TCATCACAAA	AGAGACGCTA	TTTTAGAAGT	TTTTGAATAT	300
CTAGAGTCAG	AACCACTTCT	GGCTGTCCTT	CTTTCTGAAA	ATGGGACTAA	AGAAATCCAA	360
AATTTCTTAC	GAAATAAACT	TCATATCATG	CTTAGTACAG	ATTTACAAAA	GCGATTTATG	420
CAACTGAATC	TAAATACCAC	CGAATTAGAA	TATAGTAGCA	TCTATCTAAC	TCATGCACTT	480
TTTGGTGTCT	GCCAAACTTG	GATTGCACAT	GGAAAAAAG	AAAGTTCTCA	AGAAATAACA	540
GACTTCCTTA	TGAAATGCT	TGGTGATACA	AATTGA			576

(2) INFORMATION FOR SEQ ID NO:700:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

ATGTTTTTAC	ATCATTTTAC	AGAGATTTAC	GAACTTTTG	CCCCTTTTTT	GCCCCTTTTG	60
AGCAAACAAA	AAAACCGCAA	GCCTGAGCCT	GCGGTGAAAG	AACAATTTAG	AAAGTTTCCT	120
TTCTATTTAT	TTAACTGTAA	TCAAGCCATC	TGGCTCTACT	GTGAACTCTG	GCTTGTCTGC	180
CATGCTACCG	TCTGGTTTGA	GGTAGTACCA	GCCTGTTCCG	TCCGCTGA		228

(2) INFORMATION FOR SEQ ID NO:701:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

ATACTCTTAC	AGACCGTGAA	AGAAAATGTT	CTGCGTCTAC	GTTTTGGACT	AGATGATGGA	60
AAAATGCGCA	CACTTGAAGA	TGTGGGGAAA	GTCTTTAACG	TAACTCGTGA	GCGTATCCGT	120
CAGATTGAAG	CAAAGGCTTT	GAGAAAATA	CGCCAACCAA	GTCGCAGCAA	ACCGCTTCGT	180
GATTTTATTG	AAGACTAA					198

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

ATAGGAAGTC	TTACAATTAT	ACTTCTAAAA	CAAGTGACAT	TGAAAAGAAA	TCGACTCAGG	60
AAGCAGTTCT	CAATAAAAAAC	TTCCGTCAGG	CTATCAATTT	TGCTTTTGAC	AGAACATCTT	120
ATGGGGCTCA	GTCTGAAGGG	AAAAGGAAGT	GCAACAAAAG	TTTTGCGTAA	CCTAGTGGTT	180
CCTCCAAACT	TTGTCAGTAT	CAAGGGAAAA	GACTTTGGTG	AAGTTGTAGC	CTCTAAGATG	240
GTCAACTATG	GTAAGGAATG	GCAAGGTATC	AACTTTGCGG	ATGGTCAAGA	CCCTTACTAC	300
AATCCTGAGA	AAGCCAAGGC	TAAGTTTGCG	GAAGCTAAGA	AAGAACTCGA	AGCAAAGGGT	360
GTTCAATTCC	CAATCCACTT	GGATAAGACT	GTGGAAGTAA	CAGATAAAGT	AGGCATACAA	420
GGAGTTAGTT	CTATCAAACA	ATCAATTGAA	TCTGTTTATG	GTTCTGATAA	TGTAGTGATT	480
GACATTCAGC	AATTAACATC	AGATGAGTTT	GACAGTTCAG	GCTACTTTGC	TCAAACAGCT	540
GCTCAGAAAG	ACTATGATTT	ATATCATGGC	GGTTGGGGAC	CTGATTATCA	AGACCCGTCA	600
ACCTATCTCG	ATATTTTTAA	TACTAATAGT	GGAGGAGTTC	TACAAAATCT	TGGACTAGAG	660
CCTGGAGAAG	CCAATGACAA	GGCTAAGGCA	GTTGGACTGG	ATGTCTATAC	TCAAATGTTG	720
GAAGAAGCTA	ATAAAGAGCA	AGATCCAGCC	AAACGTTATG	AGAAATATGC	TGATATTCAA	780
GCTTGGTTGA	TTGATAGTTC	TTTAGTTCTT	CCAAGTGTTT	CGCGTGGGGG	AACACCATCA	840
TTGAGAAGAA	CCGTACCATT	TGCTGCTGCC	TATGGTTTAA	CCGGTACAAA	AGGGGTTGAA	900
TCATATAAAT	ACCTCAAAGT	ACAAGATAAG	ATTGTCACAA	CAGACGAATA	TGCAAAAGCC	960
AGAGAAAAAT	GGTTGAAAGA	AAAAGAAGAA	TCCAATAAAA	AAGCCCAAGA	AGAATTGGCA	1020
AAACATGTCA	AATAA					1035

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GGAGGAAGTC TTATGATACA ACCAGCAAGT TTAGAAGAAT TGGCATCTTT AGTAGAAAAA	60
GACGGTAAGA AGGTCTTCCT TTTTGTGGCG GACTGGTGTG GCGATTGCCG TTATATCTAT	120
CCTGCCTTAC CAGAAATTGA GGAGAGTAAT CCAGAGTTTA CCTTTATTCG AGTGGATAGA	180
GACCAAGTATA TAGATTTGGC CAAACTCTGG GATGTATATG GAATCCCTAG CCTTGTTGTT	240
CTAGAAAAGG ACAAGGAAAT CGGTCGTTTT GTCAATCGCG ACCGTAAAAG CAAGCAACAA	300
ATTAAACGATT TTTTAGCAGG ATTGAAATAG	330

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

AAACTGTTAC AATGTAGAAA AAGAAAAGAG GCCCTCATGA CTTCACTTTA TGATTTTTCC	60
GTTTTGAACC AAAACAACCA AGCAACTCCC TTGGATAGCT ATCGTGGCAA AGTTCTCTTG	120
ATTGTCAACA CTGCTACTGG ATGTGGTTTA ACGCCCCAGT ACCAGGGACT TCAAGAACTC	180
TATGAACGCT ATCAAGATCA GGGCTTCGAA ATATTGGATT TCCCTTGCAA TCAGTTTATG	240
GGACAAGCAC CCGGCAGCGC AGAGGAAATC AACCGCTTCT GTAGCCTACA TTTTCAAACC	300
ACTTTCCAC GTTTTGCCAA GATTAAGGTC AACGGTAAGG AAGCAGACCC TCTCTATGTC	360
TGGTTAAAAG ACCATAAATC TGGCCCACTA GGAAAACGAA TCGAATGGAA TTTCGCTAAG	420
TTTCTCATTA GTCGTGATGG GCAAGTCTTT GAACGCTTTT CTTCAAAAAC AGACCCAAAA	480
CAAATTGAAG AGGCGATACA AACTCTACTA TAA	513

(2) INFORMATION FOR SEQ ID NO:705:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...996
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

TCCTTGAGTC	TATGTGCCTA	TGCACTAAAC	CAGCATCGTG	CGCAGGAAAA	TAAGGACAAT	60
AATCGTGTCT	CTTATGTGGA	TGGCAGCCAG	TCAAGTCAGA	AAAGTGAAAA	CTTGACACCA	120
GACCAGGTTA	GCCAGAAAGA	AGGAATTCAG	GCTGAGCAAA	TTGTAATCAA	AATTACAGAT	180
CAGGGCTATG	TAACGTCACA	CGGTGACCAC	TATCATTACT	ATAATGGGAA	AGTACCTTAT	240
GATGCCCTCT	TTAGTGAAGA	ACTCTTGATG	AAGGATCCAA	ACTATCAACT	TAAAGACGCT	300
GATATTGTCA	ATGAAGTCAA	GGGTGGTTAT	ATCATCAAGG	TCGATGGAAA	ATATTATGTC	360
TACCTGAAAG	ATGCAGCTCA	TGCTGATAAT	GTTCGAACTA	AAGATGAAAT	CAATCGTCAA	420
AAACAAGAAC	ATGTCAAAGA	TAATGAGAAG	GTTAACTCTA	ATGTTGCTGT	AGCAAGGTCT	480
CAGGGACGAT	ATACGACAAA	TGATGGTTAT	GTCTTTAATC	CAGCTGATAT	TATCGAAGAT	540
ACGGGTAATG	CTTATATCGT	TCCTCATGGA	GGTCACTATC	ACTACATTCC	CAAAAGCGAT	600
TTATCTGCTA	GTGAATTAGC	AGCAGCTAAA	GCACATCTGG	CTGGAAAAAA	TATGCAACCG	660
AGTCAGTTAA	GCTATTCTTC	AACAGCTAGT	GACAATAACA	CGCAATCTGT	AGCAAAAGGA	720
TCAACTAGCA	AGCCAGCAAA	TAAATCTGAA	AATCTCCAGA	GTCTTTTGAA	GGAACTCTAT	780
GATTACCTA	GCGCCCAACG	TTACAGTGAA	TCAGATGGCC	TGGTCTTTGA	CCCTGCTAAG	840
ATTATCAGTC	GTACACCAAA	TGGAGTTGCG	ATTCCGCATG	GCGACCATTA	CCACTTTATT	900
CCTTACAGCA	AGCTTTCTGC	TTTAGAAGAA	AAGATTGCCA	GAATAGGTGC	CTATCAGTGG	960
AACTGGTTCT	ACAGTTTCTA	CAAATGCAAA	ACCTAA			996

(2) INFORMATION FOR SEQ ID NO:706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 891 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GTTGTTATAC	AGGGAGTAAG	CATGCAAATT	CAAAAAAGTT	TTAAGGGGCA	GTCTCCCTAT	60
GGCAAGCTGT	ATCTAGTGGC	AACGCCGATT	GGCAATCTAG	ATGATATGAC	TTTTCGTGCT	120
ATCCAGACCT	TGAAAGAAGT	GGACTGGATT	GCTGCTGAGG	ATACGCGCAA	TACAGGGCTT	180
TTGCTCAAGC	ATTTTGACAT	TTCCACCAAG	CAGATCAGTT	TTCATGAGCA	CAATGCCAAG	240
GAAAAAATTC	CTGATTTGAT	TGGTTTCTTG	AAAGCAGGGC	AAAGTATTGC	TCAGGTCTCT	300
GATGCCGGTT	TGCCTAGCAT	TTCAGACCCT	GGTCATGATT	TGGTTAAGGC	AGCTATTGAG	360
GAAGAAATTG	CAGTTGTTAC	AGTTCCAGGT	GCCTCTGCAG	GAATTTCCGC	CTTGATTGCC	420
AGTGGTTTAT	CGCCGCAGCC	ACATATCTTT	TACGGCTTTT	TACCGAGAAA	ATCAGGCCAG	480
CAAAAGCAAT	TTTTTCGACTC	GAAAAAAGAC	TATCCTGAAA	CTCAGATTTT	TTATGAATCG	540
CCCCATCGTG	TGGCAGATAC	ATTGGAAAAT	ATGCTAGAAG	TCTACGGTGA	CCGCTCCGTT	600
GTCTTGGTCA	GGGAATTGAC	CAAAATCTAT	GAAGAATACC	AAAGAGGTAC	AATTTCTGAA	660
TTGCTGGAAA	GCATTGCTGA	AACGTCTCTC	AAGGGTGAAT	GTCTTCTGAT	TGTTGAAGGT	720
GCCAGTCAGG	ATGTGGAAGA	AAAAGACGAG	GAAGACTTGT	TCTTAGAAAT	CCAAGCTCGT	780
ATCCAGCAAG	GTATGAAGAA	AAATCAAGCT	ATTAAGGAAG	TAGCTAAGAT	TTACCAGTGG	840
AATAAGAGTC	AACTCTACGC	TGCCTACCAC	GACTGGGAAG	AAAAACAATA	A	891

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

AAGGAGAGTC	TCATGACGGT	GGTTAAAGTT	GAGAAATTGA	GTAAGAAAAT	AAAAGACAAG	60
GAAATTTTGC	GGAACATCTC	CTTTGAAATC	AACGATGGTG	AATGTGTTGC	CTTAATTGGT	120
CCAAATGGTG	CCGGAAGAC	AACACTCTTA	GATTGTTTGC	TTGGAGATAA	ACTGGTCACA	180
AGCGGTCAAG	TATCTATTCA	AGGTTTACCA	GTGACGAGTT	CTAAGTTAGA	CTATACTAGG	240
GCTTACCTCC	CTCAAGAAAA	TATAATCGTT	CAGAAATTAA	AAGTTAAAGA	GTTGATTGCT	300
TTCTTTCAAC	GTATCTATCC	AAATCCTTTG	AGCAATCAGG	AAATTGATCA	ACTATTGCAG	360
TTTGTCAAGC	AACAAAAAGA	ACAGTTGGCA	GAAAAATTAT	CAGGCGGTCA	AAAGCGTCTC	420
TTTTCTTTCA	TCTTGACCTT	AATTGGGCGA	CCAAAGATTG	TTTTTTTAGA	TGAGCCTACT	480
GCGTCCATGG	ATACCTCAAC	TCGTCAACGT	TTTTGGGAAA	TTGTCCAGGA	GTAAAAGCG	540
CAAGGAGTCA	CCATTCTCTA	TTCGTCCCAT	TATATTGAGG	AAGTGGAACA	CACTGCAGAC	600
CGCATTTTGC	TCTTAAATAA	GGGAGAGTTG	ATTTCGAGATA	CGACGCCCTCT	AGCTATGCGT	660
AGCGAGGAAA	TAGAAAAGCA	CTTTATCCTT	CCTATAGCTT	ACAAGGAAGT	CGTAGAGCAG	720

TCAAATTTGG TTGAAAAC TG GACCCTAAAG CAAGATTCTT TACAAGTAGT CACTCGAGAA	780
GCAGATGCTT TCTGGGAACT ATTAGCCCAA GCAGGATGTA GGATGCAAAG AAATCGAAGT	840
TAA	843

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

CCTGAAATAC AGTATTGGCT TGGTCAATTT TCACGCCAAA AAGAAGGGAG GGATCTCCAA	60
GAAATCTTTG CTCGCTTTAC AAATTTTAAAC TTTTGTTCGTT GGGTAACCTC GCAAGTTGCC	120
ATCGACAGTA GTCACAAAAA ACAAAGATAT AAAGTGTGTT TCTCAGATGC GGCTTATGCC	180
TGCCGTTTGT TTTTAAACGG TTCCCTTTCT TCCCTCCAGT TGAAAAACTA CCTCAAGAAA	240
CAGTTATCTA TTATTCGACC GAATCGAAAA TATTCAAGAA AGATAAAAGC TCAATCGGTA	300
GTTGATTTC TCTATAGAGT AACATAA	327

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GCTGAAATAC	AAGAAATGAG	GGAGGATTTC	TATGAAAAAG	TATCAACTTC	TATTCAAAAT	60
AAGTGCAGTC	TTCTCTTACT	TATTTTTCGT	ATTTGGTCTT	TCTCAGCTGA	CGCTTATCGT	120
CCAAAAATTAT	TGGCAATTTT	CTTCCCAGAT	TGGCAATTTC	GTCTGGATTG	AAAATATCTT	180
GAGTTTACTA	TTTAG					195

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

AGGAGAATAC	ACATGAGCTT	ACTAGATATC	GCAAAATCAA	TCAAAAAGA	GGGCTTTGAC	60
CCACGCAAAG	ACAGCGCCAA	CGGTCCTGCA	CCAATCCCAG	CTGGTACTTA	TCCAGTAGTC	120
CTGAAGAAAG	CAACCTTCAA	CGTATCGGAC	AAAGGCTGGG	AAAGCCTTGG	TTATCAATTT	180
GAAATCCGTG	GCGGTGATTA	CAGTGGACGC	TCTGAATTTG	CAACATTTGG	CACACTGACT	240
GAATGGAACG	GTAAGAACCT	TGACTGGGCA	GTTGAACGCA	CTATGAAATT	CTTTATCAAA	300
GCCTTGGTCC	TTGCTGGCGA	CAGTATGCAA	GGAAATGAAG	AAGACGGTAA	AGCCTTGGAA	360
GAGGCTCTAC	AACGTAAGGC	AGTTGGCTCT	TACTACAACC	TTGTTATCTC	TGTGACTAAG	420
GGGAAAGATG	GCCGTGAGTT	CCGAAACTAT	GACCTTGAAG	AAGAAGAAGC	ACAACCGCTG	480
ACTGAAGCTG	ATATCGATGA	AGATGACCTC	CCTTTCTAA			519

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

AGTTGTTTAC	ATCTTATTTT	AATTCACAT	AGAAGGAGGA	AAAGGATGAT	TCTCAGACAT	60
CTGGGAATTA	GCCCGACCAA	TGACTTGGTT	GCTAAGAAAA	TTTTTCAGCAA	CCCAGAAATC	120
ACTTGTCAAT	TTATCCGCGA	TATGCTGGAC	TTGCCAGCCA	AAAATGTGAC	TATTTTGGAG	180
GGAAGTAACA	TTCATGTCTT	GCCTTCCATG	CCCTACTCGG	TGCAGGATTT	TTATACCAGT	240
ATAGACGTCT	TGGCGGAGTT	GGATAACGGT	ACTCAAGTAA	TTATTGAGAT	TCAAGTCCAT	300
CATCAGAATT	TTTTTCATCA	TCACTTGTGG	GCTTACCTGT	GCAGTCAGGT	TAATCAAAAT	360
CTTGAAAAAA	TTCATCAGCG	AGAAGGTGAT	ACTCACTAG			399

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

TTTATCTCAC	ACAAAGTGGA	GGTGTTCAT	CACATTGTGT	TCACCCCTAA	GTATAGACGA	60
AAAGTCATCT	ATAATCAATA	TAGAAGTAGT	TTAGGCGAAA	TATTTTCATCG	CTTGTGTAGT	120
TATAAAGGTG	TTGAAATGAT	CGAGGGTCAC	TTAATGCCAG	ACCATGTACA	CATGTTAGTC	180
AGTATTCCGT	CGAGGCTAAG	TGTTTCAAGT	TTTATGGGGT	ATTTAAAAGG	CAAAAGTGCA	240
CTCATGATGT	TTGACAAACA	CGCCAATCTC	AAGTACAAGT	TTGGGAATCG	GCATTTCTGG	300
GCGGAAGGTT	ATTATGTAAG	TCCAGTAGGG	CTTAATGAAG	CCACAATTAA	GAAATATAGT	360
CAAGATTAA						369

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GGGTTATCAC	ATATAACTCA	AAAAAAGAAA	GAACAAAAGG	AGAGTCAAAC	TATGGCTTCT	60
AAAGATTTCC	ACGTAGTGGC	AGAAACAGGT	ATTCACGCAC	GTCCAGCAAC	ATTGTTGGTA	120
CAAACTGCTA	GCAAATTTGC	TTCAGATATC	ACTCTTGAGT	ACAAAGGTAA	ATCAGTTAAC	180
CTTAAATCAA	TTATGGGTGT	TATGAGTCTT	GGTGTGGCC	AAGGTGCTGA	CGTAACTATC	240
TCAGCTGAAG	GTGCAGATGC	AGATGACGCT	ATCGCTGCAA	TCTCAGAAAC	AATGGAAAAA	300
GAAGGATTGG	CATAA					315

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

CCACATGGTC	TGCACGGAAA	TGAACCGTCG	CCGCTGCCTT	GGATGAATAA	GAANACCCTA	60
CCCAACAATC	CTGCTACAAG	CAAGGATAGC	CATGGAGTTG	CTGCTCCAAA	TTGTTCTGCA	120
AATTCAAGGT	TAAAGACAAC	TCCAGAAAAG	GCACCCATAA	CCATAATTCC	TTCAAGGCCA	180
ACGTTTACCA	CACCACCACG	TTCAGAGAAA	ACACCACCGA	TACTTGTAAG	GATGAGAGGT	240
GCTGAGTAA						249

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

TTCTTTACAC	AATCTTTACA	TGAATCAGGG	ATAAACCTTT	ACAAAGACTT	GTTAGACTAT	60
AAATGTAGTA	AGCCTACACA	AGAAAAATAC	ATAGAGATAA	AGGTGATTAT	TATGAAATTC	120
AAAAAAATGC	TTACTCTTGC	AGCCATTGGC	TTATCAGGAT	TTGGGCTTGT	TGCCTGTGGC	180
AATCAGTCAG	CTGCTTCCAA	ACAGTCAGCT	TCAGGAACGA	TTGAGGTGAT	TTCACGAGAA	240
AATGGCTCTG	GAACACGGGG	TGCCTTCACA	GAAATCACAG	GGATTCTCAA	AAAAGACGGT	300
GATAAAAAAA	TTGACAACAC	TGCCAAAAACA	GCTGTGATTC	AAAAATAGTAC	AGAAGGTGTT	360
CTCTCAGCAG	TTCAAGGGAA	TGCTAATGCT	ATCGGCTACA	TCTCCTTGGG	ATCTTTAACG	420
AAATCTGTCA	AGGCTTTAGA	GATTGATGGT	GTCAAGGCTA	GTCGAGACAC	AGTTTTAGAT	480
GGTGAATACC	CTCTTCAACG	TCCCTTCAAC	ATTGTTTGGT	CTTCTAATCT	TTCCAAGCTA	540
GGTCAAGATT	TTATCAGCTT	TATCCACTCC	AAACAAGGTC	AACAAGTGGT	CACAGATAAT	600
AAATTTATTG	AAGCTAAAAC	TGAAACCACA	GAATATACAA	GCCAACACTT	ATCAGGCAAG	660
TTGTCTGTTG	TAGGTTCCAC	TTCAGTATCT	TCTTTAATGG	AAAAATTAGC	AGAAGCTTAT	720
AAAAAAGAAA	ATCCAGAAGT	TACGATTGAT	ATTACCTCTA	ATGGGTCTTC	AGCAGGTATT	780
ACCGCTGTTA	AGGAGAAAAAC	CGCTGATATT	GGTATGGTTT	CTAGGGAATT	AACTCCTGAA	840
GAAGGTAAAG	GTCTCACCCA	TGATGCTATT	GCTTTAGACG	GTATTGCTGT	TGTGGTCAAT	900
AATGACAATA	AGGCAAGCCA	AGTCAGTATG	GCTGAACTTG	CAGACGTTTT	TAGTGGCAAA	960
TTAACCACCT	GGGACAAGAT	TAAATAA				987

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 561 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

CTCAGGACAC	ACCAAAAGAA	CCAGGTAACA	AAAAACCATC	TGCTCCAAAA	CCAGGTATGC	60
AACCAAGTCC	TCAACCAGAG	GTTAAACCGC	AGCTGGAAAA	ACCAAAACCA	GAGGTTAAAC	120
CGCAACCAGA	AAAACCAAAA	CCAGAGGTTA	AACCGCAGCC	GGAAAAACCA	AAACCAGAGG	180
TTAAACCGCA	GCCGGAAAAA	CCAAAACCAG	AGGTTAAACC	GCAGCCGGAA	AAACCAAAAC	240

CAGAGGTTAA	ACCGCAGCCG	GAAAAACCAA	AACCAGAGGT	TAAACCGCAG	CCGGAAAAAC	300
CAAAACCAGA	GGTTAAACCG	CAGCCGGAAA	AACCAAAACC	AGAGGTTAAA	CCGCAGCCGG	360
AAAAACCAAA	ACCAGAGGTT	AAACCGCAGC	CGGAAAAACC	AAAACCAGAG	GTAAACCGC	420
AGCCGGAAAA	ACCAAAACCA	GAGGTTAAAC	CGCAACCAGA	AAAACCAAAA	CCAGAGGTTA	480
AACCGCAACC	AGAAAAACCA	AAACCAGATA	ATAGCAAGCC	ACAAGCAGAT	GATAAGAAGC	540
CATCAACTAC	AAATAATTTA	A				561

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...435
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

CCTAAAGCAC	ATATTAAGCT	GTTAGCAAAT	CAACAAAAAC	ATAGTGATGC	AGGAGCAACT	60
ATTGAAGATG	AATATTATGT	ATTTATCGCT	GAGAGTAAAA	TTGATGGCAA	GAAGGAAGTT	120
ATTCACTGTT	GCATGGGTGC	GGCAAGGGAT	TTTTTAGAAC	TAATTAATCA	CAAAGGGCTA	180
CCTTTTTTTT	ATCCGCTTGT	AGGTGATTCT	CATGTAAATA	ATAGACAAGA	ATATGACAAT	240
ACAGGGAGTG	GAAATTTACA	ACCTGAAAAG	TGGAATGAAA	CTGCACAGCA	GCTTTATAAT	300
GCTATAATGT	GGTTGATTAT	TTTATGGAAT	GCTAAGCCGG	ATACACCTTT	ATTTATTTTT	360
AAAGACGAAG	TAATTAAGTA	TAAAACATAT	GAGCCTTTTG	AAAGCAGTAT	AAAATTGGTA	420
TCAATCAATG	AGTAA					435

(2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 575 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

AAAATGGCAC	ATTTATTAGA	AAAAACTAGA	AAAATTACAT	CAATTTTGAA	ACGCTCAGAG	60
GAGCAGTTGC	AGGATGAGCT	CCCTTACAAC	GCTATTACGC	GTCAGTTAGC	GGATATTATT	120
CATTGCAATG	CCTGCATTAT	CAATAGTAAG	GGACGTCTGC	TTGGCTATTT	TATGCGTTAT	180
AAAACAAATA	CAGATCGCGT	AAAGCAATTC	TTCCAAACTA	AGATTTTCCC	AGATGACTAC	240
GTTCAAGGGG	CTAATATGAT	TTACGAAACA	GAAGCAAAC	TGCCTGTTGA	GCATGATATG	300
AGTATTTTCC	CTGTTGAGAG	TAGAGATGAT	TTTCCAGATG	GCTTGACGAC	TATTGCACCG	360
ATTCATGTAT	CGGGGATTCG	CCTTGGTTCT	TTGATTATTT	GGCGTAATGA	TAAAAAATTC	420
GAAGATGAGG	ACTTGGTTCT	TGTTGAGATT	GCCAGTACCG	TTGTTGGGAT	TCAGCTTCTT	480
AACTTCCAAC	GTGAAGAAGA	TGAGAAAAAT	ATTCGTCGTC	GTAAGTCTGT	CACCATGGCG	540
GTCAATACCC	TTTCTTACTC	CGAACTCCGT	GCTGT			575

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

ATAATACAAC	AAAACAAAAA	ACTTGTCAAG	CAAAAAGAAG	AATTGTTTTG	GGAATCGCTT	60
AAAAAATGGT	ATAATGAAAA	GAAAACGATA	AGGAGGGAAA	GGATGCGTTG	TCCAAAATGT	120
GGGGCTACCA	AGTCAAGTGT	TATCGATAGT	CGCCAAGCAG	AAGAAGGGAA	CACCATTCGT	180
AGAAGACGAG	AGTGCGACGA	GTGCCAACAC	CGTTTTACAA	CCTACGAACG	AGTAGAAGAA	240
AGAACCCTTAG	TGGTTGTAA	AAAAGATGGC	ACACGGGAAC	AATTCCTCCAG	AGATAAAATC	300
TTTAATGGGA	TTATCCGCTC	AGCCCAGAAA	CGTCCTGTGT	CAAGTGATGA	AATCAACATG	360
GTAGTCAATC	GTATCGAACA	GAAACTCCGT	GGTCGAAATG	AAAATGAAAT	TCAAAGTGAG	420
GACATTGGTT	CACTCGTCAT	GGAGGAGTTG	GCTGAATTGG	ACGAGATTAC	CTATGTACGT	480
TTTGCTAGTG	TCTATCGTAG	TTTTAAGGAT	GTCAGTGAGT	TAGAGAGCTT	GCTCCAACAA	540
ATCACCCAGT	CCTCTAAAAA	GAAAAAGGAA	AGATAA			576

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

CTAAGTAAAC	AAAAAGAGGT	AAAGAATATG	AATAACAACCT	TTAATAATTT	TAATAACATG	60
GATGATTTAT	TTAACCAATT	GATGGGTGGT	ATGCGAGGAT	ATAGTTCTGA	AAATCGCCGT	120
TACTTAATTA	ATGGACGCGA	AGTCACACCT	GAGGAATTTG	CTCACTATCG	TGCGACTGGT	180
CAATTACCAG	GAAATGCAGA	AACTGATGTG	CAAAATGCCAC	AACAGGCATC	AGGTATGAAA	240
CAAGATGGTG	TCCTTGCAAA	ACTAGGTCGA	AACTTAACAG	CAGAAGCGCG	TGAGGGCAAG	300
TTGGACCCTG	TTATCGGACG	AAACAAGGAA	ATTCAAGAAA	CATCTGAAAT	CCTCTCACGC	360
CGCACCAAGA	ACAATCCTGT	TTTGGTCGGA	GATGCAGGTG	TTGGTAAGAC	AGCAGTTGTC	420
GAAGGTCTAG	CGCAAGCCAT	TGTGAACGGA	GATGTTCCCTG	CTGCTATCAA	GAACAAGGAA	480
ATTATTTCTA	TTGATATCTC	AGGTCTTGAG	GCTGGTACTC	AATACCGTGG	TAGCTTTGAA	540
GAAAAATGCC	AAAACTTGGT	CAATGAAGTG	AAAGAAGCAG	GGAATATTAT	CCTCTTCTTT	600
GATGAAATTC	ACCAAAATCT	TGGTGCTGGT	AGCACTGGTG	GAGACAGTGG	TTCTAAAGGG	660
CTTGCGGATA	TTCTCAAGCC	AGCTCTCTCT	CGTGGAGAAT	TGACAGTGAT	TGGGGCAACA	720
ACTCAAGACG	AATACCGTAA	CACCATCTTG	AAGAATGCTG	CTCTTGCTCG	TCGTTTCAAC	780
GAAGTGAAGG	TCAATGCTCC	TTCAGCAGAG	AATACTTTTA	ACATTCTTCA	AGGCATTCCGT	840
GACCTCTATC	AACAACACCA	CAATGTCATC	TTGCCAGACG	AAGTCTTGAA	AGCAGCGGTG	900
GATTATTTCTG	TTCAATACAT	TCCTCAACGT	AGCTTGCCAG	ATAAGGCTAT	TGACCTTGTC	960
GATGTAACGG	CTGCTCACTT	GGCGGCTCAA	CATCCAGTAA	CAGATGTGCA	TGCTGTTGAA	1020
CGAGAAATCG	AAACGGAAAA	AGACAAGCAA	GAAAAAGCAG	TTGAAGCAGA	AGATTTTGAA	1080
GCAGCTCTAA	ACTATAAAAC	ACGCATTGCA	GAATTGGAAA	GGAAAATCGA	AAACCACACA	1140
GAAGATATGA	AAGTGACTGC	AAGTGTC AAC	GATGTGGCTG	AATCTGTGGA	ACGAATGACA	1200
GGTATCCCAG	TATCGCAAAT	GGGAGCTTCA	GATATCGAAC	GTTTGAAAGA	TATGGCTCAT	1260
CGCTTGCAAG	ACAAGGTGAT	TGGTCAAGAT	AAGGCCGTAG	AAGTTGTAGC	TCGTGCTATC	1320
CGTCGTAAAC	GTGCTGGTTT	TGATGAAGGA	AATCGCCCAA	TCGGCAGCTT	CCTCTTTGTA	1380
GGGTCTACTG	GGGTGTTGTA	GACGGAGCTT	GCTAAGCAAT	TGGCACTCGA	TATGTTTGGA	1440
ACCCAGGATG	CGATTATCCG	TTTGGATATG	TCTGAATACA	GTGACCGCAC	AGCTGTTTCT	1500
AAGCTAATTG	GTACAACAGC	AGGCTATGTG	GGTTATGATG	ACAATAGCAA	TACCTTAACA	1560
GAACGTGTTT	GTCGCAATCC	ATACTCTATC	ATTCTCTTGG	ATGAAATTGA	AAAGGCTGAC	1620
CCTCAAGTTA	TTACCCCTCT	CCTCCAAGTT	CTAGATGATG	GTCGTTTGAC	AGATGGTCAA	1680
GGAAATACAG	TAAACTTCAA	GAACACTGTC	ATTATTGCGA	CCTCAAATGC	TGGATTTGGC	1740
TATGAAGCCA	ACTTGACAGA	AGATGCGGAT	AAACCAGAAT	TGATGGACCG	TTTGAACCCC	1800
TTCTTCCGTC	CAGAACTCCT	CAACCGCTTT	AATGCAGTCA	TCGAGTTCTC	ACACTTGACT	1860
AAGGAAGACC	TTTCTAAGAT	TGTAGATTTG	ATGTTGGCTG	AAGTTAACCA	AACCTTGGCT	1920
AAGAAAGACA	TTGACTTGGT	AGTCAGTCAA	GCGGCTAAAG	ATTATATCAC	AGAAGAAGGT	1980
TACGACGAAG	TCAATGGGGT	TCGTCTCTCT	CGTCGAGTGG	TTGAACAAGA	AATTCGTGAT	2040
AAGGTGACAG	ACTTCCACTT	GGATCATTTA	GATGCTAAAC	ATCTGGAAGC	AGATATGGAA	2100
GATGGCGTTT	TGGTTATTCG	TGAGAAAGCC	TAA			2133

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

ATCTACAAAC	ACATCGCTCC	TGTTTACGTC	ATTGCTATCG	TGGATAGTAA	TTATTTCTCA	60
GATGACCTGG	CTTTTCATAG	CTTTAGTATG	CGCGAAGACA	CAACAGGTGA	GGTATTGGCG	120
ATTACCAACA	ATGGACAGGA	AAACCATCTG	GTTAAGATGG	CATTCTTGGA	ATTAAAAAAT	180
ACAGAGAAAC	CAGCAAAGAC	AAGGTTTCGCA	AGCCATGGTT	GGAGTTTTTC	GGCAACAAGC	240
CCTTTACCCA	GCAACCGCAA	CGAGCCATTA	GCCAAGCAAA	TCAACTGCTG	GACTACAAGA	300
GCTGGTCCGA	GGAGGACAGG	AAAATGTTTA	GTCAACTACA	TATGCGAGAA	GAACAAGTCT	360
TGTTAG						366

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

TGCTCAAAAC	ACCGTTTTGA	GGTGGCAGAT	AGAACTGACG	AAGTCAGCTC	AAAACACCGT	60
TTTGAGGTGG	CAGATAGAAC	TGACGAAGTC	AGCTCAAAAC	ACCGTTTTGA	GGTGGCAGAT	120
AGAACTGACG	AAGTCAGCTC	AAAACACCGT	TTTGAGGTGG	CAGATAGAAC	TGACGAAGTC	180
AGCTCAAAAC	ACCGTTTTGA	GGTGGCAGAT	AGAACTGACG	AAGTCAGCTC	AAAACACCGT	240
TTTGAGGTGG	CAGATAGAAC	TGACGAAGTC	AGCTCAAAAC	ACCGTTTTGA	GGTGGCAGAT	300
AGAACTGACG	AAGTCAGCTC	AAAACACCGT	TTTGAGGTGG	CAGATAGAAC	TGACGAAGTC	360

AGCTCAAAAC	ACCGTTTTGA	GGTGGCAGAT	AGAACTGACG	AAGTCAGCTC	AAAACACCGT	420
TTTGAGGTGG	CAGATAGAAC	TGACGAAGTC	AGCTCAAAAC	ACCGTTTTGA	GGTGGCAGAT	480
AGAACTGACG	AAGTCAGTAA	CATATATACG	GCAAGGCGAA	GCTGA		525

(2) INFORMATION FOR SEQ ID NO:723:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...708
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

ATGACAAAAC	AAGTCTTATT	AGTGGATGAT	GAAGAACACA	TTCTGAAATT	GCTTGACTAC	60
CATTTAAGTA	AGGAAGGCTT	TTCTACTCAA	TTGGTAACAA	ATGGACGGAA	GGCCTTAGCT	120
TTGGCAGAAA	CAGAACCCTT	TGATTTTATC	TTGCTTGATA	TCATGTTACC	ACAATTAGAT	180
GGCATGGAAG	TTTGTAAGCG	GCTGAGAGCC	AAAGGCGTCA	AAACTCCAAT	TATGATGGTT	240
TCTGCGAAAA	GTGATGAATT	TGATAAGGTT	TTAGCCTTGG	AATTAGGGGC	TGATGACTAC	300
CTGACCAAGC	CTTTTAGCCC	TAGAGAATTG	CTGGCGCGTG	TCAAGGCTGT	CCTCAGGCGA	360
ACTAAAGGAG	AACAAGAAGG	AGATGATTCA	GATAATATCG	CTGACGATTC	TTGGCTATTT	420
GGGACCTTGA	AAGTATACCC	TGAGCGTCAT	GAAGTCTACA	AGGCGAATAA	GTTACTGAGT	480
TTGACCCCAA	AAGAATTTGA	ACTCTTGCTC	TATCTTATGA	AACATCCCAA	CATGACACTG	540
ACTAGAGAGC	GTCTTTTGGG	ACGTATCTGG	GGGTATGACT	TTGGGCAGGA	AACACGTTTG	600
GTGGACG TTC	ATATTGGTAA	GTTGAGGGAA	AAAAATTGAAG	ACAATCCTAA	AGCCCCCTCAA	660
TTTATTTCGAA	CCATTGCGGG	TTATGGTTAT	AAGTTCAAGG	AGTTATAG		708

(2) INFORMATION FOR SEQ ID NO:724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

CTGGCAAAAC	AGTTTGTGTT	AAAAACGGAA	CTGGCGCTCA	ACGTGTTTCCT	TGAAACAATC	60
AAAGATAAAT	ACGGCTTTAC	TATCAAAACA	TTTGACACTG	GTGATTTAAT	GAACAACAGC	120
TTGAGTGCTG	GTGCCATCGA	TGCCATGATG	GATGACAAAC	CTGTTATCGA	ATATGCCATT	180
AACCAAGGTC	AAGACCTCCA	TATTGAAATG	GATGGTGAAG	CTGTAGGAAG	TTTTGCTTTC	240
GGTGTGAAAA	AAGGAAGTAA	ATACGAGCAC	CTGGTTACTG	AATTTAACCA	AGCCTTGGCT	300
GAAATGAAAA	AAGATGGTAG	TCTTGATAAA	ATTATCAAGA	AATGGACTGC	TTCATCATCT	360
TCAGCAGTGC	CAACTACAAC	TACTCTCGCA	GGATTAAAAG	CTATTCCTGT	TAAGGCTAAA	420
TATATCATTG	CCAGCGATTC	TTCTTTTGCA	CCTTTTGTTT	TCCAAAATTC	AAGCAACCAA	480
TACACTGGTA	TTGATATGGA	ATTGATTAAAG	GCAATCGCTA	AAGACCAAGG	TTTTGAAATT	540
GAAATCACCA	ACCTTGTTTT	TGATGCTGCT	ATCAGTGCTG	TCCAAGCTGG	TCAAGCCGAT	600
GGTATCATCG	CTGGTATGTC	TGTCAAAGAT	GCTCGTAAGG	CAACTTTTGA	CTTCTCAGAA	660
TCATACTACA	CTGCTAATAC	CATTCTTGGT	GTCAAAGAAT	CAAGCAATAT	TGCTTCTTAT	720
GAAGATCTAA	AAGGAAAGAC	AGTCGGTGTT	AAAAACGGAA	CTGCTTCTCA	AACCTTCCTA	780
ACAGAAAATC	AAAGCAAATA	CGGCTACAAA	ATCAAAACCT	TTGCTGATGG	TTCTTCAATG	840
TATGACAGTT	TAAACACTGG	TGCCATTGAT	GCCGTTATGG	ATGATGAACC	TGTTCTCAAA	900
TATTCTATCA	GCCAAGGTCA	AAAATTGAAA	ACTCCAATCT	CTGGAACTCC	AATCGGTGAA	960
ACAGCCTTTG	CCGTAAAAA	AGGAGCAAAT	CCAGAACTGA	TTGAAATGTT	CAACAACGGA	1020
CTTGCAAACC	TTAAAGCAAA	CGGTGAATTC	CAAAAGATTC	TTGACAAATA	CCTAGCTAGC	1080
GAATCTTCAA	TGCTTCAAC	AAGTACTGTT	GACGAAACAA	CGCTCTGGGG	CTTGCTTCAA	1140
AACAACCTACA	AACAACCTCT	TAGCGGTCTT	GGTATCACTC	TTGCTCTAGA	CTCTTATCTC	1200
ATTTGCTATT	GCCATTGTCA	TCGGAATTAT	CTTCGGTATG	TTTAG		1245

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

AAAATGAAAC	AAGAACGATT	TCCATTGGTG	TCAGATGACG	AGGTCATGTT	GA CTGAAATG	60
CCAGTCATGA	ATCTCTATGA	TGAGTCTGAT	CTGATCAGTA	ATATCAAGGG	TGAGTATCGA	120
GATAAAAAAT	ATTTAGAAATG	GGCTCCTATT	ACTGAAGAAA	AACCAGTAAA	ACCGATTGAA	180
AAGCAAGTCG	AAAAACCTAA	AAAGGCTCCT	TTAGGGGTTA	AAAAAGAAGG	AAAGAGCTAT	240
GCGGAGGTGG	CGCGTGAAGA	AGCGCGTGCG	GACTTGAAAA	AGAAACGCTC	TGCTAACTAC	300
CTAACTCAGG	ATTTCACTCT	TGCGAGACGT	CATTCTCAGC	CCAGTCTAGT	TAGACAGGGC	360

AATCAACCGA	CAGCTCCTTT	CCAAAAGGAA	AATCCTGGTG	AATTTGTCAA	ATATAGCCAA	420
AAATTGACCC	AGTCTCATTA	TATCTTGGCG	GAAGAAGTTC	ATTCTATCCC	TACCAAGAAT	480
GAAGAAGTGT	CAGCACCTGC	TCCAAAGAAA	AACAATTATG	ATTTTCTAAA	GAAGAGCCAA	540
ATCTACAATA	AAAAAAGTAA	ACAAACAGAA	CAAGAACGTC	GGGTTGCCCA	AGAGTTGAAT	600
CTGACCAGAA	TGACAGAATA	G				621

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

CTGCCTGAAC	ATACTTTTTTA	TGTCGATAAT	CTCTTTGTCT	TTACGCCCCT	TCAGCAGGTC	60
AAGACCATGT	ACTATCTGCC	TGTCGATTTT	TATCGTTATT	TGATTGGGCG	TGAGGACCAG	120
TCTGTCAATG	AGCAAGTGAT	GATTAAGTGC	ATTGACCAGC	AACTCAAGGT	CAATCGACTC	180
TTGGTAGACC	AACTTGATTT	GTCCCAAGTG	AGTCATCCCA	AAATGCGAGA	ATATCTGCTG	240
AATCATATTG	AAATCACGAC	GGTGATTTCC	AGTACCCTGC	TCAACCGATC	TGGAACAACG	300
GAGCATCTGG	CAAAAAAACG	CCAATTGTGG	ACCTATATTC	AGCAGAAAAA	TCCAGAAGTC	360
TTTCAGGCTA	TTTCGTAAGAC	CATGTTGAGC	CGTTTGACCA	AACATTCTGT	CTTGCCAGAT	420
CGCAAACGTG	CCAATGTCGT	CTATCAAATC	ACCAAATCTG	TTTATGGATT	TAATTAA	477

(2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GTATTAGAAC	ATACAATGGA	GGTCGTCATG	GACAATATCA	TCGATGTGTC	AATTCCTGTT	60
GCAGAAGTGG	TGGACAAGCA	TCCAGAAGTC	TTGGAAATTC	TAGTGGAGTT	GGGTTTTTAAA	120
CCCCTTGCCA	ATCCCTTAAT	GCGCAATACA	GTTGGTCGTA	AAGTATCACT	TAAACAGGGT	180
TCTAAGCTAG	CAGGAACTCC	TATGGACAAG	ATTGTACGCA	CACTGGAAGC	GAATGGCTAC	240
GAAGTGATTG	GATTAGACTA	A				261

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

AAGTTGGAAC	ACTCTTCGAG	AAAACATTTT	GTGAAGATTG	TTAAGGAACC	GGGCTTGAAG	60
GGGGCTTTGC	GCTCCTTTAT	TCATCCTGAA	AAGCAGACCT	TTGAAGCGGT	CAAGGATTTG	120
ACCTTTGAGG	TTCCAAAAGG	GCAGATTTTA	GGATTTATCG	GGGCAAATGG	TGCTGGGAAG	180
TCGACAACCA	TTAAAATGCT	GACAGGAATT	TTGAAACCAA	CATCTGGTTT	TTGTCGGATT	240
AACGGCAAGA	TTCCCCAGGA	CAATCGGCAA	GATTATGTCA	AAGATATTGG	CGTAGTCTTT	300
GGACAACGCA	CCCAGCTATG	GTGGGATTTG	GCTCTGCAAG	AGACCTACAC	TGTCTTAAAA	360
GAGATTTATG	ATGTGCCAAA	CTCGCTCTTT	CATAAGCGCA	TGGACTTTTT	GAATGAAGTC	420
TTGGATTTGA	AGGACTTTAT	CAAGGATCCC	GTGCGGACTC	TTTCACTGGG	ACAACGGATG	480
CGGGCGGATA	TTGCGGCCTC	CTTGCTCCAC	AATCCCAAGG	TTCTTTTTTT	AGATGAGCCG	540
ACCATTGGTT	TGGACGTTTC	GGTTAAGGAT	AATATTCTGC	GGGCAATTAC	TCAGATCAAT	600
CAAGAGGAAG	AAACTACCAT	TCTTTTGACC	ACTCACGATT	TGAGTGATAT	TGAGCAACTT	660
TGTGATCGGA	TTTTTCATGAT	TGACAAGGGG	CAAGAGATTT	TTGATGGAAC	GGTGAGCCAA	720
CTCAAGGAGA	CCTTTGGTAA	GATGAAGACT	CTCTCTTTTG	AACTGCTACC	AGGTCAAAGT	780
CATCTCGTCT	CTCACTATGA	AGGTCTGTCT	GATATGACCA	TTGATAGACA	AGGAAACAGC	840
CTCAACATTG	AATTTGATAG	TTCTCGCTAC	CAGTCAGCTG	ACATTATCAA	GCAAACCCTG	900
TCTGATTTTG	AAATCCGCGA	TTTGAAGATG	GTGGATACGG	ATATTGAGGA	TATTATCCGT	960
CGCTTCTACC	GAAAGGAGCT	CTAG				984

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

CAAGACAGAC	AAACATCTCT	TTCTCAACCC	AAAAATTTTCG	CAAATCGAGG	AATGTCTTTT	60
GAAAAGATGA	TCAATGCTAC	CAACGACTAC	TATTTGTCTC	AGGGCTTGGC	TGTTATACAT	120
AAGAAACCAA	CTCCTATTCA	AATCGTACAA	GTGGACTATC	CACAACGAAG	TCGTGCCAAG	180
ATTGTTGAAG	CCTATTTTTCG	ACAAGCTTCA	ACGACGGACT	ATTCTGGCGT	TTATAATGGA	240
TATTACATCG	ACTTTGAAGT	CAAGGAAACA	AAACAAAAAC	GTGCGATTCC	GATGAAAAAT	300
TTTCATCCAC	ATCAGATTCA	GCATATGGAA	CAAGTCCTTG	CCCAACAAGG	AATCTGCTTT	360
GTCCTTCTTC	ACTTTTCTTC	TCAGCAAGAA	ACCTACTTAT	TGCCGGCATT	CGATTTGATT	420
CGCTTCTATC	ATCAAGATAA	GGGACAAAAA	TCAATGCCAC	TTGAATATAT	TCGAGAATAT	480
GGATATGAAA	TCAAGGCTGG	TGCCTTCCCT	CAAATTCCTT	ATCTCAATGT	TATCAAAGAA	540
CATTTATTAG	GTGGTAAAC	AAGATGA				567

(2) INFORMATION FOR SEQ ID NO:730:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

ACCAGCAGAC	AAAGGAGAAT	AGACATGGCA	GAAACAAATC	AAAACACAGA	TAACTTACTA	60
GACCTTACAA	AAATCACAGA	ACCATTTGAG	CTTGCGAGCG	CTTTGCGCTA	CATGAAAGAA	120
AATGGAGAGT	TCATTCTGTT	CAAGAATGTA	AGCGATGACT	TCTATATGTA	TCGTGACGTT	180
CAAAAACGTC	CTGTGATCGT	AAATGGCCGT	CGCCAATTCA	AGGATGTTGA	AACCGTTTGG	240
CGGTTCAACC	AGTGGGGTGG	TACAATCGCA	ACAATCAACG	TAGCCGTTCT	GTTGAATCAT	300

GAATTCTATA TCATGAAATT TGATGCAGAG GGCAATCCTG ACTGGACGGT TCCAACGGTA	360
GAACCTAAAG AATAG	375

(2) INFORMATION FOR SEQ ID NO:731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GACAAAGAGAC AAGAAAAGAGG ACTTGATGTG AAGATTCGGA TGCGAAATAC GATTCAGTTT	60
GATGAGCAGT TGGAAAGTGAT TGACCAGCTT TATGATGTGG AAGTGCATGA AAAGGGAGAT	120
TATAGCTATT TACTCTTTTA TAATGAGGAA AAGGAAAAAG TAGTTATTAA ATTTTCATGGT	180
CAAGAACTGG TGATGAGCCG ATTTTCTAAT CCAAGACCA TTATGCGCTT TTTAAAGGAT	240
AGTGATAGTT TGGCCTATAT TCCTACCCCT ATGGGCATGC AGGAATTAT CATTCAAACG	300
AGCCGTTATC AAGTTGATAG GCAAAGATT GAGCTAGCTT ATCAACTACA AAATCAAGAG	360
GGGCATCCCT TTGCCAGCTA TCAATTGGAA ATTACTTGGG GCTAG	405

(2) INFORMATION FOR SEQ ID NO:732:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 840 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

CACTGCGGAC	ATGAATTTTC	TGGTGAAATC	ATAGATGTCG	GAAGCGATGT	TACCCGTGTT	60
AAAGTTGGTG	ATCGTGTTGC	TGTGGAACCA	ATTCTAGCTA	AAAATAACTT	AGTTGGTGAT	120
TATAATTTGG	ATCCAAACCT	TAATTTTGTC	GGTTTGGCTG	CAGACGGTGG	ATTTGCCAAA	180
TATTGTGTTT	TAGACGGTGA	CTTAGTACAT	GTCATTCCAG	ATAGCTTGAG	CTATGAGCAA	240
GCTGCTCTTA	CTGAACCCGC	TGCTGTTGCA	GTCTATGCTG	TTCGTCAATC	TTCTTTGAAG	300
GCTGGCGATA	CAGCTGTTGT	CTTTGGTTTA	GGCCCGATTG	GTCTATTAAT	TGTAGAAGCT	360
CTTCGTGCAG	CTGGTGCTTC	TAAGATTTAT	GCTGTTGAAC	TATCACCTGA	ACGTCAAGCA	420
AAAGCTGAAG	AGTTAGGAGC	TATCGTTGTC	CGTCCGGAAG	AAGGTGAAAC	AGCTGTTGAA	480
GCTATTCATC	GTTTAACAAA	CGGTGGTGTA	GATGTTTCTT	ATGAAGTAAC	GGGTGTGCCA	540
GTAGTTTTAG	GACAAGCCTT	AGCTGCCGTA	CATAAAGCAG	GTGAGTGCAT	GGTGGTCTCT	600
ATCTGGGAAC	GAGAAGCAAA	TATTAATCCG	AATGAATTTG	CAATCCAAGA	AAAGACACTA	660
AAAGGAATCA	TCGCTTATCG	TCATATCTTC	CCTAAAGTAT	TAGAATTGAT	GGAACAAGGC	720
TACTTCTCTG	CTGAAAAAAT	AGTTACTAAG	AAAATTAAAT	TGGAAAATAT	CGTCGAAGAA	780
GGCTTTATCG	AATTAACTCA	AGATAAGTCA	CAAATTAAAA	TTTTGGTAGA	ACCAGAATAA	840

(2) INFORMATION FOR SEQ ID NO:733:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GCTATGTTGC	AGGTAGCATT	GTTGATACAG	CAATTGATGA	TTTTACGAAT	CAATGCCGGA	60
AAAATCCTCA	TCAGTGGTTC	TGTGTTTCGTG	TATAGATATA	GTAGTGTTGT	ATTGTATAAG	120
AATTTATATA	ACTTAATGAC	CTATGCAGTG	ATAGAACTA	TTCTTTTGCA	AACGAGTCGC	180
TTATTCTGTT	ATAAGTTTAC	GTGCTCCTAG				210

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 981 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

AAGCTCCTGC	AACAGACTTT	GTTGCAGACT	TGTTTGGAGG	TAGTATTCAT	GACTAATTTA	60
ATTGCAACTT	TTCAGGATCG	TTTTGGTGAT	TGGTTGACAG	CCCTATCTCA	ACATTTGCAG	120
TTGTCACTTT	TGACCTTGTT	ACTAGCTATT	TTGCTTGCGA	TTCCCTTGGC	TGTTTATCTT	180
CGCTATCATG	AGAAGTTGGC	GGATTGGGTC	TTACAGATTG	CAGGGATTTT	CCAGACCATC	240
CCGTCTCTGG	CCTTGTGGG	ACTCTTTATT	CCCTTGATGG	GAAATGGGAC	TTTACCGGCA	300
TTGACAGCTC	TAGTGATTTA	TGCGATTTTT	CCGATTTTAC	AAAATACTAT	TACTGGGCTG	360
AAGGGAATTG	ATCCGAGTCT	TCAAGAGGCT	GGGATTGCCT	TTGGGATGAC	CAGATGGGAG	420
CGTCTCAAGA	AGTTTGAAAT	TCCACTTGCC	ATGCCTGTTA	TCATGTCTGG	AATTCGGACG	480
GCAGCGGTCT	TGATTATCGG	TACGGCTACC	TTGGCGACCT	TGATTGGGGC	AGGGGGACTG	540
GGTTCCTTTA	TCCTGTTGGG	AATTGACCGT	AATAATGCCA	GTTTGATTTT	GATTGGGGCC	600
CTTTCTTCTG	CAGTGCTAGC	TATTGCCTTT	AACCTTCCTAC	TAAAAGTAAT	GGAAAAAGCG	660
AAATTGCGGA	CGATTTTCTC	TGGTTTTGCC	TTGGTGGCTT	TATTACTGGG	TCTGTCTTAT	720
AGTCCAGCCC	TTTTGGCTCA	AAAAGAGAAG	GAAAACCTGA	TTATTGCTGG	GAAAATAGGC	780
CCAGAACCAG	AAATTTTGGC	TAATATGTAT	AAATTGCTGA	TTGAAGAAAA	TACCAGCATG	840
ACTGCGACTG	TTACACCGAA	TTTTGGGACG	ACAAGTTTCC	TTTATGAAGC	TCTGAAAAAA	900
GGTGATATTG	ACATTTATCC	TGAATTTACC	GGTACGGTGA	CTGAAAAGTT	TGCTTCAACC	960
ATCACCCAAG	GTGAGTCATG	A				981

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

TATAATATGC	AAAAGCTAGG	AGGTGGTAGG	ATGATTGAAA	AAATGGAAC	GGGGGAATTT	60
TACAAGGAAT	TACGTTTGGC	GAGAAAGCTT	AAGCAGACAG	ATGTGGCTTG	TGAGGGTCTA	120
ACAGCTTCTC	AGTTGTCCAA	GTTTGAAC	TAAGGAGTCTA	TGCTGTCTGC	GGATAAGTTG	180
ATTCTAGCTA	TCCAAGGTAT	AAATGTGACC	TTTGATGAGT	TTGGGCACAA	GCTCAACAAC	240
TATCAAGAA	TCCACATAT	GCGAATCGGT	CGAAAGGTTG	TGAATCGCTT	TGCCCCATCAG	300
GATATAGCTG	CTTTAGAGCA	GCTATTGGAG	GAAGTCGATC	AAGAACAGAT	GGCGCAGACC	360

TATCGTCGTT TGAATGCCAT CGTGATTAAA GATGCCATCC ATTCACTAAA TAAAAGTTAC	420
CCATTAGCAG AGGGGGATAG CGAGTTTTGA	450

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

AATTGGTCGC ATCGTCAAGA AAGAAAACGA AAGTGTTCATT ATCAAATGAA AAAAATAGCG	60
GTTTTTGCCT CTGGTAATGG CTCAAATTTT CAGGTGATTG CCGAAGAATT TCCAGTGGAG	120
TTTGTCTTTT CAGACCATCG TGATGCCCTAT GTGCTTGAGC GTGCAAAGCA GCTCGGCGTT	180
CTGTCCCTATG CTTTTGAACCT CAAGGAGTTT GAGAGCAAGA CAGACTACGA AGCAGCCCTT	240
GTCGAACTCT TGGAAGAACA CCAGATTGAC TTGGTTTGCC TAGCAGGCTA CATAAAAATC	300
GTTGGACCAA CCTTATTGTC GGCTTATGAA GGTCGGATTG TCAACATTCA TCCAGCCTAC	360
TTGCCAGAAAT TTCCAGGAGC TCATGGGATT GAGGATGCTT GGAATGCTGG CGTGGGTCAG	420
TCTGGTGTGA CCATTCACCTG GGTGGATTCTG GGTGTGGATA CAGGCCAGGT CATCAAACAG	480
GTTCCGCTGC CACGACTAGC TGATGATACC AGTGACAGAT GTGAAGCTCG CATCCATGAA	540
GCAGAGTACA GGTGTATCC GGAAGTAGTG AAGGCTCTAT TTACAGAT	588

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...2838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GGCAAGGCGC	ATGATAAAAT	TGTCATGCAT	GGGGCGCGTG	CCCATAATTT	AAAAAATATT	60
GATGTGGAGA	TTCCGCGAGA	CAAGTTGGTT	GTCGTGACTG	GCTTGTTCAGG	TTCAGGGAAG	120
TCCAGTCTGG	CTTTTGATAC	TCTCTATGCG	GAGGGACAAC	GTCGCTATGT	AGAGAGTTTG	180
TCCGCTTACG	CTCGTCAGTT	CTTGGGAAAT	ATGGAAAAAC	CAGATGTAGA	TGCCATTGAT	240
GGTCTCAGCC	CAGCTATTTT	CATCGACCAG	AAAACGACTA	GTAAAAATCC	TCGCTCGACG	300
GTGGGAACGA	CGACTGAAAT	CAATGACTAT	CTGCGTCTCC	TCTACGCACG	TGTGGGGACG	360
CCTTACTGTA	TCAACGGACA	TGGAGCTATC	AATGCTTCTT	CTGTGGAGCA	AATCGTTGAT	420
AAGGTTTTTG	AGTTACCTGA	ACGCCAGCGC	TTGCAGATCT	TGGCTCCTGT	CATCCGCAAG	480
AAAAAAGGCC	AACATAAGAG	TGTTATCGAG	AAGGTTTCTA	AAGACGGGTA	TGTTCTGTGT	540
CGTGTGGATG	GGGAAGTCTA	TGATGTGACC	GAAAGTGCCAG	AGTTGTCTAA	GAGCAAGCAA	600
CACAAATATCG	ATGTCGTGGT	TGACCGTATT	GTTATCAAGG	AGGGCATTCG	TAGTCGTCTC	660
TTTGATTCCA	TTGAGGCTGC	CCTTCGTATT	GCAGAAAGTT	ATGTCATTAT	CGACACCATG	720
GACGATTCCG	AGTTGCTCTT	CTCTGAGCAT	TATGCCTGTC	CAGTTTGTGG	TTTTACTGTC	780
CCAGAGTTAG	AGCCTCGTCT	CTTCTCTTTC	AATGCTCCTT	TTGGCTCTTG	TAGTGAGTGT	840
GACGGCTTGG	GCAATCAAGCT	GGAGGTGGAT	ACTGATTTGG	TAGTGCCAGA	TGCCAGCAAA	900
ACCTTACGTG	AGGGAGCGCT	AGCACCTTGG	AATCCTATCT	CATCCAACTA	CTATCCAAAC	960
ATGTTAGAGC	AGGCCATGAA	AGTCTTTGGA	GTGGCTATGG	ATAAGCCTTT	TGAGGACCTG	1020
TCAGAAGAAG	ATAAGAACTT	GATTCTCTAT	GGGTCAGATG	GTAAGGAATT	CCATTTCCAC	1080
TATGAGAATG	AATTTGGTGG	CGTGCGCGAT	ATCGACATTC	CGTTTGAGGG	AGTTATCAAT	1140
AATATCAAAC	GTCGTTACCA	TGAAACCAAT	AGCGATTACA	CTCGCACTCA	GATGCGTCTC	1200
TACATGAAATG	AGCTGACCTG	CGGAACCTGT	CAAGGCTATC	GTCTCAATGA	CCAGGCCCTG	1260
TCTGTCCGTG	TGGGCGGCCA	GCAAGGGCCA	CATATTGGAG	AAATCTCAGA	CCTGTCTATC	1320
GCTGACCACT	TGGACTTGGT	GAGCCAGTTA	ACTTTGTCTG	AAAATGAAGC	CATCATTGCT	1380
CGTCCCATTG	TCAAGGAAAT	CAAGGATCGT	TTGACCTTCC	TTAATAATGT	GGGTCTTAAC	1440
TATCTAACCC	TGTCACGTTC	AGCAGGAACC	CTTTCAGGTG	GGGAAAGTCA	GCGCATTCGT	1500
TTGGCAACCC	AGATTGGTTC	CAACCTATCA	GGCGTCCTCT	ATATCCTAGA	CGAGCCGTCA	1560
ATCGGTCTTC	ACCAGAGGGA	CAATGACCGC	CTGATTGCCA	GTCTGAAAAA	GATGCGTGAC	1620
TTGGGCAATA	CTCTTATCGT	GGTGGAAACAC	GACGAAGATA	CCATGCGTGA	AGCTGATTAT	1680
CTGATTGACG	TTGGTCCCTG	TGCCCGTGTG	TTTGGTGGTG	AGATTGTTGC	AGCAGGTACA	1740
CCTAAGCAAG	TGGCTCGCAA	CAGCAAGTCT	ATCACAGGTC	AGTACTTGTC	AGGCAAACGT	1800
GTCATCCCAG	TACCAGAAAG	GCGCCGTGTC	GGAAATGGTC	GTTTTATTGA	AGTGATAGGA	1860
GCGCGTGAGA	ACAACCTTGA	AAATGTCACG	GCTCGCTTTC	CACTAGGAAA	ATTTATCGCA	1920
GTGACAGGTG	TGTCGGGTTT	AGGGAAATCG	ACTCTAATCA	ACAGCATTCCT	CAAAAAAGCC	1980
ATTGCCCAGA	AGCTCAACCG	TAATTCAGAC	AAACCTGGTA	AGTTTAAGAC	TATTACAGGG	2040
ATTGAGCATG	TCGACCGTTT	GATTGATATT	GACCAGAGCC	CTATCGGACG	GACGCCGAGG	2100
TCTAACCAG	CTACCTATAC	AGGAGTTTTT	GACGATATAC	GTGACCTTTT	TGCTCAGACA	2160
AATGAAGCCA	AGATTGAGG	CTACAAGAAG	GGGCGCTTCA	GTTTCAACGT	CAAGGGAGGT	2220
CGCTGTGAAG	CTTGCTCAGG	TGACGGGATT	ATCAAGATTG	AGATGCACTT	CTTGCCAGAT	2280
GTTTATGTGG	CTTGTGAAGT	TTGCCACGGA	ACCCGCTATA	ACAGTGAAAC	CCTAGAAGTT	2340
CACTACAAGG	AAAAGAATAT	TTGCGAGGTC	TTGGATATGA	CGGTCAACGA	TGCGGTAGAA	2400
TTTTTTCCAAC	ACATTCCGAA	AATTCAACGC	AAACTCCAGA	CCATCAAGGA	TGTAGGGCTA	2460
GGCTATGTGA	CCTTGGGACA	GCCAGCTACC	ACCTTTTCTG	GGGGAGAAGC	CCAACGTATG	2520
AAGTTAGCTA	GCGAACTCCA	CAAACGCTCG	ACAGGAAAAAT	CTTCTTACAT	TCTGGATGAG	2580
CCGACGACAG	GGCTTCATAC	AGAGGACATT	GCTCGCCTGC	TCAAGGTTTT	AGCTCGCTTT	2640
GTAGACGATG	GCAATACAGT	CCTCGTCATC	GAGCACAATC	TGGATGTTAT	CAAGACGGCA	2700
GACCATATCA	TTGACTTGGG	ACCTGAGGGC	GGTGTGCGGT	GTGGAACCAT	CATCGTAACA	2760
GGAACTCCAG	AAGAACTAGC	TGCCAACGAA	GCCAGCTATA	CAGGACACTA	TTTGAAAGGA	2820
AAGTTACATC	ATGAATAA					2838

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GAGGGGGCGC	AGGCAGCCAT	GCCAACGGCT	CTGGGCTATG	TCAGTATCGG	CCTGGCCTGT	60
GGGACTATCG	GTGCGCCCTA	TGTGACACCT	GTTGAGATGG	GCTTGATGAG	TCTCTTTGTT	120
TATGCTGGGA	GTGCCAGTT	TGCCATGTTG	GCACTGATTG	TGGTTCAAGC	TCCTGTGGCA	180
GCTATTGCTA	TGACGGTTTT	TCTAATCAAC	TTGCGTCTCT	TTTGTGTTGAG	TTTACACGCA	240
TCGACTTATT	TCCGTCATAC	CAGTCTTTGG	TACAATATCG	GTATGTCTAG	TATCTTGACA	300
GATGAGACCT	ATGGCGTTTT	GATGGGTGAA	TTGGCCCATA	CAGACAAGGT	AAATCCTATG	360
TGGATGCACG	GAAACAATCT	TAACAGCTAT	GTGGCTTGGT	TTGTGGGGAC	AGTAGTCGGA	420
ACGGCTCTGG	GTGGCCTGCT	ACCAAATCCA	GAAATCTTTG	GCTTGGATTT	TGCCCTGGTT	480
GGGATGTTTA	TTGGTATTTT	TGCTTCGCAA	TTTCAGATGA	TGCAAAGACG	GATTCCTGTT	540
CGCAATCTGC	TCATT					555

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1608 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

AATCACCAGC	AGGCCAGAT	GTTACGGGGG	ACTGCTTTGC	TAACGGCTAG	TAACTTTATC	60
AGTCGCCTAC	TCGGGGCTGT	TTACATTATC	CCTTGGTACA	TCTGGATGGG	GGCTTATGCA	120
GCTAAGGCAA	ATGGTCTCTT	TACCATGGGT	TACACTATCT	ATGCTTGGTT	CTTGTGTTGTT	180

TCAACAGCGG	GGATTCCAGT	TGCGGTGGCC	AAGCAAGTTG	CCAAGTATAA	TACCATGCGA	240
GAAGAAGAGC	ATAGCTTTGC	CCTGATTCGG	AGCTTCTTAG	GCTTTATGAC	AGGACTAGGC	300
CTGGTTTTTG	CTTTAGTCTT	GTATGTCCTT	GCTCCTTGGC	TAGCAGACTT	GTCTGGCGTG	360
GGCAAAGACT	TGATCCCAAT	CATGCAAAGC	TTGGCTTGGG	GAGTCTTGAT	TTTCCCGTCT	420
ATGAGTGTTA	TCCGAGGATT	TTTCCAAGGG	ATGAATAACC	TCAAACCCTA	TGCCATGAGC	480
CAAATTGCTG	AGCAGGTCAT	TCGTGTTATC	TGGATGCTCC	TAGCAACCTT	TATCATTTATG	540
AAGCTCGGTT	CAGGAGATTA	TCTAGCAGCC	GTTACCCAAT	CAACCTTTGC	TGCCTTTGTC	600
GGTATGGTAG	CCAGTTTTGC	AGTCTTGATT	TATTTCCCTTG	CCCAAGAAAAG	TTCACTCAAA	660
AGAGTCTTTG	AAACAGGAGA	TAAGATTAAC	AGTAAGCGTC	TCTTGGTTGA	TACCATTAAAG	720
GAAGCCATTC	CTTTTATCCT	GACAGGGTCT	GCCATCCAGA	TCTTCCAGAT	TTTGGATCAG	780
CTGACCTTTA	TCAATAGTAT	GAGCTGGTTT	ACCAACTACA	GCAATGAGGA	CTTGGTTGTC	840
ATGTTTTCTT	ATTTCTCAGC	CAATCCTAAT	AAAAACACGA	TGATTTTGAT	TTCTGTAGGG	900
GTTTCGATTG	GGAGTGTTGG	TTTGCCACTT	TTGACGGAAA	ACTATGTCAA	GGGGGACTTG	960
AAAGCGGCTT	CTCGTCTCGT	TCAGGACAGT	CTCACCTAC	TCTTTATGTT	CTTGCTACCA	1020
GCAACGGTTG	GAGTGTTTAT	GGTAGGAGAA	CCTCTTTATA	CGGTCTTCTA	TGGTAAGCCA	1080
GATAGTTTGG	CTCTGGGCTT	ATTTGTCCTT	GCAGTTTTCG	AGTCTATTAT	TTTAGGCTTG	1140
TACATGGTCT	TGTCTCCAAT	GCTTCAGGCC	ATGTTCCGCA	ACCGCAAGGC	CGTTCTCTAT	1200
TTTATCTATG	GTTCTATTGC	CAAGCTAGTC	TTGCAACTAC	CTACCATCGC	CCTCTTCCAC	1260
AGTTATGGTC	CTTTGATTTT	AACAACCAT	GCTCTCATCA	TTCCCTAACGT	CTTGATGTAT	1320
CGGGATATTT	GTAAAGTAAC	TGGTGTC AAG	CGCAAGGTGA	TTTTGAAGCG	AACCATTTTA	1380
ATCAGTTTGC	TGACCCTAGT	CATGTTTCTG	TTAATAGGAA	CCATCCAGTG	GCTGTTAGGA	1440
TTTTTCTTCC	AACCAAGTGG	ACGTTTGTGG	AGCTTCTTTT	ATGTAGCTCT	TGTCGGTGCC	1500
ATGGGGGGTG	GACTTTATAT	GGTTATGAGT	CTGCGTACCT	ATTTATTAGA	TAAGGTAATA	1560
GGAAAAGCCC	AAGCAGATCG	CCTGCGAGCA	AAATTTAAGC	TTTCGTAA		1608

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

CAAATGCAGC	AAATTACTGA	AATCATCATT	GCTTTTGCGA	CAAGCTTTTT	AACAGTAGCA	60
GTAGGCGGTA	TTGTAAAAGC	AGTAAAAGAT	TATCTTTTGC	GTAAAGGCGG	AGAGAAAGCG	120
GTGATCATCG	CTGAAATTCT	AGCTAAAAAT	GCAGTAAATG	CCGTGGAGCA	GGTAGCTGCT	180
GAAACTGGCT	ACAAGGGAGA	TGAAAAACTG	GCACAGGCTC	GCGCTAAAGT	CCGTGCTGAG	240
CTTACAAAAT	ACAAATATTAG	CATGACTGAC	AAAGACTTAG	ACACCTTCGT	AGAGTCAGCA	300
GTGAAGCAGA	TGAATGACGC	ATGGAAAGGA	CGATAG			336

(2) INFORMATION FOR SEQ ID NO:741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

GCACATAAGC	AAAAATTTTC	GCCTGAAATG	ATGGTTAACA	AGAAGCAAGT	GAAAGTTGGT	60
ATTTCAACCA	TCTACTACTG	GTTTCATAAT	GGTCATTTAG	GATTGACGAA	GGCCGACATG	120
CTTTATCCCA	GAAAAAGGAA	AGGTGTCAAG	AAGCAAGCTA	GTCCGAACTT	TAAGCCGGCA	180
GGTAAATCTA	TCGAAGAACG	TCCTGACGTT	ATTAATTTTC	GCTTGGAAAA	TGGTCATTAT	240
GAAATTGATA	CCGTCCTACT	GACTAAGATA	AAAAATTATT	GCCTGTTAGT	TTTAACCGAC	300
CGGCGGAGCA	GACACCAAAT	TATAAGGTTA	ATTCCAAATA	AAACTGCTGA	ATCTGTCAAT	360
CAGGCGCTTA	CGTTACTATT	AGGGGAGCAT	CGTATTCTGT	CCATTACTGC	AGATAATGGT	420
TCGGAGTTCA	AACGATTGTC	TGAGGTATTT	CCTGAGGAAC	ATATCTACTA	CGCACATGCT	480
TACTCTTCAT	GGGAGAGAGG	TTCAAATGAA	AATCATAATC	GATTAATTCG	GAGATGGTTA	540
CCTAAAGGAA	CCAAGAAAAC	GACTCCGAAA	GAAGTAGCTT	TTATCGAAAA	TTGGATTAAAC	600
AACTACCCTA	AAAAATGCTT	GGACTACAAG	TCGCCAAGTG	AATTTCTTTT	GGGTGGCTAA	660

(2) INFORMATION FOR SEQ ID NO:742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GCACATAAGC	AAAAATTTTC	GCCTGAAATG	ATGGTTAACA	AGAAGCAAGT	GAAAGTTGGT	60
ATTTCAACCA	TCTACTACTG	GTTTCATAAT	GGTCATTTAG	GATTGACGAA	GGCCGACATG	120
CTTTATCCCA	GAAAAAGGAA	AGGTGTCAAG	AAGCAAGCTA	GTCCGAACTT	TAAGCCGGCA	180
GGTAAATCTA	TCGAAGAACG	TCCTGACGTT	ATTAATCTTC	GCTTGGAAAA	TGGTCATTAT	240
GAAATTGATA	CCGTCCCTACT	GACTAAGATA	AAAAATTATT	GCCTGTTAGT	CTTAACCGAC	300
CGGCGGAGCA	GACACCAAAT	TATAAGGTTA	ATTCCAAATA	AAACTGCTGA	ATCTGTCAAT	360
CAGGCGCTTA	CGTTACTATT	AGGGGAGCAT	CGTATTCTGT	CCATTACTGC	AGATAATGGT	420
TCGGAGTTCA	AACGATTGTC	TGAGGTATTT	CCTGAGGAAC	ATATCTACTA	CGCACATGCT	480
TACTCTTCAT	GGGAGAGAGG	TTCAAATGAA	AATCATAATC	GATTAATTTCG	GAGATGGTTA	540
CCTAAAGGAA	CCAAGAAAAC	GACTCCGAAA	GAAGTAGCTT	TTATCGAAAA	TTGGATTAAAC	600
AACTACCCTA	AAAAATGCTT	GGACTACAAG	TCGCCAAGTG	AATTTCTTTT	GGGTGGCTAA	660

(2) INFORMATION FOR SEQ ID NO:743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

TGTCACAAGC	ACAATATGCA	GGTACTGGAC	GTCGTAAAAA	CGCTGTTGCA	CGCGTTCGCC	60
TTGTTCCAGG	AACTGTAAA	ATCACTGTTA	ACAAAAA	GAGTTGAAGA	GTACATCCCA	120
CACGCTGACC	TTCGTCTTGT	CATCAACCAA	CCATTCGCAG	TTACTTCAAC	TGTAGGTTCA	180
TACGACGTTT	TCGTTAACGT	TGTAGGTGGT	GGATACGCTG	GTCAATCAGG	AGCTATCCGT	240
CACGGTATCG	CTCGTGCCCT	TCTTCAAGTA	GACCCAGACT	TCCGCGATTTC	ATTGAAACGC	300
GCAGGACTTC	TTACACGTGA	CTCACGTAAA	GTTGAACGTA	AGAAACCAGG	TCTTAAGAAA	360
GCTCGTAAAG	CATCACAAAT	TAGTAAACGT	TAA			393

(2) INFORMATION FOR SEQ ID NO:744:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

CTGCTAAAGC	AAAAGAAAGC	TGGTTTTAAT	ATAAAATGG	TTGATATCGC	TGGCGCTCAA	60
TTAGCAGACC	GTGTTATTGC	TGAGAAGAAT	AATGCAGTTG	CAGATATGGT	ATTTGGAATT	120
GGTGCTGTTG	ACTCAAATAA	AATTAGAGAT	CAAAAATTAC	TAGTACAGTA	CAAGCCTAAA	180
TGGTTAGATA	AAATTGATCA	ATCTTTATCA	GATAACGAGA	TAATTATTAT	AATCCTGTGA	240

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

ATGAAAAAGC	AAGAAAAATT	AGCTCTTGTC	GAGTCGGCTT	TGGAAGATTT	TTATGGAGAC	60
CAGCAGTTTG	CCTCTAGTTT	ACGGGAGTCT	GTTCTCTATT	CTATTCATGC	TGGTGGCAAG	120
CGTATTCGCG	CTTTTCTCTT	GTTAGAAGTT	CTGGAAGCCT	TGCAGGTTAC	CATCAAACCT	180
GCTCACGCGC	AGGTAGCTAC	TGCCTTGGAG	ATGATTTCATA	CAGGGAGCTT	GATTCACGAT	240
GACCTTCCTG	CTATGGATGA	TGACGATTAT	CGAAGAGGGC	GGTTAACCBA	TCACAAGAAA	300
TTCGGTGAAG	CTATGGCCAT	TTTGGCTGGA	GATGCCTTAT	TCTTAGACTC	ATATGCCTTG	360
ATTGCGCAGG	CAGATTTGCC	AAGTCAGATT	AAGGTGGACT	TGATTGCCAA	CTTATCCCTT	420
GCTTCAGGTA	GTCTGGGTAT	GGTGGCAGGG	CAAGTTTTTG	ATATGGAGGG	CGAACACCAG	480
CACTTGTCCT	TGGAAGAACT	TCAGACTATT	CATGCCAATA	AGACTGGGAA	GTTACTAGCC	540
TATCCCTTCC	AAGCGGCAGC	TATTATAGCT	GAATTGTCAC	CTGAAATGCA	GGTGAAGCTG	600
AAAACGTGTG	GTGAATTGAT	TGGACTTGCT	TTTCAAGTCA	GAGATGATGT	ACTGGATGTG	660
ACAGCTAGTT	TTGAGGAAAT	CGGCAAGACA	CCTCAAAAGG	ATCTGCAGGC	AGAAAAATCA	720
ACCTATCCTG	CCCTGTGGG	CTTGGGAAGAG	TCCATTGCCT	TTTGTAAACCA	AACCCTGGAT	780
CAAGCTAATG	AAAAATTAGA	AGAAATTGCC	CAGCAGATTC	CCTTTGAAAC	AGAATCGATT	840
GTAAGTGTAG	TAGAAAAGTTT	GAGAAATCAAT	GGCTAA			876

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

AGGAGAAAGC	AGATGCTACT	AATCAAAAAT	GGTCGTGTAA	TGGATCCTAA	GTCTGGTTTG	60
GATCAAGTTT	GTGATGTCTT	AGTTCAAGAT	GGGAAAATTA	TCAAAATTGC	GCCTGAGATC	120
ACGGAAGAAG	GAGCAGAAAC	GATTGATGCT	ACTGGTCTTG	TGGTTGCTCC	TGGTTTGGTC	180
GATATTCATG	TGCATTTCCG	TGAACCTGGT	CAAACACATA	AAGAAGACAT	TCATACTGGT	240
GCCCTGGCAG	CCGCTGCAGG	TGGTTTTACT	ACTGTCGTCA	TGATGGCTAA	TACCAGTCCA	300
ACCATTTTCAG	ACGTGGAGAC	TTTGCAAGCA	GTTCTCCAGT	CAGCTGCCAA	AGAGAAGATT	360
AATGTCAAGA	CAGTTGCGAC	CATTACTAAA	AACTTTAATG	GTAAAAACTT	GACTGACTTT	420
AAGGCGCTCT	TAGAAGCTGG	TGCGGTGGT	TTCTCTGATG	ACGGTATTCC	GCTTGAGAGC	480
AGTAAGATTG	TCAAGGAAGC	CATGGAGGAA	GCCAAAAAAC	TCAATACCTT	TATCAGCCTT	540
CATGAGGAAG	ATCCAGGTTT	GAACGGTGTT	CTTGGCTTTA	ATGAAAATAT	TGCTAGAGAA	600
CATTTCCATA	TCTGCGGTGC	TACTGGGGTG	GCTGAGTACG	CTATGATGGC	GCGTGATGTC	660
ATGATTGCCT	ATGCAACTAA	AGCCCATGTT	CACATCCAGC	ATTTGTCTAA	GGAAGAAAGT	720
GTTAAAGTAG	TGGAGTTTGC	TCAGGGGTTA	GGTGCAGAAG	TCACAGCAGA	AGTAGCGCCA	780
CAGCATTTCT	CTAAGACAGA	AGCACTTCTT	TTAACACAAG	GTAGCAATGC	TAAGATGAAT	840
CCACCGCTTC	GTTTGGAATC	AGACCGTCGT	GCCGTTATCG	AAGGTCTCAA	ATCAGGTGTC	900
ATCACAGTTA	TTGCGACTGA	CCACGCGCCT	CATCATGTAG	ATGAAAAAAA	TGTTGAGGAT	960
ATTACCAAAG	CGCCATCTGG	TATGACTGGC	TTAGAAACAT	CCCTGTCTCT	CGGCTTGACC	1020
TATTTAGTAG	AAGCTGGTGA	GTTGAGCTTG	ATGGAATTAC	TTGAAAAAAT	GACATACAAC	1080
CCAGCCAAGC	TTTACAACTT	TGAAGCAGGT	TACTTGGCTG	AGAATGGTCC	AGCAGATATC	1140
ACTATTTTTG	ATGCCAAGGC	TGACCGCCTT	GTGGACTCCC	ATTTTGCCTC	CAAAGCAGCT	1200
AATTCACCAT	TCATCGGTGA	AACCTTAAAA	GGGCAGGTTA	AATATACCAT	CTGTAAGGGA	1260
CAAATCGTCT	ATCAAGCTTG	A				1281

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

AGGAGGAAGC	ACACGATGAC	TGGATCTAAC	AAATTAACAA	AACGTGATTA	TCTTAAAACG	60
TCTTTGCGGG	CATTCTTTTG	TCAAAATGGA	TTTAACTATA	GTAACATATCA	AGGGTTGGGA	120
TATGCCAATG	TGATGTATCC	TGCTTTGAAA	AAACACTATG	GAGAGGATCA	GGAAGGTTTC	180
TACCAAGCCT	TGGAAGAAAA	CTGTGAATTC	TATAATACCA	ACCCACACTT	CCTGCCTTTT	240
ATTACCAGCT	TGCACCTTGT	AATGTTGGAA	AATGGCCGTC	CGGCAAAAGA	AACACGTAGT	300
ATCAAGATGG	CCTTGATGGG	ACCATTGGCA	GGTATTGGGG	ATTCTCTTTC	TCAATTCTGT	360
TTAGCTCCAT	TGTTCTCAAC	CATCGCAGCT	TCGTTTGCTC	AAAAAAGCTT	GGTTGTCGGT	420
CCAATCTTGT	TCTTCCTTGC	GATGAATACC	ATTTTAAACAG	CGATTAAATT	GTCAACTGGT	480
CTGTATGGAT	ACAAACTAGG	AACAACTGTG	ATTGATAAAC	TAAGCGAACA	GATGGCAACG	540
ATTTCTCGTA	TTGCCAATAT	TATCGGTGTA	ACCGTAATTG	CTGGTTTGGC	AGGGACATCT	600
GTTAAGATTA	TGGTGCCGAT	TACCTTTGCT	GCAGGGGAAG	TTAAAGCAGA	CGCTAAACAA	660
AGTATCGTAA	GTATTCAGGG	AATGCTTGAT	AAGGTTGCTC	CAGCTCTTCT	ACCAGCCCTA	720
TTTACACTTT	TAGTTTACTA	CTTGATCAAA	GAAAAGAAAT	GGACAACATA	TAAACTCGTT	780
ATTTTAACAG	TTATCATCGG	AATTATCGGA	AGCTGGCTTA	AGATTATAGC	TTAA	834

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1548 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

AAGGAAGAGC	ACATGGCACA	CGAAAATGTC	ATTGAGATGC	GTGATATTAC	CAAGGTGTTT	60
GGTGGATTTG	TTGCTAACGA	CAAAATCAAC	TTGCACCTAC	GAAAAGGTGA	AATTCATGCA	120
CTTTTAGGAG	AAAATGGGGC	TGGTAAGTCC	ACGCTAATGA	ACATGTTAGC	AGGCCTTCTT	180
GAACCAACTA	GTGGTGAAAT	CGCGGTCAAC	GGTCAAGTTG	TCAATCTCGA	CTCCCCATCT	240
AAAGCAGCTA	GCTTGGGAAT	CGGGATGGTT	CACCAGCACT	TTATGTTGGT	TGAAGCCCTC	300
ACAGTGGCTG	AAAACATCAT	TTTAGGTAAGT	GAATTGACTA	AAAATGGTGT	GCTAGATATC	360
GCTGGAGCTA	GCAAAGAAAT	CAAGGCTCTT	TCTGAACGTT	ATGGCTTAGC	TGTTGACCCT	420
TCTGCCAAGG	TAGCAGATAT	CTCAGTTGGA	GCCCAACAAC	GTGTAGAAAT	TTTAAAAACA	480
CTTTATAGGG	GGGCTGATAT	CCTTATCTTT	GACGAACCAA	CGGCTGTTTT	GACTCCATCA	540

GAAATTGATG	AGTTGATGGC	TATTATGAAA	AATCTTGTCA	AAGAAGGAAA	ATCAATTATC	600
TTGATTACCC	ACAAATTGGA	TGAAATTCGC	GCAGTTTCTG	ACCGTGTTAC	AGTTATCCGT	660
CGTGGGAAAT	CAATTGAAAC	CGTTGAAATT	GCAGGGGCTA	CCAATGCTGA	TTTGGCGGAA	720
ATGATGGTAG	GACGTTCTGT	TTCCTTTAAA	ACAGAGAAGC	AAGCCTCTAA	ACCAAAAGAA	780
GTGGTTTTGT	CTATCAAAGA	TTTGGTGGTG	AATGAAAACC	GTGGTGTTCC	AGCTGTTAAA	840
AATCTGTCC	TGGATGTTTC	TGCTGGAGAG	ATTGTTGGTA	TTGCGGGGAT	TGATGGAAAT	900
GGTCAGTCTG	AACTGATTCA	AGCCATTACA	GGTCTTCGTA	AGGTTGAATC	TGGTAGCATT	960
GAGCTAAAAG	GAGATTCAAT	TGTAGGCTTG	CACCCACGTC	AGATTACAGA	ACTAAGTGTT	1020
GGGCACGTTT	CAGAAGACCG	TCACCGTGAT	GGCTTGATTT	TGGAAATGAT	GATATCTGAA	1080
AATATTGCC	TTCAAACCTA	CTATAAAGAA	CCACATAGTA	AAAATGGAAT	TTTGAATTAT	1140
TCAAATATTA	CTTCTTATGC	TAAAAAGCTG	ATGGAAGAGT	TTGATGTTCG	CGCTGCCAGT	1200
GAATTAGTTC	CTGCAGCTGC	ACTCTCAGGA	GGAAATCAAC	AAAAAGCAAT	TATTGCTCGT	1260
GAAATTGATC	GAGATCCTGA	TCTCCTTATC	GTTAGTCAGC	CAACTCGTGG	GTTGGATGTC	1320
GGTGCCATTG	AGTATATCCA	CAAACGCTTG	ATTGAAGAGC	GTGATAATGG	CAAGGCTGTC	1380
CTTGTGTGTC	GCTTTGAATT	GGATGAGATT	TTAAACGTCT	CAGACCGTAT	TGCCGTTATC	1440
CACGATGGTA	AGATTCAAGG	TATTGTATCA	CCAGAAACAA	CCAATAAACA	AGGACTTGGT	1500
GTCTTGATGG	CTGGTGAAAA	CTTGGGAAAG	GAGAAGAGTG	ATGTCTAA		1548

(2) INFORMATION FOR SEQ ID NO:749:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...348
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

CTGGAATGGC	ATTTGAAAAA	GCTCTTGTTG	TGGGGGTTCT	TCCCTTTATC	ATTCCAGACC	60
TTGGCAAAC	TCTGGCTATT	AGTTTTATTA	GCCGTCCCCT	ACTTCAACGC	CTTAAAAATC	120
AGACTTACTT	TACTAACTAA	AAAAGGATAC	CGAGTTATCA	TGACTCAATA	TCCTTTTTTTT	180
TATTTTGAAA	ACTTATACTC	AATGAAAATC	AAAGAGCAAA	CTAGGAAGCT	AGCCGCAGGC	240
TGCTCAAAAC	ACTGTTTTGA	GGTTGTAGAT	GAAACTGACG	AAGTCAGTAA	CCATACATAC	300
GGCAAGGCAA	AGCTGATGCG	GTTTGAAGAG	ATTTTCGAAG	AGTATTAG		348

(2) INFORMATION FOR SEQ ID NO:750:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1434
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

AGTGGATGGC	AAGCTTGCAG	CCAGTGGTAC	CCTTACTTTT	GCAATTGGGA	ACTAAGGAGG	60
TTCTCCATGT	TTCGAAAAAT	TTTAATTGCC	AATCGTGGTG	AAAT'GCGGT	TCGTATTATC	120
CGTGCGGCAC	GTGAATTGGG	GATTGCGACG	GTAGCGGTTT	ATTCAACTGC	TGATAAGGAA	180
GCTCTTCATA	CGCTGTTGGC	AGATGAAGCA	GTTTGTATTG	GTCTTGGCAA	GGCAACAGAG	240
TCTTATCTCA	ATATTAATGC	AGTTCATATCA	GCTGCAGTCT	TGACTGAGGC	AGAAGCTATT	300
CACCC'GGTT	TTGGATTTCT	CAGTGAAAAAT	TCCAAATTTG	CGACCATGTG	TGAAGAAATA	360
GGTATCAAGT	TTATCGGTCC	ATCTGGTTCAT	GTTATGGATA	TGATGGGGGA	TAAAATCAAT	420
GCGCGTGCTC	AGATGATTAA	AGCAGGTGTG	CCTGTTATAC	CAGGTT'GAGA	TGGAGAAGTG	480
CATAACTCTG	AAGAAGCTTT	GATTGTTGCT	GAAAAAATTG	GCTATCCTGT	TATGCTCAAG	540
GCTTCAGCAG	GTGGAGGTGG	TAAAGGGATT	CGTAAGGTTG	AAAAACCAGA	TGACCTCGTT	600
TCTGCCTTTG	AAACTGCCTC	TAGTGAGGCC	AAGGCCAATT	ATGGCAATGG	TGCCATGTAC	660
ATAGAACGGG	TTATCTATCC	AGCTCGGCAC	ATTGAGGTTT	AAATCCTAGG	TGATGAGCAT	720
GGACATGTGA	TTCACTTGGG	TGAACGGGAT	TGTTCTCTTC	AAAGGAATAA	CCAAAAGGTT	780
TTGGAAGAAA	GTCCCTCGAT	TGCAATCGGA	AAAACGCTGC	GTCATGAAAT	AGGTGCTGCT	840
GCTGTT'CGAG	CGGCAGAGTT	TGTTGGCTAT	GAGAATGCAG	GAACCATTGA	ATTTCTTCTT	900
GATGAAGCAA	GTAGCAATTT	CTATTTTCATG	GAGATGAATA	CTCGTGTTC	GGTAGAACAT	960
CCAGTAACAG	AGTTTGTTTC	AGGTGTTGAT	ATCGTTAAGG	AACAGATTTG	CATTGCGGCA	1020
GGTCAGCCTT	TGTCGTGTTAA	GCAAGAAGAT	ATTGTCCTAC	GCGGT'CATGC	CATCGAGTGT	1080
CGTATCAATG	CAGAAAACCC	AGCCTTTAAC	TTTGCTCCAA	GTCCAGGTAA	GATTACTAAT	1140
CTCTATCTGC	CAAGTGGTGG	AGTTGGCTTG	CGCGTGGATT	CAGCAGTTTA	TCCAGGTTAT	1200
ACCATTC'CGC	CTTATTATGA	TAGTATGATT	GCCAAAATCA	TAGTACACGG	CGAAAATCGT	1260
TTTGACGCCT	TGATGAAAAT	GCAACGTGCC	CTCTATGAAT	TAGAAATTGA	AGGAGTGCAG	1320
ACCAATGCAG	ATTTCCAGCT	TGACCTCATT	TCAGATCGCA	ATGTCATTGC	TGGGGATTAT	1380
GATACTTGCT	TCTTGATGGA	AACCTTCTTA	CCTAAATATC	AAGAAAAAGA	ATAA	1434

(2) INFORMATION FOR SEQ ID NO:751:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

```
TTGAGGTGGC ACCGCGAATT TCGTCCTCAC GCAAGTTATT TTGCGTGGGG ATTTTTCATA      60
CAGTCGCTAC GAACTAGAAT TAGAACTGAA AGGGAAATTA CAATGGAACG AATCATTCAT      120
GGAGATGTCT TATCACCAAT CTTGGCTTAT ATGCGCTTAA AGGGGCAACA CAAGGTTATC      180
TTAGAGAGTA TTCCGAGAGA CAAGGAAACA GCTCGTTTTT CTATCCTAGC CTATAATCCT      240
GTTTTTGAGA TTAAGTTTGA AAATGGAGTT CTTTATCAAA ATGGTCAAGT GATTGATCGG      300
GATCCCTTGG ATTTCCCTTA TGAAGTGATT CATAAGAGTC AGCACCATTC AGAGCTACCT      360
TTTGGTGGTG GAGCCATTGG TTTTGTGGGT TACGATATGA TTTGCTTTTA TGAAGAAATT      420
GGTCAAATCC CTGAGGATAC AATTGGGACG CCAGACATGC ATTTCTTTGT CTATGAGAGC      480
TATATAGTCT TTGACCACAA GAAGGAGAAG ATACATGTCA TAGAGGATGC ACTTTATAGT      540
GAGCGCAGTC AAGAGGCCCTT GGA AAAATCC TTGAACCAAG TGCTTGAGGA ATTACGCATT      600
CCTGCTCCAA ATGAATTTGA AGACTTGGAT TTATCACCAC TTGACTTCAA ACCGCATATC      660
GCTCCACATA AGTTTGAGGG AATGGTAGAA ACAGCTCGTG ACTTGATTCG TAACGGCGAT      720
ATGTTCCAAT GTGTACTCAG CCAGCGTTTC TCAGCAGAAG TTA CTGGAAA TCCATTTGAC      780
TTCTACAGAA ATCTCCGCGT AACTAATCCT TCTAATTACC TTTATTTCTA TGATTTTGGG      840
GATTATCAAA TCATCGGAGC TAGTCCAGAA AGTTTGGTTT CTGTCAAAAA TGGCATCGTG      900
ACAACCAATC CGATTGCAGG GACGCGACCA AGAGGGGCTA CGGATGAAGA AGACAAGGCC      960
TTGGCGACTG ACCTCCTCTC TGATGAGAAG GAAACAGCAG AACATCGAAT GTTGGTAGAC     1020
TTGGGGCGTA ACGATATTGG CCGCATCTCT GAAACGGCCA GTGTCCAAGT TACTAAGTAT     1080
ATGGAGGTGG AGCTCTTCCG CTACGTCATG CATTTGACCA GTGTGGTCAA GGGACGTTTG     1140
CTTGACAGAA TCACTGCCAT GGATGCCCTG AAAGCAACGC TTCCTGCTGG AACCCTTTCT     1200
GGAGCGCCAA AGATTGAGC GATGAGACGT ATCTATGAAC TGGAAACGGA AAAACGGGGA     1260
GTATACGCTG GGGCAATCGG CTACTTGTCT GCGACGGGTG ATATGGATTT GGCCATCGCC     1320
ATCCGAACCA TGATTCTCAA AAATCAAAGA GCCTATGTGC AGGCTGGGGC AGGGATTGTC     1380
TACGACTCTA TCGCCCAAAA CGAATACCAA GAAACCATTA ACAAAGCAAA ATCTATGACT     1440
AGAATTGGAG AACTAAGACC ATGA                                             1464
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(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

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CAAGGGTGGC AGGTCATGTT TTTGAAGCAG AGTAGACTGA AACCTTATCC AATGCGACGG      60
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TTTGAAAAGA	CTGTCACTGA	GGAAGGTGTC	GCGAAAGAAG	GGTATGCCAA	GGAAGCTGAG	120
ACAGTCCGCC	TTGAATTGTG	GCCAGCTAGT	AGCAAGCTAC	AATCTGAATT	GTATGGCGAG	180
CGTGTCAATG	ATATTTTGAA	CGCAAATGCC	AACAAGTCAG	CTACTATCAA	AGTAAAAGAT	240
GGTGTGTGTA	TCGATAGTCA	GACGGAAGTG	ACTCATAGGG	TTATTTCTAA	AAAGGTCTAC	300
ACACATCATC	AAGTTTTTGA	GTTAGAGCGT	GTCAGGGGCTA	CTAGGGGCAG	ATAG	354

(2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

AAAAGCAGGC	ATCGTATAAT	GCCTACTTTT	TCTTCAAATG	CTCCCTTTAA	TCCAATCCG	60
ATCTCTAAGA	TATTAGTCGT	ATTTATCACA	GGCTTAACTG	TTATGCATAG	CATAAACATC	120
CGTTTTGAGC	TGGCAATTGT	TTGTCTTATT	GGTATTTTGC	TTTATTTGAA	TGGATACAAA	180
AAAACACTTT	TCAAATGGAT	TATATTGTGT	GGGATACTTT	ACTCCTTGCC	TAATTTTATG	240
GTGTTATCTG	AATTAAACCC	TATAGTTAAG	ATGTTTTTGA	GTATACCTAT	TGTTATTAGA	300
ATGTTTATTT	TACCATTTAT	GGCAGCAAGC	TTTATGATAA	AGACCTCGGA	TGTAGGCGCA	360
ATAATTTTCAT	CGATGGATAA	GCTTAAGATT	TCAAAGAATG	TATCCATACC	TATTGCGGTT	420
ATGTTTAGAT	TCTTCCCATC	TTTTAAGGAG	GAGAAGAAAA	ACATCAAAAT	GGCTATGAGA	480
GTAAGAGGGA	TAAATTTTAA	AAACCCAGTC	AAATATCTTG	AATATGTTTC	TGTGCCACTA	540
CTCATTATAT	CATCTAATAT	ATCAGATGAC	ATTGCAAAAG	CGGCAGAAAC	AAAGGCAATA	600
GAAAATCCAA	TTGCCAAGAC	CAGATACATT	CGCGTAAAGA	TACAGCTAAT	TGATTTTGTG	660
TATGTTTTAG	CGGTTGCTGG	ACTTATTGTG	GGAGGCTTAA	TATGGTTGAA	ATAA	714

(2) INFORMATION FOR SEQ ID NO:754:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GAAAGGAGGC	AAATAATGTC	TACAATCGAT	AAAGAAAAAT	TTCAGTTTGT	AAAACGTGAC	60
GATTTTGCCT	CTGAAACTAT	TGATGCGCCA	GCATATTCTT	ACTGGAAATC	AGTGTTTAAA	120
CAATTTATGA	AGAAAAAATC	AACTGTAGTC	ATGTTGGGAA	TCTTGGTAGC	CATCATTTTG	180
ATAAGTTTCA	TCTACCCAAT	GTTTTCTAAG	TTTGATTTCA	ATGATGTCAG	CAAGGTAAAC	240
GACTTTAGTG	TTCGTTATAT	CAAGCCAAAT	GCGGAGCATT	GGTTCGGTAC	TGACAGTAAC	300
GGTAAATCGC	TCTTTGACGG	TGTCTGGTTC	GGAGCTCGTA	ACTCCATCCT	CATTTCTGTG	360
ATTGCGACAG	TGATTAACCT	GGTATCGGT	GTTTTTGTCT	GTGGTATTTG	GGGTATTTCA	420
AAATCAGTTG	ACCGTGTCAT	GATGGAAGTT	TACAACGTCA	TCTCAAACAT	CCCACCTCTT	480
TTGATTGTTA	TTGTCTTGAC	TTACTCAATC	GGAGCTGGAT	TCTGGAATCT	GATTTTTGCC	540
ATGAGCGTAA	CAACATGGAT	TGGTATTGCC	TTCATGATCC	GTGTGCAAAT	CTTGCGCTAT	600
CGTGACTTGG	AATACAACTT	GGCGTCACGT	ACTTTGGGAA	CACCAACCTT	GAAGATTGTT	660
GCCAAAAATA	TCATGCCTCA	ATTGGTATCT	GTTATTGTGA	CAACCATGAC	TCAAATGCTT	720
CCAAGCTTTA	TCTCATACGA	AGCCTTCTTG	TCTTTCTTCG	GTCTTGGAAT	ACCGATTACA	780
GTGCCAAGTT	TGGGTCGTTT	GATTTCTGGAT	TATTCACAAA	ACGTAACAAC	CAATGCCTTAC	840
TTGTTCTGGA	TTCCATTGAC	AACCCTTGTC	TTGGTATCCT	TGTCCCTTTT	CGTAGTTGGT	900
CAAAACTTAG	CGGATGCTAG	TGATCCACGT	ACACATAGAT	AG		942

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAGACTGGGC	AAAGAGTCGT	TAAAAGCAAA	AACGCATACT	ATCAGGTATT	GAAAAAAGTT	60
GATACTATGC	GTTTTATTGT	GGGAAGATTT	ACTTCCTTTT	CTACTGAAAT	TGAGTC'TTTT	120
CCCAGATCT	TTTTATACTC	AATGAAAAATC	AAAGTGCAAA	CTAGGAAGCT	AGCCGCAGGT	180
TGCTCAAAAC	ACTGTTTTGA	GGTTGTGGAT	AGAAGTGACG	AAGTCAGCTC	AAAACATGGT	240
TTTGAGGTTG	TAGATGAAAC	TGACGAAGTC	AGCTCAAAAC	ATGGT'TTTGA	GGTTGCAGAT	300
GAAACTGACG	AAGTCAGCTC	AAAACATGGT	TTTGAGGTTG	CAGATAGAAC	TGACGAAGTC	360
AGTAACATAT	ATACGGTAAG	GCGACGCTGA				390

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

AATAAGGGGC	AAAGCCCTAA	TAAATTGGAG	GATCTAATGA	AAAAATTAGG	TACATTACTC	60
GTTCTCTTTC	TTTCTGCAAT	CATTCTTGTA	GCATGTGCTA	GCGGAAAAAA	AGCAACAACCT	120
TCTGGTCAAA	AACTAAAAGT	TGTTGCTACA	AACTCAATCA	TCGCTGATAT	TACTAAAAAT	180
ATTGCTGGTG	ACAAAATTGA	CCTTCATAGT	ATCGTTCCGA	TTGGGCAAGA	CCCACACGAA	240
TACGAACCAC	TTCTGAAGA	CGTTAAGAAA	ACTTCTGAGG	CTGATTTGAT	TTTCTATAAC	300
GGTATCAACC	TTGAAACAGG	TGGCAATGCT	TGGTTTACAA	AATTGGTAGA	AAATGCCAAG	360
AAAACTGAAA	ACAAAGACTA	CTTCGCAGTC	AGCGACGGCG	TTGATGTTAT	CTACCTTGAA	420
GGTCAAAATG	AAAAAGGAAA	AGAAGACCCA	CACGCTTGGC	TTAACCTTGA	AAACGGTATT	480
ATTTTGTGTA	AAAATATCGC	CAAACAATTG	AGCGCCAAAG	ACCCTAACAA	TAAAGAATTC	540
TATGAAAAAA	ATCTCAAAGA	ATATACTGAT	AAGTTAGACA	AACTTGATAA	AGAAAGTAAG	600
GATAAAATTA	ATAAGATCCC	TGCTGAAAAG	AAACTCATTG	TAACCAGCGA	AGGAGCATTC	660
AAATACTTCT	CTAAAGCCCTA	TGGTGTTCCA	AGTGCCTACA	TCTGGGAAAT	CAATACTGAA	720
GAAGAAGGAA	CTCCTGAACA	AATCAAGACC	TTGGTTGAAA	AACTTCGCCA	AACAAAAGTT	780
CCATCACTCT	TTGTAGAATC	AAGTGTGGAT	GACCGTCCAA	TGAAAACTGT	TTCTCAAGAC	840
ACAAACATCC	CAATCTACGC	ACAAATCTTT	ACTGACTCTA	TCGCAGAACA	AGGTAAAGAA	900
GGCGACAGCT	ACTACAGCAT	GATGAAATAC	AACCTTGACA	AGATTGCTGA	AGGATTGGCA	960
AAATAA						966

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

ATGGCTTTTA	ACCCATTGT	TAAATATTCT	TTGGCTTTGG	TCTATGATTT	GAGGAAAAAC	60
CTTAAAGGAT	TAACAGTATT	GAGTTTATTG	ATTACAGGTC	TCTTTTCTT	GACCAAGTAT	120
CCACTGGAAA	ATGAAATCAC	CATGCTGGAT	GTGGGGCAAG	GAGAAAGTAT	TTTCCTACGG	180
GATGTAAGT	GGAAAACCAT	TCTCATAGAT	GTAGGTGGTA	AGGCAGAATC	TTATAAGAAA	240
ATCGAAAAAT	GGCAAGAAAA	GATGACGACC	AGCAATGCCC	AGCGAACCTT	GATTCCCTAT	300
CTCAAAAGTC	GAGGAGTAGC	TAAGATTGAC	CAGCTAATTT	TGACTAACAC	GGACAAGGAG	360
CATGTTGGAG	ATTTGTCAGA	GGTGACCAAG	GCTTTCCATG	TAGGGGAGAT	TTTAGTATCA	420
AAAGGCAGTT	TGAAGCAGAA	GCAATTTGTG	GTAGAACTAC	AGGCGACTAA	AACAAAGGTG	480
CGTAGTATGA	CAGTAGGGGA	GAACCTGCCC	ATTTTGGAA	GTCAGTTAGA	AGTTCTATCT	540
CCAAGGAAAA	TGGGAGATGG	AGGACACGAT	GATACCCTAG	TTCTGTATGG	GAAATTCCTG	600
GATAAGCAAT	TTCTCTTCAC	GGGAAATTTG	GAGGAGAAAAG	GAGAGAAGGA	CTTGCTGAAG	660
CACTATCCAG	ACTTGAAAGT	TTATGTTTTG	AAAGCTAGCC	AACATGGCAA	TAAAAAATCA	720
TCAAGCCAG	CCTTTNTATA	A				741

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 903 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

AATGACTTTA	AGAGTTTAAA	CCGAAAAGGG	GAATCAATGG	CTCTATTTAG	TAAAAAAGAT	60
AAGTATATTC	GAATCAATCC	CAATCGTTCG	GTTAGGGAAA	AACCTCAAGC	TAAGCCAGAG	120
GTTCCAGATG	AATTATTTTC	CCAGTGTCCA	GGCTGTAAGC	ATACCATCTA	TCAGAAGGAT	180
CTGGGAAGTG	AACGTATCTG	TCCGCACTGT	AGCTATACCT	TTCGTATTTT	TGCCCAAGAA	240
CGCTTGGCTT	TGACGATTGA	TATGGGAACC	TTCAAAGAAT	TGTTTACAGG	GATTGAAAGC	300
AAGGATCCCT	TGCATTTCCT	TGGTTACCAA	AAGAACTGG	CATCTATGCG	TGAAAAACA	360
GGTCTGCATG	AAGCCGTTGT	GACAGGAAC	GCTCTTATTA	AAGGTCAGAC	TGTGGCTCTT	420
GGGATTATGG	ATTCTAACTT	TATCATGGCT	TCTATGGGTA	CGGTTGTAGG	TGAAAAATC	480
ACTCGTTTGT	TTGAGTATGC	GACTGTCGAA	AAATTGCCAG	TTGTCCTATT	CACAGCCTCT	540
GGTGGAGCCC	GTATGCAGGA	AGGAATCATG	AGTCTCATGC	AGATGGCTAA	GATCTCTGCG	600
GCGGTTAAAC	GCCATTCAAA	TGCTGGTCTC	TTTTACCTGA	CCATTTTGAC	AGATCCAACG	660
ACTGGTGGTG	TGACAGCTTC	TTTCGCTATG	GAAGGCGATA	TCATTCTGGC	TGAACCACAG	720
AGCTTGGTTG	GTTTTGCTGG	ACGTCGTGTG	ATTGAAAATA	CGGTTCTGTA	AAGCTTGCCT	780

GAGGATTTCC AAAAGGCAGA ATTCCTATTA GAACATGGCT TTGTGGATGC TATTGTCAAA	840
AGAAGAGACT TACCAGATAC GATTGCTAGC CTAGTCAGAT TGCATGGAGG GAGTCCTAGA	900
TGA	903

(2) INFORMATION FOR SEQ ID NO:759:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

GATGGCTTTA AATTTGCGTG GAAGATGGAT ATTCTCACAA GTCTTCAAGA GTCGGAGAGC	60
CTGATTTCTGA TTCAGAATTG GCATAATTCC TGCATGAATG GGAACATCAA TCCCAGCCAA	120
GATGCACTTG TCCTGAAAAT CATAGAAGCG CTCATTGTCA AAGAAGAGCT GAGTTACGAG	180
GCTCGAACAG CCTGCATCCA CTTTCTTCTT AAGATTTTGA ATATCTGA	228

(2) INFORMATION FOR SEQ ID NO:760:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

ATAATGTTTA AACGAATTCG AAGAGTGCTT GTACTAGCAG TCTTCCTTTT TGCTGGCTAT	60
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AAAGCTTACC	GCGTTCATCA	AGATGTCAAA	CAAGTCATGA	CCTATCAACC	CATGGTGCGA	120
GAAATCTTGA	GTGAAAAAGA	CACCCAGCA	AACGAAGAGC	TTGTGCTTGC	TATGATTTAT	180
ACTGAAACAA	AAGGAAAAGA	AGGCGATGTT	ATGCAGTCTA	GTGAGTCTGC	AAGTGGTTCC	240
ACCAACACCA	TCAATGATAA	TGCCTCTAGC	ATTCGGCAAG	GCATTCAAAC	TCTGACAGGC	300
AATCTCTATC	TGGCGCAGAA	GAAGGGGGTA	GATATCTGGA	CAGCTGTTCA	AGCCTATAAT	360
TTTGGACCTG	CCTATATCGA	TTTTATCGCC	CAAAATGGCA	AGGAAAATAC	CTTGGCTCTA	420
GCCAAACAGT	ACTCTCGTGA	GACTGTTGCC	CCCTTGCTTG	GTAATACGAC	TGGAAAGACT	480
TATAGTTATA	TTCACCCCAT	TTCCATTTTT	CACGGTGCTG	AACTCTATGT	AAATGGAGGA	540
AATTATTATT	ATTCTAGACA	GGTACGACTT	AACCTTTACA	TCATCAAATG	TTTCACTCTC	600
TTTTCAACAT	CTGGCTAG					618

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

CAGAATTTCC	TTACATGGTC	AATAAAACCA	ATGTGCATGA	GCATATTGTT	CGCTTGGTTC	60
AGGAAAAACG	CATTGAGGGT	ATCACAGCAG	TACGTGATGA	GTCAAACCGT	GAAGGTGTTC	120
GATTTGTTAT	TGAAGTCAAG	CGCGACGCCT	CAGCCAATGT	TATTCTCATA	TAACCTCTTC	180
AAAATGACCC	AAATGCAAAC	CAATTTTGGT	TTCAATATGC	TCGCTATCCA	AAATGGTATA	240
CCGAAATTT	TGTCTCTTCG	TCAGATTTTG	GATGCTTATA	TCGAGCACCA	AAAAGAATGG	300
TTGTTCTGTCG	TACACGTTTT	GATAAGGAAA	AAGCGGAAGC	GCGCGTCAT	ATCTTAG	357

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

AGAGATTTCC	TCAGCAATCT	TCTGAAAGGA	TTTAGTCTAG	GCCTGGCACT	TTTTCTTCTG	60
ACCTTGTTAG	GTTTAGTGGT	CTTAGGTCAA	TATCGTTTGG	AATCCATTCA	CTTGAATCCT	120
TATTCTCTTG	CCTTTGTCGT	CTTTACTATC	CCATTTTGGA	TTTTACAGGG	GACAGCAGAA	180
GAAGTGGTGG	CCCGTGCTTG	GCTACTTCCT	CAATTGGCCT	CAAGAACCAA	TCTAAACTA	240
GCTATTCTTA	TATCTAGCCT	GTTCTTTACC	CTGCTTCATA	TGGGCAATTC	TGGCCTCACC	300
CCTCTATCTC	TAGTAAATCT	CTTTTTATTC	GGAGTTGCCA	TGGCTCTTTA	CCTTCTCAAA	360
ACTGATACAG	TTTGGGGTGT	TGCAGGTATT	CATGGTGCCT	GGAATTTTGC	TCAGGGTAAT	420
CTCTTTGGGA	TTTGTAGTTAG	TGGTCAACCG	TCAGGAACGT	CTCTGATGAC	CTTTTTACCA	480
CAAGGCAATC	AAGATTGGCT	ATCAGGTGGT	TCTTTTGGCA	TAGAAGGTTT	CATTATGACA	540
AGTCTGGTAT	TACTACTGCT	GATTGTCTAT	CTTGCTAATA	AATTAAAGAA	AGAAAATGAA	600
AGGATGTGA						609

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

ATGAATATTA	AAATTATAAG	GAGGACGAAG	GTGGTTAAAA	ATTTAAAATT	AAAATTAGCT	60
CGGGTAGAGC	TTGATTTAAC	TCAAGGTCAA	CTAGCAGATG	CTGTCGGGGT	GACGCGCCAG	120
ACTATTGGTT	TGATAGAGGC	GGGGAAATAC	AATCCAGTC	TCTCGCTCTG	CCAGTCCATT	180
TGCAGATGTT	TAGGGAAAAC	CCTAGACCAA	CTATTTTGGG	AGGAAGAAGA	TGAAAAATAG	240

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

TCGATTTGTT	TACATCTTAT	TTCAATCTAC	TATATTATCT	CAATAAATGA	TGATGGCGAC	60
TGTTTTGTTT	GTGCTTGTCT	ATTTTTGAAT	CCTGATCGAG	CGGAAGAATA	TTTCTGCCGA	120
GGTTGCCAAG	GGGAAAATCC	TGAAGATATT	GAATTTTATG	ATGAACAATT	ACAGGCAGAA	180
AAGGTGGAGG	TTTTGAATAT	TCGATTGGAA	GTAAAAAATT	GA		222

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1641 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

AGGAGTATTA	AAATGAAAAA	AATTGTTAAA	TTAGCTTTAA	CAGCTGCAGC	AGTTTTTAATA	60
GCTGTAGTAG	GATTGGTTGC	TTGTAGTTCG	GGAAGCAAAA	AATCTGATTT	TTCAGAGTCT	120
GGAAAAAGAAA	AAGTATTCTA	TTTATCAGGT	TTGCTTCAAG	GAACTGGAGA	TCGTATCCCT	180
TACGTTTGGC	AAAATGGTGA	TGGTTTAGTT	CCATATTTGT	TATACCGTAC	ACTGTTAATG	240
GCAGATTCAA	AATATGAAAA	ATCAACTCCA	GATTTAGCTA	AAGATTGGAA	AAAATCTGAT	300
GATGAAAAAA	CTTATGAATT	TACACTTAAA	GATGGATTGA	AATGGTCTGA	TGGAGAAGCT	360
TTGACAGCTT	CCGATGTGGA	ATTCAGTGTT	AAATTAGCAT	TGAAAGCTTC	AGTAATTAAT	420
GGAATTTTCC	CTTCAACATT	CACAAAAATT	GAAGGAGCTA	AAGATTTCAA	AGACGATAAA	480
GCAGATAAAA	TTTCTGGTCT	TACAGTTGAT	GGAAATAAAG	TAACATTTAA	ACTTACTGCT	540
CCAGTTGGTG	ACTTTGAGCA	AATGATGACT	CAATTCTTTA	TTCTTCCAAA	ACATAAATTA	600
GAGTCTGAAA	ATCCTCTTGA	ATTAAATAAT	AGCTCATTTT	GGACAGCTCC	TGTTACAAGC	660
GGTATGTACA	AAGTAAAAAG	AATTAGTGCA	GGTAATTTCT	TAGAGTATGA	CAAAAAATGAA	720
AACTATGAAA	ATGAAAAACC	AAAATTTGAT	AAAGTAGTAT	TCAACTATAT	TTCAGATCCA	780
GTTTTAGCAT	TGCAAGATGG	TAAATCATAC	TTCTATTCAA	CAAACAAACC	TCAAGAAATT	840
AGTCAGTTGG	ATGCTGTATC	TACTTTAACT	AAAAAACCAA	TTGATATCCT	ATTCTATCGC	900
TACTTTATCG	CTAACTTAGC	AGGTGTCGAA	GGTAATGGAG	ATTCCTTGAT	TGCTAATCCT	960

AAAGTTAGAG	AAGCTATTCT	ATATGCAATT	AATCGTGATG	AATTAGCTAA	ATCTGTATTT	1020
AGTGGAATTG	CAGATGTTAA	TAATACTGGT	GTTCCTTCAA	GCTTAGAAGC	TCATCTGAAA	1080
TCAGCAAATA	AATTTGAATA	TAATCCAGAA	AAAGCAAAAC	AACTTCTTAA	AGAAGCTAAA	1140
TACGATAATA	GCAGAAATCT	AATTTTAGCT	TATTACTATA	AAGATCAAGC	CTCTCAAGAT	1200
TTCATGCAAG	CAGTAAGTTA	TCAATTGAAT	GAGGTTGGAA	TCAAGAACGA	AGTTGTCCAA	1260
ATTACTTCTG	ATGCAACAAC	AGGATTGTTT	AAAACACGTA	AATATGACCT	AGCTTATAAA	1320
GGATTATCAT	CATTTGGTTA	TGAAACTTGG	TATGGTGAAT	ATAGTTCAAC	AAATACTAAC	1380
TTTAAAAATA	TTACAAATGG	CGAAACAAGT	TTTGATGAGT	TGAGCAAAAA	ATTGTCTGAA	1440
ACTTCTGATG	TAAAAGAAA	AAACAAAATT	TTAGCAAGTC	TACAAAAATT	AGAACAAGAA	1500
AAACTATTGA	AGTTAAACTT	ATTCACATTT	AAAAACTTCT	TGTATTTAAA	TACTGAAAAA	1560
GTTTTAATTC	CTGACGATGT	TCAATTTGGT	AATCCATTCT	ATAAATTTGA	TTACAAATTC	1620
GAAAAATGGG	ATGCTAAATA	A				1641

(2) INFORMATION FOR SEQ ID NO:766:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

ATCCCCATTA	AAGACATTGA	TTTCAGCATC	GTTAACCAAA	TGAATGACCT	TGTCTCTCTT	60
ACGATAGTGG	CACTGAGGAG	CTTCAAAACT	GAGTTGATCT	TTTTGTGGGG	GATTGAGCAG	120
GTCTTGCATG	AGCTGATTGA	TAGCATCAAT	CCCTGCCGTC	CCTCGGTACA	TAGGAGCCAG	180
AACTTGATA	TCACGGGCAG	GAATACCATT	TCTGAGGGCG	GCACCTAA		228

(2) INFORMATION FOR SEQ ID NO:767:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

ATGGAAATTA	AAATTGAAAC	TGGTGGTCTG	CGTTTGGATA	AGGCTTTGTC	AGATTTGTCA	60
GAATTATCAC	GTAGTCTCGC	GAATGAACAA	ATTAAATCAG	GCCAGGTCTT	GGTCAATGGT	120
CAAGTCAAGA	AAGCTAAATA	CACAGTCCAA	GAGGGTGATG	TCGTCACTTA	CCATGTGCCA	180
GAACCAGAGG	TATTAGAGTA	TGTGGCTGAG	GATCTTCCGC	TAGAAATAGT	CTACCAAGAT	240
GAGGATGTAG	CTGTTGTCAA	CAAACCTCAG	GGAATGGTTG	TGCATCCGAG	TGCTGGTCAT	300
ACTAGTGGAA	CTCTAGTCAA	TGCCCTCATG	TATCATATTA	AGGACTTGTC	TGGTATCAAT	360
GGGGTTCTGC	GTCCGGGAAT	TGTTCAACCGT	ATTGATAAGG	ATACGTCAGG	TCTTCTCATG	420
ATTGCTAAAA	ACGATGATGC	GCATCTAGCA	CTTGCCCAAG	AACTCAAAGA	TAAAAAGTCT	480
CTCCGCAAAT	ATTGGGCGAT	TGTTTCATGGA	AATCTGCCTA	ATGATCGTGG	TGTAATTGAA	540
GCGCCGATTG	GCCGGAGTGA	AAAAGACCGT	AAGAAACAGG	CTGTAACTGC	TAAAGGGAAG	600
CCTGCAGTGA	CGCGTTTTC	CGTCTTGGAA	CGCTTTGGCG	ATTATAGCTT	AGTAGAGTTG	660
CAACTGGAGA	CAGGGCGCAC	TCATCAAATC	CGTGCCACA	TGGCTTATAT	CGGCCATTCA	720
GTGCTGGTG	ATGAGGTCTA	TGGTCCTCGC	AAGACTTTGA	AAGGACATGG	ACAATTTCTT	780
CATGCCAAGA	CTTTAGGTTT	TACTCATCCG	AGAACAGGTA	AGACCTTGGA	ATTTAAAGCA	840
GATATCCCAG	AGATTTTAA	GGAAACCTTG	GAGAGATTGA	GAAAGTAA		888

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1347 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

TTTATGATTA	AAATCTATGA	CACCATGTCT	CGTGATTGTC	GAGAATTGTT	CCCGATTGAG	60
GACGGCAAGA	TCAAGATGTA	TGTTTGTGGG	CCAACCGTGT	ACAACTATAT	TCACGTGGGA	120
AACGCCCGTT	CGACGGTAGC	TTTTGATACG	ATTTCGTCGCT	ATTTTGAGTA	CCGTGGGTAT	180
AAGGTTGCCCT	ATATTTCCAA	TTTTACAGAT	GTGGATGATA	AGATTATCAA	CCGTGCCAGG	240
GAAGAAGGCA	TCACACCTCA	GGAGGTTGCG	GATAAGTACA	TCGCTGCCTT	TCGTGAGGAT	300
GTGACGGCAT	TGGGCGTGAA	ACCTGCGACT	CGCCATCCGC	GTGTAGTGGA	GTTTATGGCA	360
GACATCATCC	GTTTTGTGGA	AGACTTGATC	GAGAAAGGCT	TTGCCTATGA	GAGTCAAGGG	420
GATGTCTATT	TCCGTGTAGA	AAAATCCCAC	AACTATGCTA	AATTGGCTAA	TAAAACCTTG	480
GAAGATTTGG	AGCTAGGTGC	TTCAAGTCGT	ACCGATGAAG	AAACGGCTCG	TAAGGAAAAT	540
CCTGTAGACT	TTGCTCTATG	GAAATCTTCC	AAACCAGGTG	AGATTTCTTG	GGATAGTCCT	600
TGGGGACCTG	GACGTCCGGG	TTGGCATATT	GAGTGTTTCA	TCATGTCGAC	AGAGATTTTA	660

GGTGATACCA	TTGATATCCA	CGGTGGTGGA	GCTGACCTAG	AGTTTCCACA	CCACACCAAT	720
GAAATTGCC	AGTCTGAAGC	TAAAAACAGG	AAGGCTTTTG	CTAACTACTG	GATGCACAAT	780
GGCTTTGTCA	ATATCGACAA	TGTCAAAATG	TCTAAGTCCT	TGGGTAACTT	CATTACGGTA	840
CACGATGCC	TTAAAACTCT	TGATGGGCAA	GTACTTCGTT	TCTTCTTTGC	GACCCAGCAC	900
TACCGTAAGC	CTATCAACTT	CACGGAAAAG	GCAGTTCGCG	ATGCCGAGAC	CAATCTCAAG	960
TATCTCAAGA	ATACTTACGA	ACAACCATT	ACAGGAAATG	TGGATGCCCA	AGAGTTACAA	1020
AACTTTAAAG	ATAAGTTTGT	AGCAGCTATG	GATGAAGATT	TTAATGCTGC	CAACGGTATC	1080
ACAGTTGTCT	TTGAAATGGC	CAAATGGATC	AACTCAGGGA	ACTATGATGC	AAGTGTCAAG	1140
CAAGCTCTTG	CAGATATGTT	AGAAATTTTT	GGAATTGTCT	TTGTTGAGGA	AGTTTTGGAT	1200
GCAGAGATTG	AAGACTTGAT	TCAAAAACGC	CAAGAGGCGC	GTGCCAATCG	TGACTTTGCG	1260
ACAGCAGACC	AAATCCGTGA	CCAATTGGTT	ACTCAAGGAA	TTAAGCTCCT	TGATACCAAG	1320
GATGGAGTGA	GGTGGACACG	TGATTGA				1347

(2) INFORMATION FOR SEQ ID NO:769:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

ACTATGATTA	ACAATGTTGT	ACTTGTAGGG	CGTATGACAC	GTGACGCTGA	GTTGCGTTAT	60
ACCCCATCAA	ATGTAGCAGT	TGCGACTTTT	ACTCTTGACG	TAAACCGTAC	ATTTAAGAGT	120
CAAAATGGTG	AACGTGAGGC	TGATTTTATC	AATGTCGTTA	TGTGGCGCCA	ACAGGCTGAA	180
AATCTTGCTA	ACTGGGCTAA	AAAAGGCTCA	CTTATCGGGG	TGACAGGTCG	TATCCAGACT	240
CGTAGTTACG	ATAACCAGCA	AGGACAACGT	GTCTACGTGA	CAGAGGTCGT	GGCTGAGAAT	300
TTCCAAATGT	TGGAAAGCCG	TAGTGTGCGT	GAGGGCCACA	CAGGTGGAGC	TTACTCTGCA	360
CCAAC TGCAA	ACTATT CAGC	ACCTACA AAT	TCAGTACCAG	ACTTTTCACG	TAATGAAAAT	420
CCATTTGGAG	CAACAAACCC	ATTGGATATT	TCAGATGATG	ATTTACCATT	CTAA	474

(2) INFORMATION FOR SEQ ID NO:770:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1572 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: *misc_feature*
 - (B) LOCATION 1...1572
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

CTAATGATTA	AAAAGGAGAA	TATAATGACT	AAACGCGTCT	TAATCAGCGT	CTCAGACAAA	60
GCGGGCATTG	TTGAATTTGC	CCAAGAAGTC	AAAAAACTTG	GTTGGGAGAT	TATCTCAACA	120
GGTGGAAC TA	AGGTTGCCCT	TGATAATGCT	GGGGTGGATA	CCATTGCTAT	CGATGATGTG	180
ACTGGTTTCC	CAGAAATGAT	GGACGGTCGT	GTGAAGACCC	TCCACCCAAA	TATCCACGGA	240
GGGCTTCTCG	CTCGTCGTGA	CTTGGATAGC	CACTTGGAAG	CGGCTAAGGA	CAACAAGATT	300
GAGCTCATTG	ACCTTGTGGT	GGTCAACCTT	TACCCATTTA	AGGAAACTAT	CCTTAAACCA	360
GATGTGACTT	ATGCTGATGC	AGTTGAAAAT	ATCGATATTG	GTGGGCCGTC	TATGCTTCGT	420
TCAGCAGCGA	AAAATCATGC	CAGTGTTACA	GTTGTGGTAG	ATCCTGCTGA	CTACGCTGTG	480
GTTTTGGACG	AATTGGCAGC	AAACGGCGAA	ACCTCTTATG	AAACTCGCCA	ACGTTTAGCA	540
GCCAAAGTAT	TTCGTCACAC	AGCGGCTTAT	GACGCCTTGA	TTGCAGAATA	CTTCACAGCT	600
CAAGTGGGTG	AAAGCAAGCC	TGAAAACTC	ACTTTGACTT	ATGACCTCAA	GCAACCAATG	660
CGTTACGGTG	AGAATCCTCA	ACAAGACGCG	GACTTTTACC	AGAAAGCTTT	GCCTACAGAT	720
TACTCTATTG	CTTCAGCCAA	ACAGCTCAAC	GGGAAAGAAT	TGTCATTTAA	TAATATCCGT	780
GATGCAGATG	CTGCTATCCG	TATCATCCGT	GACTTCAAAG	ATAGTCCAAC	CGTTGTGGCT	840
CTCAAACACA	TGAATCCATG	TGGAATTGGT	CAAGCTGATG	ACATCGAGAC	TGCTTGGGAC	900
TACGCTTATG	AGTCTGACCC	AGTATCTATC	TTTGGTGGGA	TTGTCGTCCT	CAACCGTGAG	960
GTGGATGCTG	CGACAGCTGA	GAAGATGCAC	GGCGTTTTCC	TCGAAATCAT	CATTGCACCA	1020
AGCTATACGG	ATGAAGCGCT	AGCCATTTTG	ATCAATAAAA	AGAAAAACTT	GCGTATCCTT	1080
GCCTTGCCAT	TTAATGCTCA	AGAGGCTAGC	GAAGTGAAG	CAGAATACAC	AGGTGTAGTC	1140
GGTGGACTTC	TCGTGCAAAA	TCAAGACGTG	GTCAAGGAAA	GCCCAGCTGA	CTGGCAAGTG	1200
GTGACCAAAC	GTCAGCCAAC	TGAGACAGAA	GCGACTGCTC	TTGAGTTCGC	TTGGAAGGCT	1260
ATCAAGTACG	TCAAATCAAA	TGGTATTATC	GTGACCAACG	ACCACATGAC	ACTTGGTGTT	1320
GGTCCAGGTC	AAACCAACCG	TGTGGCTTCT	GTTCGCCTTG	CCATTGACCA	AGCCAAAGAT	1380
CGTCTGGACG	GGGCGGTCCT	TGCTTCAGAT	GCCTTCTTCC	CATTTGCGGA	TAACGTGGAA	1440
GAAATCGCCA	AAGCAGGAAT	TAAGGCCATC	ATCCAGCCCC	GTGGCTCTGT	CCGTGACCAA	1500
GAATCCATCG	AAGCAGCGGA	TAAATACGGC	TTGACTATGG	TCTTTACAGG	TGTGAGACAT	1560
TTTAGACATT	AA					1572

(2) INFORMATION FOR SEQ ID NO:771:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

ATGATGATTA	AGGTAATTGC	GACAGATATG	GATGGGACCT	TGCTGGATGC	TAGAGGTCAG	60
CTTGATCTCC	CACGATTGGA	AAAGATTTTA	GATCAGTTGG	ATCAAAGGGG	CATTCGTTTT	120
GTCATTGCGA	CGGGCAATGA	AATTCACCGC	ATGAGACAAC	TACTGAGTCC	CTTGGTGGAT	180
CGAGTGGTTC	TGGTTGTTGC	TAATGGCGCT	CGTATTTTTG	AAAACAATGA	ATTGATTCAG	240
GCTCAGACAT	GGGATGACGC	CATTGTCAAC	AAGGCTTTGG	CTCATTTCAA	GGGTCGAGCG	300
TGTCAGAAC	AGTTTGTGT	AACGGGGATG	AAGGGTGATT	TTGTCAAGGA	AGGTACGATT	360
TTTACAGATC	TTGAAAGTTT	TATGACTCCA	GAAATGATTG	AAAAATTCTA	CCAACGGATG	420
CAATTTGTGG	ATGAATTAAC	ATCTGACCTC	TTTGGTGGTG	TGCTCAAGAT	GAGCATGGTT	480
GTTGGTGAGG	AACGTTTGAG	TTCGGTTTTG	GAAGAAATCA	ATGCTCTCTT	TGATGGCCGT	540
GTCCGAGCTG	TATCCAGTGG	CTATGGTTGC	ATTGATATCC	TCCAAGCTGG	GATTCATAAA	600
GCAATGGGGCT	TGGAGGAATT	ACTCAAGCGC	TGGGACTTGA	AATCCCAAGA	AATCATGGCT	660
TTTGGTGATA	GTGAAAATGA	TGTTGAAATG	CTTGAAATGG	CTGGAATTGC	CTATGCGATG	720
GAAAATGCTG	ATGAGAAAAG	CAAAGCTGTG	GCGACTGCTC	TAGCACCAGC	CAACAGCCAA	780
GGAGGAGTTT	ATCAAGTCTT	GGAAAACCTG	TTAGAAAAAG	GAGAATGA		828

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...2256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GCGAGGATTA	AAATGAATAC	ATTATTGACA	TTACGAGGTA	AAAGCTTTAC	ACAAAAATCA	60
AGAAATAATG	GTATGGGACC	AATAACTATA	CCCAAAAAAA	CAATAATTAC	ATTGGAACAT	120
TTGAAGTATC	TTCATTTTTT	ATTAGAAGAG	ACGAAAACAT	ATTGGGAGAA	AAATAACATT	180
ATCGATGGTA	TTTTGATCAG	TATTTACTAT	AATCGAATTG	TTGCCAAAAG	TAACCGTATT	240
AATGGCTATT	TCAATGTAGG	AGGAGGGAAT	CCATTCCCTA	ATGATACTAT	TGTGGGAGCA	300
AAATTCAATG	ATGAGAAGAC	AAAACATATT	GTTACTCATT	ATATTTCTAG	AGATGCTCTT	360
AATAAAACAA	TAACCGTTTT	AAGTAAGATA	ATTGAAGTTT	TTGAGGAACA	TTTTTGATAGA	420
GCGATAACAT	GTGAGATGTT	TTCTGATTCA	TCAACGTTTG	CTTCTATAAA	TTTTTCGGAG	480
TATGGTATTT	CAAAAAGCAA	ATTTCAACAG	TATTTGAGAG	ATTCTTGCTT	TATTGAGAAT	540
TTTGGAGTTG	AGCACACTAC	TGTTTCTGAT	ATTCAAAATT	CTATCGTGAC	ATTTTATGAT	600
GTCCATACAG	ACATTTTTAG	ATTACTGAAT	AAATTAATAA	TTGATATTTT	AGAAGCTAAT	660
ATCATGAATC	AGACCACGGT	CTTGCTTGAT	GAAAAAATAA	TTGAATTACT	ACTATCAAAA	720
GCGCCCTATC	TTGTCTCCAT	GATTGTGGAA	GATTTTTCTA	AGTTATCTGT	AGATGATTTT	780
TCTTTAGATA	ATAATGATTT	AAAAATAAAT	CTTCCATCTC	CAATGAACGA	ACCAGTTGTT	840

GGCGTTATTG	ATACCTTATT	TGACAAAAGA	GTTTACTTTA	ATGAGTGGGT	AGAATATCAT	900
GATTTTGTCT	CACCTGATAT	TAGCAAAGAT	AGCCAAGATT	ACAAGCATGG	GACAGCTGTG	960
ACTTCTTTAA	TCGTTGATGG	AGCCAATTTG	AACCCTAATC	TGGATGATGG	TTGTGGAAAT	1020
TTTAGAGTGA	GGCATTTTGG	TGTGTCACCTA	CAAAGTGGAT	TTAATTCATT	TACAATCATA	1080
AAACAGATAA	AAGAGATTGT	TTCTCAGAAT	GCTGATATTA	AGGTTTGGAA	TCTTTCTTTA	1140
GGGTCCAATG	ATGAAATAAG	AGAAAATTTT	ATCTCTGCAG	AGGGAGCATT	ATTAGACGAA	1200
ATTCAATTTG	AGAATGATGT	AATTTTTATC	ATAGCTGGGA	CAAATGCTTC	AGTAATAAAT	1260
GGGAAACGCA	AAAGAATAGG	TGCTCCTGCT	GATTCACCTA	ATTCTATAAT	AGTAAATTCT	1320
GTTGATTTTA	ATAATCAATC	AGTGTTCATAT	TCACGAGAGG	GTATTGTTTT	ATCATTCTTT	1380
GTAAACCAG	ATGTGTCATA	TTATGGAGGA	GGAAATGGTG	ACTTTATAAA	TGTTTGTGAA	1440
CCTCTAGGAT	TAGGTCGTGT	AGCTGGAACA	AGTTTTGCGG	CACCTTTTAT	TGCAAGGAAA	1500
ATGGCCTATC	TCATTTCATAT	TATGGGACTT	AGCCGAGAAG	AAGCGAAGGC	TTTGCTAATT	1560
GATGCAGCAA	TACCCTGGAA	TGATAAGAAA	ACATTCACTG	ATTTATCTTT	GATAGGAAAT	1620
GGTATTGTTT	CAATAAAAAAT	GGATGATATT	TTATCTACAC	CTGATGATGA	AATTAAATTT	1680
ATTGTGTCAG	ATATCTCTAG	GGCTTATGAT	ACCTATAATT	ATGATTTTCC	AGTACCTATT	1740
TCTAGTGAGA	GTTATCCATA	TGTAGCTAAA	GCAACAATGT	GTTATTTCCC	TAAGTCTCA	1800
AGAAAACAAG	GGGTTGATTA	TACAAATACT	GAGATGCAGC	TTACTTTTGG	TAGGTTAAAG	1860
TCAGACGGTA	TCAAATCGAT	AAATAAAGAC	AACCAGCATG	CCGAAGATTC	CCCAGGATAT	1920
GTGAGAGAAA	ATGCTGCTAG	AAATATATTT	AGGAAATGGG	ATAATGTCAA	GCATATTGGA	1980
GAGTCGTTTA	CTTCTCGAAA	GAGAGCTAAA	GCAATTTTAA	ATCCATCTAA	TCCTCAGTGG	2040
GGGATGAGTA	TTAAAACAAT	CGAACGTTTG	AAAAGCGGTG	ATGGACAAGG	AGTACGTTTT	2100
GGTGTAGTAG	TTACATTAAA	AGAATTAAAT	GGGGTTAATC	GTATTGAAGA	TTTTATTTCAG	2160
CAAGCTGAAT	TACGCGGTTG	GCTAGTTAAT	AGATTGCAAG	TAGAAGCTCA	AGTAGACCTC	2220
TTTAATAGTT	TAAATGAAGA	AATTGAATTT	GAATAG			2256

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

AACGTTGTTA	AATCAACGTT	TTTTATTTTT	ATCTTTGGTA	TTCCTTTGCA	TTCTTTTGCT	60
AAAAAGGGAG	TCACAAACAG	ACCCTATTTT	AAAAAAAGGA	TAGAAAAAAG	GATACAACAT	120
TTGTGCGCATC	CTAAAAATAA	TCTTTTTTCG	ACGGAAGACA	TGGGATTTCGA	ACCCACGCAC	180
GCTATTACAC	GCCTACCGCG	TTTCCAACAC	GGCCTCTTAA	GCCTCTTGAG	TAATCTTCCA	240
ATACTTACTC	AAATAGTCTA	CCATAAAGGC	TCTTATCTTG	CAATAAAAAAT	TCTAGAAATA	300
AGAAAAAATG	ATAGATTTTG	A				321

(2) INFORMATION FOR SEQ ID NO:774:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2370
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

AATTCCTGTTA	AAAAAAATGA	TATAATAGAA	TTTATGGATA	AAAATAAGAT	TATGGGATTA	60
ACCCAAAGAG	AAGTCAAGGA	AAGACAGGCT	GAGGGTTTGG	TCAATGACTT	TACCGCATCA	120
GCCAGTACCA	GCACTTGGCA	AATCGTTAAA	CGAAATGTCT	TTACCCTTTT	TAACGCTTTG	180
AACTTAGCCA	TTGCTTTGGC	TCTTGCCTTT	GTGCAGGCTT	GGAGCAATCT	GGTCTTCTTT	240
GCTGTTATCT	GCTTTAACGC	TTTTTCTGGG	ATTGTGACCG	AGCTACGAGC	CAAACACATG	300
GTGGACAAGC	TCAATCTCAT	GACCAAGGAA	AAGGTCAAAA	CCATCCGTGA	TGGTCAGGAA	360
GTTGCTCTTA	ATCCTGAAGA	ATTAGTGCTA	GGAGATGTCA	TTCGTTTGTC	TGCAGGAGAG	420
CAGATTCCTA	GTGATGCCTT	GGTTTTGGAA	GGCTTTGCGG	AAGTCAATGA	AGCCATGTTA	480
ACGGGAGAAA	GTGATTTGGT	GCAAAAGGAA	GTTGACGGCT	TACTTTTGTC	AGGAAGTTTC	540
CTAGCCAGTG	GGTCAGTTTT	ATCTCAAGTT	CACCATGTCT	GTGCAGACAA	CTATGCTGCC	600
AAACTCATGC	TTGAGGCTAA	GACCGTTAAA	CCCATCAACT	CCCGTATCAT	GAAATCGCTG	660
GACAAGTTGG	CTGGTTTTAC	TGGGAAGATT	ATCATTCCCT	TTGGTCTGGC	TCTCTTGCTG	720
GAAGCCTTGC	TTTTTAAAAG	CCTGCCTCTC	AAGTCATCTG	TTGTAAACTC	GTCGACAGCT	780
CTTTTGGGAA	TGTTGCCTAA	GGGAATTGCC	CTTTTGACCA	TTACTTCGCT	CTTGACTGCA	840
GTTATCAAGC	TAGGTTTGAA	AAAGGTCTTG	GTGCAGGAGA	TGTACTCTGT	TGAGACCTTG	900
GCGCGCGTGG	ATATGCTCTG	TCTGGACAAG	ACGGGTACCA	TCACCCAAGG	AAAGATGCAG	960
GTGGAGGCTG	TTCTTCCGTT	GACGGAAACG	TATGGTGAAG	AGGCTATTGC	CAGCATCTTG	1020
ACTAGCTACA	TGGCCCATAG	TGAGGATAAG	AATCCAAC TG	CCCAAGCCAT	TCGCCAGCGT	1080
TTTGTGGGAG	ATGTTGCTTA	TCCATATGATT	TCCAATCTTC	CCTTCTCCAG	CGACCGCAAG	1140
TGGGGGGGCTA	TGGAGTTAGA	AGGCTTGGGG	ACAGTTTTCT	TAGGGGCACC	TGAGATGTTG	1200
CTGGATTCTG	AAGTCCCAGA	AGCCAGGGAG	GCCTTGGAGA	GAGGATCACG	TGTCCTGGTC	1260
TTAGCTCTCA	GTCAGGAGAA	ATTAGACCAT	CACAAACCAC	AGAAACCATC	TGATATTCAG	1320
GCTCTAGCCT	TGCTGGAAAT	CTTGGAACCC	ATTCGAGAGG	GAGCAGCAGA	GACGCTGGAC	1380
TATCTCCGTT	CTCAGGAGGT	AGGACTCAAG	ATTATCTCTG	GTGACAATCC	AGTTACGGTG	1440
TCTAGCATTG	CCCAGAAGGC	TGGTTTTGCG	GACTATCACA	GCTATGTAGA	TTGCTCAAAA	1500
ATCACCGATG	AGGAATTGAT	GGCCATGGCG	GAGGAGACAG	CTATTTTCCG	ACGTGTTTCC	1560
CCTCATCAAA	AGAAACTCAT	CATCCAAACG	TTGAAAAAAG	CGGGTCATAC	AACGGCTATG	1620
ACAGGGGACG	GGGTTAATGA	TATCTTGGCC	CTTCGTGAGG	CGGATTGTTC	TATCGTGATG	1680
GCGGAGGGGG	ATCCAGCAAC	CCGTCAGATT	GCCAATCTGG	TTCTCTTGAA	CTCAGACTTT	1740
AATGATGTTT	CTGAGATTCT	CTTCGAGGGT	CGTCGCGTGG	TCAATAACAT	TGCCCACATC	1800
GCCCCGATTT	TCTTGATAAA	GACCATCTAT	TCCTTCCTGT	TAGCAGTCAT	CTGTATTGCC	1860
AGTGCTTTAC	TAGGTCGGTC	AGAGTGGAAT	TTGATTTTCC	CCTTCATTCC	GATCCAGATT	1920
ACCATGATTG	ACCAAGTTGT	GGAAGGTTTC	CCACCATTCG	TTCTGACTTT	TGAGCGAAAT	1980
ATCAAACCTG	TTGAGCAGAA	TTTCCTCAGA	AAATCCATGC	TTCGTGCCCT	ACCAAGCGCT	2040
CTCATGGTCG	TCTTCAGCGT	CCTGTTTGTG	AAAAATGTTG	GCGCGAGTCA	AGGTTGGTCT	2100
GAGTTAGAAA	TCTCAACTCT	ACTCTATTAT	CTCTTGGGGT	CAATTGGTTT	CTTATCCGTA	2160

TTTAGAGCCT	GCATGCCATT	TACCCTATGG	CGTGTCTCT	TGATTGTTTG	GTCAGTAGGA	2220
GGTTTCCTAG	CCACAGCTCT	CTTCCCAAGA	ATTCAAAAAC	TGCTTGAAAT	TTCAACCTTA	2280
ACAGAACAAA	CGTTGCCTGT	TTATGGTGTC	ATGATGTTGG	TCTTTACCGT	GATTTTCATC	2340
CTGACCACTC	GTTACCAAGC	GAAAAAATAA				2370

(2) INFORMATION FOR SEQ ID NO:775:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

TCTTTAGTTA	AAGTGAGAAG	AAATCTGATA	GATAGTTTGA	TTCAGTATAT	GCTTATAATA	60
GGGGTAAACA	ACTCAGGAGG	TTCTTGTAGG	TTGCGAGAGT	TTGGCGAAAA	AATTAAAAGA	120
TTACGTTTGG	CTAAAAAAT	CAGTCGTTCA	GAATTTTGTG	GTGATGAGTC	TGAATTAAGT	180
ATCCGTCAAT	TAATTAGAAT	TGAAAATGGA	GAATCCAGAC	CAACACTAAC	AAAGTTAAAA	240
TATATCGCTG	AACGTTTGGG	GGTTGAAGAT	TACAAGTTGA	TGCCAAGTTA	TATAGAGTTG	300
GATAAGGAAT	ACCTAGAATT	GAAGTATTTT	TTGATGAGAA	CTCCTACATA	CGAAGATGAA	360
ACTATCGCCC	AAAAGAAAAG	GAGTGTTTTT	ATAAGATTTT	TGAAGAGTAT	TATGATAGGC	420
TACCTGAGGA	AGAAAGATTT	ATCATCCCAA	ATTATTCATA	TCTGGCACTA	A	471

(2) INFORMATION FOR SEQ ID NO:776:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

ACTATAGTTA	AGGAGGTATT	TCCCATGATA	AAACAGATAA	AAGCCCACTT	GAATAAGAGT	60
ATTCAGAGTA	TCATTGGCCA	AAAAGTTGAG	TTCGTCAAAC	AAGATGAACA	GGCCTTTACT	120
CGTAAAAGAA	GGTTATCACT	AGAAACTATG	ATTCGTACAA	TTCTGGGCAT	GGGAGGAAAA	180
TCACTATCAA	AAGAATTACT	AGATGCCAGA	CTGACAGTTT	CAAATTCAGC	CTTTGTTCAA	240
AGACGCTATC	AGATAAAAACC	TGAAGCTTTC	TATGCTCTAT	TTAAAGAATT	TACAGCACCT	300
ATTCCACTTA	ATACTGATTT	TCCAATATTC	GCTGCAGATG	GGAGTGATAT	CTGTATTCCT	360
CGAAATCCCA	TGGATACAGA	AACCTCTATC	CAAACCCAAA	CGGATGTTAA	ATCCTATAAT	420
CTCATACACA	TAAATGCCCT	ATACGACTTG	ACGACTGGAG	TGTATAGAGA	TGTCTCTATT	480
CAAGACAAAC	ATGCACAACA	TGAGCGCTTA	GCTCTGATTC	AGATGATGGA	GGCTTCTCCC	540
TTTCGAGAAA	GCTCTTGTTA	TCATGGATAG				570

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

ACTATAGTTA	AGGAGGTATT	TCCCATGATA	AAACAGATAA	AAGCCCACTT	GAATAAGAGT	60
ATTCAGAGTA	TCATTGGCCA	AAAAGTTGAG	TTCGTCAAAC	AAGATGAACA	GGCCTTTACT	120
CGTAAAAGAA	GGTTATCACT	AGAAACTATG	ATTCGTACAA	TTCTGGGCAT	GGGAGGAAAA	180
TCACTATCAA	AAGAATTACT	AGATGCCAGA	CTGACAGTTT	CAAATTCAGC	CTTTGTTCAA	240
AGACGCTATC	AGATAAAAACC	TGAAGCTTTC	TATGCTCTAT	TTAAAGAATT	TACAGCACCT	300
ATTCCACTTA	ATACTGATTT	TCCAATATTC	GCTGCAGATG	GGAGTGATAT	CTGTATTCCT	360
CGAAATCCCA	TGGATACAGA	AACCTCTATC	CAAACCCAAA	CGGATGTTAA	ATCCTATAAT	420
CTCATACACA	TAAATGCCCT	ATACGACTTG	ACGACTGGAG	TGTATAGAGA	TGTCTCTATT	480
CAAGACAAAC	ATGCACAACA	TGAGCGCTTA	GCTCTGATTC	AGATGATGGA	GGCTTCTCCC	540
TTTCGAGAAA	GCTCTTGTTA	TCATGGATAG				570

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

ACTATAGTTA	AGGAGGTATT	TCCCATGATA	AAACAGATAA	AAGCCCACTT	GAATAAGAGT	60
ATTCAGAGTA	TCATTGGCCA	AAAAGTTGAG	TTCGTCAAAC	AAGATGAACA	GGCCTTTACT	120
CGTAAAGAA	GGTTATCACT	AGAAACTATG	ATTTCGTACAA	TTCTGGGCAT	GGGAGGAAAA	180
TCACTATCAA	AAGAATTACT	AGATGCCAGA	CTGACAGTTT	CAAATTCAGC	CTTTGTTCAA	240
AGACGCTATC	AGATAAAACC	TGAAGCTTTC	TATGCTCTAT	TTAAAGAATT	TACAGCACCT	300
ATTCCACTTA	ATACTGATTT	TCCAATATTC	GCTGCAGATG	GGAGTGATAT	CTGTATTCCCT	360
CGAAATCCCA	TGGATACAGA	AACCTCTATC	CAAACCCAAA	CGGATGTTAA	ATCCTATAAT	420
CTCATACACA	TAAATGCCCT	ATACGACTTG	ACGACTGGAG	TGTATAGAGA	TGTCTCTATT	480
CAAGACAAAC	ATGCACAACA	TGAGCGCTTA	GCTCTGATTC	AGATGATGGA	GGCTTCTCCC	540
TTTCGAGAAA	GCTCTTGTTA	TCATGGATAG				570

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2061 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

TCAACAGTTA	AAAAAAATCT	AGTCATCGTG	GAGTCGCCTG	CTAAGGCCAA	GACGATTGAA	60
AAATATCTAG	GCAGAAACTA	CAAGGTTTTA	GCCAGTGTGC	GGCATATCCG	TGATTTGAAG	120
AAATCCAGTA	TGTCCGTCGA	TATTGAAAAT	AATTATGAAC	CGCAATATAT	CAATATCCGA	180
GGAAAAGGCC	CTCTTATCAA	TGACTTGAAA	AAAGAAGCTA	AAAAAGCTAA	TAAAGTTTTT	240
CTCGCGAGTG	ACCCGGACCG	TGAAGGAGAA	GCGATTTCTT	GGCATTTGGC	CCATATTCTC	300
AACTTGATG	AAAATGATGC	CAACCGTGTG	GTCTTCAATG	AAATCACCAA	GGATGCAGTC	360
AAAAATGCTT	TTAAAGAACC	TCGTAAGATC	GATATGGACT	TGGTCGATGC	CCAACAAGCT	420
CGTCGGATCT	TGGATCGCTT	GGTAGGGTAT	TCGATTTGCG	CTATTTTGTG	GAAGAAGGTC	480
AAGAAGGGCT	TGTCAGCAGG	TCGCGTTCAG	TCCATTGCCC	TTAAACTCAT	CATTGACCGT	540

GAAAATGAAA	TCAATGCCTT	CCAGCCAGAA	GAATACTGGA	CAGTTGATGC	TGTCTTTAAA	600
AAGGGAACCA	AACAATTTCA	TGCTTCCTTC	TATGGAGTAG	ATGGTAAAAA	GATGAAACTG	660
ACCAGCAATG	ACGAAGTCAA	GGAAGTCTTG	TCTCGTCTGA	CTAGTAAAGA	CTTTTCAGTA	720
GATCAGGTGG	ATAAGAAAGA	GCGCAAGCGC	AATGCTCCTT	TACCCTATAC	CACTTCATCT	780
ATGCAGATGG	ATGCTGCCAA	TAAAATCAAT	TTCCGTACTC	GAAAAACCAT	GATGGTTGCC	840
CAACAGCTCT	ATGAAGGAAT	TAATATCGGT	TCTGGTGTTC	AAGGTTTGAT	TACCTATATG	900
CGTACCGATT	CGACTCGTAT	CAGTCCTGTA	GCGCAAAATG	AGGCGGCAAG	CTTCATTACG	960
GATCGTTTTG	GTAGTAAGTA	TTCTAAGCAC	GGTAGCAAGG	TCAAAAACGC	ATCAGGTGCT	1020
CAGGATGCCC	ATGAGGCTAT	TCGTCCGTCA	AGTGTCTTTA	ATACACCAGA	AAGCATCGCT	1080
AAGTATCTGG	ACAAGGATCA	GCTCAAGCTA	TATACCCTTA	TCTGGAATCG	TTTTGTGGCT	1140
AGCCAGATGA	CAGCGGCCGT	TTTTGATACC	ATGGCTGTTA	AATTGTCTCA	AACAGGGGTT	1200
CAATTTGCTG	CCAATGGTAG	TCAGGTTAAG	TTTGATGGTT	ATCTTGCCAT	TTATAATGAT	1260
TCTGACAAGA	ATAAGATGTT	ACCGACATGG	TGTTGGAGAT	GTGTCCCACA	GGTCAATAGC	1320
AAACCAGAGC	AACATTTTAC	CCAACCGCCT	GCCCGTTATT	CTGAAGCAAC	ACTGATTAAA	1380
ACCTTAGAGG	AAAATGGGGT	TGGACGTCCA	TCAACCTACG	CGCCAACCAT	TGAAACCATT	1440
CAGAAACGTT	ATTATGTTTC	CCTGGCAGCC	AAACGTTTTG	AACCGACAGA	GTTGGGAGAA	1500
ATTGTCAATA	AGCTCATCGT	TGAATATTTT	CCAGATATCG	TAAACGTGAC	CTTCACAGCT	1560
GAAATGGAAG	GTAAACTGGA	TGATGTCGAA	GT'TGGAAAAG	AGCAGTGGCG	ACGGGTCATT	1620
GATGCCTTTT	ACAAACCAT	CTCTAAAGAA	GT'TGCTAAGG	CTGAAGAAGA	AATGGAAAAA	1680
ATCCAGATTA	AGGATGAACC	AGCTGGATT	GACTGTGAAG	TGTGTGGCAG	TCCAATGGTC	1740
ATTAAACTTG	GTCGTTTTTG	TAAATTCTAC	GCTTGTAGCA	ATTTCCCAGA	TTGCCGTCAT	1800
ACCCAAGCAA	TCGTGAAAGA	GATTGGTGT	GAGTGTCCAA	GCTGTCATCA	GGGACAAATT	1860
ATTGAGCGAA	AAACCAAGCG	TAATCGCCTA	TTCTATGGTT	GCAATCGCTA	TCCAGAATGT	1920
GAATTTACCT	CTTGGGACAA	GCCTGTTGGT	CGTGACTGTC	CAAAATGTGG	CAACTTCCTC	1980
ATGGAGAAAA	AAGTCCGTGG	TGGTGGCAAG	CAGGTTGTTT	G'TAGCAAAGG	AGATGACTCT	2040
TCACCACGAG	TGCNGNGCAC	A				2061

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

AGGGAGGTTA	ATATGATTGA	ACTTAAACAG	GTGAGTAAAT	CTTTTGGAGA	ACGAGAGTTA	60
TTTTCGAATC	TTTCAATGAC	ATTTGAGGCT	GGAAAAGTCT	ATGCCTTAAT	TGGTTCAAGT	120
GGTAGCGGAA	AAACAACCTT	GATGAACATG	ATTGGGAAAT	TAGAACC'TTA	TGATGGGACG	180
ATTTTTTACC	GAGGTAAAGA	CTTGGCCAAT	TATAAATCGA	GTGATTTTTT	CCGTCACGAA	240
TTGGGTTACC	TCTTCCAGAA	CTTTGGCTTA	ATTGAAAACC	AAAGTATTGA	AGAAAACCTT	300
AAGCTAGGTC	TCACTGGTCA	AAAGTTGAGT	CGGTCGGAAC	AGCGGTTGAG	GCAGAAGCAG	360
GCTTTAGAAC	AGGTCGGCCT	GGCTTATCTT	GACCTAGATA	AGCGCATCTT	TGAGTTATCG	420

GGCGGAGAAT	CGCAACGGGT	TGCCTTGGCA	AAAGTTATCT	TAAAGAATCC	ACCCTTTATT	480
CTGGCAGATG	AGCCAACAGC	TTCAATAGAC	CCAGCAACCT	CTCAGTTGAT	TATGGAGATT	540
TTGCTATCTC	TTCGAGATGA	TAATAGGCTA	ATCATTATCG	CAACACATAA	TCCAGCAATT	600
TGGGAGATGG	CTGATGAAGT	GTTACAGATG	GATCGTCTGA	AATAA		645

(2) INFORMATION FOR SEQ ID NO:781:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...600
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

TTTGGGGTTA	AGTATCTGCA	AAGAATGATT	GCCCTTACAG	ATACTGGCTT	AACCTTTACA	60
AAAGATCCTT	TTGACTGTGA	GCGCTACGAG	GACTTGCGAA	GTCTGTTATC	TGAAATGTTG	120
AATCAGGGAT	CAGACCTGGA	TGCAGAAGAA	GTAGCAGAAG	TCTTGAAACC	AACTTCAGCT	180
TATGCGACTC	CCTTAATGGA	CGTCCGTGCT	TGGATTGTTG	AGGATGAGAA	GATTTGTCTG	240
GTTAGGGGAC	AAGGAGAGGA	TAGTTGGGCT	TTGCCAGGTG	GCTTTGGTGA	AGTCGGCTAT	300
TCTCCAAC TG	AAAAATATTCT	CAAGGAAATT	GAAGAAGAAA	CCGGTTTTTAA	AGCCAAAGTT	360
GAAAGACTGC	TAGCTGTTTT	TGATACCAAT	CGTTTCCAAC	TACAGAGCAA	ACAATATGCA	420
AAGTTTGTTT	TTGAATGTAA	GCTTCTCGAT	GGACAAATTC	AAGAAAATCA	AGAAATCGCT	480
GACCTTCAAT	TTTTTGCAAT	TGACCAACTG	CCGAATTTAT	CTGAAAAACG	CATTACCAAG	540
GAGCAAATCG	AGATTCTTTG	GCAGGTTTAT	CAAGGTCAGA	GGGAGCAATA	TCTTGACTAA	600

(2) INFORMATION FOR SEQ ID NO:782:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

ATTAATTCTA	AAGAATTGAG	TATTTCTATG	TTAAAAAAAT	ATCCTTGTAC	GATGCAACAT	60
GACCAGTCAG	ATTGTGCTGC	GGCAGTTGTT	TCAACAGTTC	TTTTATCTTA	CAAAAAGGAA	120
CTATCAATCA	TGAAGATTCG	GGAAATTATT	GGTACAGACA	TGTATGGAAC	GA CTGTCAGT	180
GGTATTGTTT	CAGGTCTGAA	TAAGTTGAAT	TTTACAGTAA	AAGCTGTTTC	AGTAGCACTG	240
GAAGATTTGA	CTCCAAAATT	AACATTTTCCT	GCGATTCTTC	AAGTTAAGAA	TGATTTAGGT	300
CAAAATCATT	TTGTGGTATT	ACATAGTATA	AAGGAGAAAA	TAAAGGGAAC	TCGTATTACC	360
AAATAA						366

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GCTTTCTCTA	AGGAAAACTT	ATACTCAATG	AAAATCAAAG	AGCAAAC TAG	GAAGCTAACC	60
GCAGGTTGCT	CAAAACACTG	TTTTGAGGTT	GTGGATGAAA	CTGACGAAGT	CAGCTCAAAA	120
CATGGTTTTG	AGGTTGTAGA	TGAAACTGAC	GAAGTCAGCT	CAAAACACCG	TTTTGAGGTG	180
GCAGATAGAA	CTGACGAAGT	CAGTAACATA	TATACGGTAA	GGCGACGCTG	A	231

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

TCCTCATCTA	AACTTGTTTT	TTTAAAATTG	AAGGATGATT	TTGGAGGATA	TAAGATGACA	60
TTGACTATTC	ATGTATATTA	TAAAGGTGAT	GGAGATAGTG	CAATAAAGTT	TGCAAGAGAA	120
ATGCTTGATA	GTGGCCTTGT	TGAAGAAATT	AGAAATCAAA	AAGGTAACCT	GAAATACGAA	180
TATTTTTTAC	CAATTGAAAA	AGAGGGAAC	ATTCTCCTTA	TTGATCAGTG	GATAAATCAA	240
GAAACTTTAG	ATAAACATTA	TCAATCAAAG	ACAATGCAGA	AAATCTTAGA	TTTAAGAAAA	300
AAATATCACT	TGCAGATGCA	AGTTGAACGT	TATATAGAAG	ATGATTCTGG	GATGCCAGAA	360
AGCGATAAGT	CGTTTATAGA	CACAGGGAAT	TAG			393

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

ATGTCATCTA	AGGTTATTGT	TACAATTTTC	GGTGCGAGTG	GAGACCTGGC	TAAACGCAAG	60
CTCTACCCTT	CCCTTTTATG	ACTATATCAA	TCCGGCAATC	TTTCCAAGCA	CTTTGCCGTT	120
ATTGGAAGTG	CCCGTAGACC	TTGGAGTAAG	GAATATTTTG	AATCTGTAGT	TGTCGAGTCC	180
ATCCTTGATT	TGGCAGATAG	TACCGAGCAA	GCCCAAGAAT	TTGCTAGCCA	CTTCTACTAT	240
CAAAGCCATG	ATGTCAATGA	TTCGGAACAT	TATATTGCTT	TGCGTCAATT	ACAAGCTGAG	300
CTTAATGAAA	AATACCAAGC	TGAACACAAT	AAGCTCTTCT	TCTTGTCTAT	GGCACCTCAG	360
TTCTTTGGAA	CCATTGCCAA	ACACCTCAAA	TCTGAAAACA	TTGTGCGATG	CAAAGGTTTT	420
GAGCGCTTGA	TCGTTGAAAA	ACCATTGCGT	ACAGATTACG	CAACTGCAAA	CAAGTTGAAT	480
GACGAACTCC	TAGCAACATT	TGACGAAGAA	CAAATTTTCC	GTATCGACCA	TTATCTTGGT	540
AAGGAAATGA	TCCAAAGCAT	CTTTGCAGTT	CGCTTTGCAA	ACTTGATTTT	TGAAAACGTT	600
TGGAACAAGG	ATTTTATCGA	CAATGTTCAA	ATTACCTTTG	CGGAGCGCTT	GGGTGTAGAA	660
GAACGTGGTG	GCTACTATGA	CCAATCCGGT	GCCCTCCGTG	ACATGGTCCA	AAACCACACT	720
CTACAACTTC	TTTCGCTCCT	CGCCATGGAC	AAACCAGCAA	GCTTCACAAA	AGACGAGATT	780
CGTGCTGAAA	AGATTAAGGT	CTTTAAAAAC	CTCTATCATC	CAACTGATGA	AGAACTCAAA	840
GAACACTTTA	TCCGTGGGCA	ATACCGCTCT	GGTAAGATTG	ATGGCATGAA	ATACATCTCT	900
TATCGTAGCG	AGCCAAATGT	GAATCCAGAA	TCAACAACCT	AAACCTTTAC	ATCTGGTGCC	960
TTCTTTGTAG	ACAGCGATCG	ATTCCGTGGT	GTTCTTTTCT	TTTTCCGTAC	AGGTAAACGA	1020
CTGACTGAAA	AAGGAACTCA	TGTCAACATC	GTTTTTAAAC	AAATGGATTG	TATCTTTGGA	1080
GAACCACTTG	CTCCAAATAT	TTTGACCATC	TATATTCAAC	CAACAGAAGG	CTTCTCTCTT	1140

AGCCTAAATG	GGAAGCAAGT	AGGAGAAGAA	TTTAACTTGG	CTCCTAACTC	ACTTGATTAC	1200
CGTACAGATG	CGACTGCAAC	TGGTGCTTCT	CCAGAACCAT	ACGAGAAATT	GATTTATGAT	1260
GTCCTAAATA	ACAACCTAAC	TAACTTTAGC	CACTGGGATG	AAGTTGGTGC	ATCATGGAAG	1320
TTGATTGACC	GTATTGAAGA	GCTCTGGGCT	GAAAATGGTG	CCCCACTTCA	TGACTATAAA	1380
GCTGGAAGCA	TGGGACCTCA	AGCCAGCTTT	GACCTACTTG	AAAAATTCGG	TGCCAAATGG	1440
ACTTGGCAAC	CAGATATCGC	CTATCGTCAA	GATGGTCGTT	TCGAATAA		1488

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

TTTACTTGTT	TTTGTGATAT	AATAGTCTTA	TCTTTACACA	GAGGTATAGT	AATGAAAGAA	60
ACTGTTTATT	TTGGAACCTTA	TACACGTCGT	ACTTCTCAAG	GGATTTACAA	GGCAGACTTT	120
GATACAGAAA	CTGGTCAGCT	TTCAAATCTA	GAACTTTTTTG	CAGCTGAGCC	AAGTCCAACC	180
TACCTTGCCCT	TTGACCAGCA	CCAACATTTA	TACACTGTTG	GTAGCCAAGA	CGATAAGGGG	240
GGAATTGCAG	CCTATCAAAC	TGACGGGACT	GTGTTAAATC	ATGTTGTTGA	AGAAGGAGCT	300
CCCCACTGTT	ATGTTGCTGT	CGATGAAAAG	CGTGATTTGG	TTTACGCAGC	TAACTATCAC	360
AAGGGACAAG	TCCTTGTTTA	TAAACGCCAG	GAAGATGGTA	GTCTTCTACT	TAGTGATATG	420
GATCAACACA	GTGGCCAAGG	TCCACATGAA	AATCAAGCTT	CCCCCATGT	TCACTATACA	480
GATTTAACAC	CTGACCACTA	TCTAGTGACC	TGCGACTTGG	GAACTGACCA	AGTCATCACC	540
TATGACCTCG	ATCAAGAAGG	AAAATTATCT	AAGCTCTATA	CCTATCACAG	CAAGCCAGGA	600
GCAGGCTCAC	GCCATATCAT	TTTCCATAAC	CACTATAAAA	TCGCTTATCT	CATTTGTGAA	660
CTCAATAGTA	CTATCGAAGT	TTTAATCTAC	GATGGCGTTG	GCGAATTTGA	ACGTATGCAG	720
GTCATTTCAA	CTTTACCGGA	AGCTTACGAA	GGCTTTAATG	GAACCGCTGC	TATTCATCTC	780
TCTAAAGACG	GTAAATACCT	CTACGCTTCT	AACCGTGGCC	ATGATTCTAT	CGCAGTATAT	840
ACCATCCTTG	CGGACGGTAG	CTTAGAGTTA	TTAGAAATCG	TTCCAACGCA	TGGTCAGACT	900
CCACGTGATT	TTGATTTGAC	ACCCGACCAA	AAATTTCTCA	TTGTTGTCCA	TCAAGACTCT	960
GACAATGCAA	CTGTCTTTAA	ACGTAATTGT	GACAATGGTC	GTCTAGCAGA	ACTCTCCAAC	1020
GACTTCCATG	TTCCCGAAGC	AGTCTGCATC	CGTTTTGCTC	CTTAA		1065

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1086
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

CATATGTCTA	AATTACAACA	AATCCTAACA	TATCTTGAAT	CAGAAAAACT	AGACGTCGCT	60
GTCGTATCTG	ACCCCGTCAC	AATCAATTAC	CTCACTGATT	TTTACAGTGA	TCCCCATGAA	120
CGCCAAATGT	TCCTCTTTGT	CCTAGCAGAT	CAGGAACCTC	TCCTCTTTGT	CCCAGCTCTT	180
GAAGTAGAAC	GTGCAAGTAG	CACCGTTTCC	TTCCCACTAG	TGGGCTATGT	CGATTCTGAA	240
AATCCATGGC	AAAAAATCAA	ACATGCTCTT	CCACAACCTG	ACTTCAAACG	TGTCGCTGTT	300
GAGTTTGACA	ATCTCATCTT	GACCAAATAC	CATGGTTTGA	AAACAGTTTT	TGAGACTGCT	360
GAGTTTGACA	ACCTCACTCC	TCGTATCCAA	CGCATGCGCC	TCATCAAATC	AGCTGATGAA	420
GTGCAAAAAA	TGATGGTTGC	AGGTCTTTAT	GCTGACAAGG	CTGTTTCATGT	TGGTTTTGAC	480
AATATTTCTC	TTGATAAGAC	TGAGACAGAT	ATCATCGCAC	AAATTGACTT	TGCCATGAAA	540
CGTGAAGGTT	ACGAAATGAG	CTTTGATACC	ATGGTCTTGA	CTGGTGATAA	TGCTGCGAAT	600
CCACACGGCA	TTCCAGCAGC	TAATAAGGTT	GAAAAATGATG	CTCTTCTCCT	CTTTGACCTG	660
GGTGTTCCTG	TCAATGGCTA	TGCGTCAGAT	ATGACTCGTA	CAGTCGCTGT	CGGCAAACCA	720
GACCAATTCA	AGAAAGATAT	TTACAACTTG	ACTCTTGAAG	CCCAACAAGC	TGCTCTTGAC	780
TTTATCAAGC	CAGGTGTGAC	TGCTCATGAA	GTGGACCGCG	CTGCCCCTGA	GGTCATCGAA	840
AAAGCTGGTT	ATGGTGAGTA	CTTCAACCAC	CGTCTCGGGC	ATGGTATCGG	TATGGATGTC	900
CATGAATTCC	CATCTATCAT	GGAAGGAAAC	GACATGGTCA	TCGAAGAAGG	CATGTGCTTC	960
TCTGTTGAAC	CAGGTATCTA	TATCCCTGGT	AAAGTCGGTG	TTCGTATTGA	AGACTGCGGT	1020
GTTGTTACCA	AGGATGGCTT	CGACCTCTTT	ACAAGCACCA	GCAAAGATTT	GCTTTATTTT	1080
GATTAA						1086

(2) INFORMATION FOR SEQ ID NO:788:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

ATGATGTCTA	ACAAAAATAA	GGGAATTCTG	ATTTTTGCGA	TTCTCTATAC	AGTCCTCTTT	60
GTGTTTGATG	GCGTTAAATT	GCTGGCTTCT	TTAATGCCAT	CTGTCATTGC	AAATTATCTT	120
GTTTATGTAG	TTTTAGCTTT	ATATGGCTCC	TTCTTGTTCA	AGGATAGATT	GATCCAACAA	180
TGGAAGGAGA	TTAGAAAGAC	TAAAAGAAAA	TTCTTCTTTG	GCGTCTTAAC	AGGATGGCTC	240
TTTCTCATTC	TGATGACTGT	TGTCTTTGAA	TTTGTATCAG	AGATGTTGAA	GCAGTTTGTG	300
AGACTAGATG	GACAAGGTCT	AAATCAGTCT	AATATTCAAA	GTACCTTTCA	AGAACAACCA	360
CTACTGATAG	CTGTTTTTGC	TTGTGTCATT	GGACCTCTGG	TAGAAGAATT	ATTTTTCCGT	420
CAGGTCTTAT	TGCATTACTT	GCAGGAACGG	TTGCCAGGTT	TACTAAGCAT	TATTCTGGTA	480
GGACTTGTTT	TTGCTCTGAC	TCATATGCAC	AGTTTGGCCC	TATCAGAGTG	GATTGGTGCA	540
GTTGGTTACT	TAGGTGGAGG	CCTTGCCTTT	TCTATTATTT	ATGTGAAAGA	AAAAGAGAAT	600
ATCTACTATC	CCCTACTTGT	TCACATGTTA	AGCAACAGCC	TCTCCTTAAT	CATTTTAGCT	660
ATCAGTATAG	TAAAATGA					678

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: *misc_feature*
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GCATGGTCTA	ATAAAGCTAT	GGCATATAAT	ACTGATTTTA	AACAAGGAGC	ATTAGATTCC	60
ATCAAAGGAG	GGCACAGACA	TGTCGAGGCG	GCCAAAGTTT	TTTGGTGTTG	GCGTCAGAAC	120
TCTCTTCACG	TGGGAAAAGA	AAGACGTGAA	CAAAGGAAC	TAGAGCGGAA	AAAGCGAGTC	180
GTCAAAAAGC	GTAAGATCCC	TTTAGAAGAA	TTGAAAGCCT	TTGTAGAGGC	TCATCCAGAT	240
GCTTTTTTAC	GGGAAATTGC	GGCACATTTT	GATTGTGCTG	TTCCCTTCAGT	ATGGGCAGCT	300
TTAAAGCAGA	TTAAGGTCAC	TTTAAAAAAA	GATGACGATC	TTTAA		345

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

CCGCTGCCTA	AAGGAGAAGC	CATGTCAACA	TATAACTGGG	ATGAGAAGCA	TATCCTTACC	60
TTTCCTGAAG	AAAAAGTAGC	CCTTTCTACT	AAGGATGTCC	ATGTTTACTA	TGGTAAAAAT	120
GAATCCATTA	AGGGGATTGA	TATGCAATTT	GAAAGAAATA	AAATTACAGC	TTTGATTGGT	180
CCGTCCGGAT	CGGGGAAATC	TACCTACTTA	CGCAGTCTCA	ATCGCATGAA	TGATACCATT	240
GATATTGCTA	AAGTAACTGG	GCAGATTCTC	TATCGTGGAA	TTGATGTCAA	CCGTCCAGAA	300
ATCAACGTTT	ATGAAATGCG	TAAACACATT	GGAATGGTTT	TTCAACGCCC	CAATCCATT	360
GCTAAGTCAA	TTTACCGTAA	TATTACCTTT	GCGCATGAAC	GTGCTGGAGT	TAAGGATAAG	420
CAAGTCCTAG	ATGAAATCGT	AGAAACCTCC	CTTCGTCAGG	CTGCCCTCTG	GGATCAGGTT	480
AAAGACGATC	TCCACAAGTC	AGCCTTGACC	TTATCAGGTG	GTCAGCAACA	ACGTCTCTGT	540
ATCGCTCGTG	CCATCTCTGT	TAAGCCAGAT	ATCCTCTTAA	TGGATGAGCC	AGCCTCAGCC	600
TTGGATCCGA	TTGCGACCAT	GCAACTAGAA	GAGACCATGT	TTGAGCTCAA	GAAAAACTTT	660
ACCATCATCA	TTGTAACGCA	TAATATGCAG	CAGGCTGCTC	GTGCAAGTGA	CTATACAGGC	720
TTCTTTTACT	TGGGTGATTT	GATTGAGTAT	GACAAGACTG	CAACTATTTT	CCAAAATGCC	780
AAGCTACAGT	CCACCAATGA	CTATGTATCT	GGTCACTTTG	GTTAG		825

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 966 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

ATCATGCCTA	AGAAAATCCT	TGTTTTACAT	ACGGGTGGAA	CTATTTCCAT	GCAGGCCGAT	60
GCTTCTGGCG	CTGTTGTGAC	GAGTTCAGAT	AATCCCATGA	ACCATGTGTC	CAACCCACTT	120
GAAGGAATCC	AAGTCCACGC	CTTGGACTTT	TTTAACCTTC	CAAGTCCCCA	TATCAAACCC	180
AAACATATGC	TGGTCTCTA	CCAGAAAATT	AAAGAGGAAG	CAGATAACTA	CGATGGAGTG	240
GTGATCACAC	ACGGAACCGA	TACTTTAGAG	GAAACAGCCT	ATTTCTTGA	TACCATGGAA	300
GTTCCCCATA	TGCCTATCGT	TCTAACAGGA	GCCATGCGTA	GCTCCAATGA	GCTCGGTAGT	360
GATGGTGT	TTTATAATTACCT	AAGTGCTTTA	CGAGTGGCCA	GTGATGACAG	GGCTGCTGAC	420

AAAGGAGTTT	TGGTCGTTAT	GAACGATGAA	ATCCACGCTG	CCAAGTATGT	CACCAAAACA	480
CATACGACTA	ATGTCAACAC	CTTCCAGACT	CCAACACATG	GCCCCCTCGG	TCTCATCATG	540
AAACAGGAAA	TCCTCTACTT	CAAAACAGCT	GAACCTCGTG	TTCGCTTTGA	CCTTGATCAC	600
ATACAAGGTT	TAGTCCCTAT	CATCTCGGCT	TATGCTGGTA	TGACAGATGA	GCTGATTGAT	660
ATGCTGGATT	TAGAACACTT	GGACGGTTTG	ATTATCCAAG	CCTTCGGAGC	TGGTAATATT	720
CCCAAAGAAA	CGGCTCAAAA	ATTAGAAAAGC	CTTCTGCAAA	AAGGAATCCC	AGTCGCTCTG	780
GTATCACGAT	GCTTTAACGG	TATTGCCGAG	CCTGTTTATG	CCTACCAGGG	TGGGGGCGTA	840
CAGTTGCAAA	AAGCAGGCGT	TTTCTTTGTT	AAAGAACTCA	ACGCCCCAAA	AGCCCGCTTG	900
AAACTCCTCA	TCGCCCTCAA	TGCCGGACTA	ACAGGACAGG	CTTTGAAAGA	CTATATGGAA	960
GGCTAA						966

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

AAAGCGCCTA	AACAACTCAT	TAGAAAGTAT	CTTATGGAAC	ACATCAATCA	TACCACATTA	60
CTCATCGGAA	TAAAAGACAA	AAACATCACC	TTAAATAAAG	CCATTTCAGCA	CGATACCCAT	120
ATCGAAGTCT	TCGCTACACT	TGATTATCAC	CCACCTAAAT	GTAAACACTG	TAAAGGAAAA	180
CAAATCAAAAT	ACGACTTCCA	AAAGCCTTCT	AAAAATCCCTT	TTATCGAGAT	TGGTGGTTTC	240
CCTAGCCTCA	TTCATTTGAA	AAAGAGACGA	TTTCAATGCA	AGTCCTGTCG	GAAAGTCACT	300
GTAGCTGAAA	CAACTCTCGT	TCAGAAAAAT	TGCCAAATCT	CGGAAATGGT	GAGACAGAAA	360
ATTGCCCAAC	TCCTACTCAA	CAGAGAGGCT	CTTACACATA	TCGCTTCTAA	ATTAGCCATC	420
TCTACCTCTA	CCTCTACCGT	CTATCGTAAAG	CTCAAGCAAT	TTCATTTCCA	AGAGGATTAC	480
ACCACTTTGC	CTGAAATCCT	CTCCTGGGAT	GAATTCTCCT	ACCAGAAGGG	GAAATTGGCT	540
TTCATTGCTC	AGGATTTCAA	CACTAAGAAA	ATCATGACCA	TTCTTGATAA	CAGACGTCAA	600
ACAACCATCC	GAAATCATTT	CTTCAAGTAC	TCGAAAAGAAG	CTAGAAAAAA	AGTTAAAGTC	660
GTCACGTGTG	ATATGTCTGG	AAGTTATATC	CCTCTCATTA	AGAAATTATT	TCCCAATGCT	720
AAAATTGTTT	TCGATCGTTT	CCACATTGTC	CAACACATGA	GCAGGGCTCT	TAATCAGACT	780
AGAATCAACA	TCATGAAGCA	ATTTGATGAT	AAATCTCTGG	AATACAGAGC	TCTTAAATAT	840
TACTGGAAAT	TTATCCTAAA	AGATAGTCGG	AAACTCTCTC	TTAAGCCTTT	CTATGCTAGA	900
ACTTTCAGAG	AGACCTTAAC	TCCTAGGGAG	TGTCTGAAGA	AAATCTTTAC	TCTAGTACCT	960
GAACTTAAAG	ATTACTATGA	CCTGTATCAA	CTACTCCTAT	TTCATCTACA	AGAGAAGAAT	1020
ACTGACCAGT	TTTGGGGCTT	AATTCAAGAC	ACGTTACCTC	ATCTCAACCG	CACCTTTTAA	1080
ACCACTTTGA	GCACATTTAT	TTGCTATAAA	AACTACATCA	CTAACGCCAT	TGAATTGCCCT	1140
TATTCTAACG	CTAAACTTGA	GGCCACTAAC	AAACTCATCA	AAGACATCAA	GCGCAATGCC	1200
TTTGGTTTTT	GGAACCTTGA	AAACTTCAAA	AAACGGATTT	TCATCGCTCT	GAACATCAAA	1260
AAAGAAAGGA	CAAAATTTGT	CCTTTCTCGA	GCTTAG			1296

(2) INFORMATION FOR SEQ ID NO:793:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...510
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

ACCTACACTA	AAACATATAA	AGGGGGGAAA	CTTATGACAA	TTGTAGGATG	CCGTATTGAT	60
GGACGTTTGA	TCCACGGACA	AGTAGCCAAT	CTTTGGGCTG	GAAAACTAAA	TGTTTCACGC	120
ATTATGGTTG	TAGACGACGA	AGTTGTCAAC	AACGATATTG	AAAAGAGTGG	TTTGAAACTT	180
GCGACACCAC	CAGGTGTGAA	ATTGAGTATT	TTGCCAGTTG	AGAAAGCTGC	AGCCAATATT	240
CTTGCTGGCA	AATACGATAG	CCAACGTCTC	TTTATCGTGG	CTCGTAAACC	AGACCGCTTC	300
CTTGTTTGG	TAGAAGCAGG	TGTACCACTT	GAAACTCTTA	ATGTTGGGAA	TATGTCTCAA	360
ACACCAGAAA	CTCGTTCTAT	TACACGTTCT	ATCAACGTAG	TAGACAAGGA	TGTGGAAGAC	420
TTCCACAAAC	TGGCAGAAAA	AGGTGTTAAA	CTTACTGCTC	AGATGGTTCC	AAATGATCCA	480
ATTCAGACT	TTTGAGCTT	ATTAAAATAG				510

(2) INFORMATION FOR SEQ ID NO:794:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...924
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAAATGACTA	AAACAGCCTT	TTTATTTGCT	GGTCAAGGTG	CCCAGTATCT	AGGGATGGGA	60
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CGGGATTTCT	ATGATCAGTA	TCCGATTGTT	AAAGAAACGA	TTGATCGAGC	GAGTCAGGTG	120
CTCGGTTATG	ATTTGCGTTA	TCTCATCGAT	ACGGAAGAGG	ACAAACTCAA	TCAGACCCGC	180
TATACGCAAC	CAGCCATTCT	AGCGACTTCG	GTTGCTATCT	ACCGTTTATT	GCAAGAAAAG	240
GGCTATCAGC	CTGATATGGT	CGCTGGTTTG	TCTCTTGGAG	AATACTCTGC	CTTGGTGGCA	300
AGCGGCGCCT	TGGATTTTGA	AGATGCGGTT	GCCTTGGTAG	CTAAGCGTGG	AGCCTATATG	360
GAAGAAGCGG	CTCCTGCTGA	CTCTGGCAAG	ATGGTAGCAG	TTCTCAATAC	GCCAGTAGAG	420
GTCATTGAAG	AAGCCTGTCA	AAAAGCTTCT	GAAC TTGGAG	TGGTTACTCC	AGCCAACTAT	480
AACACACCTG	CACAAATCGT	CATTGCTGGA	GAAGTGGTTG	CAGTTGATCG	AGCGGTTGAA	540
CTTTTGCAAG	AAGCAGGTGC	CAAACGCTTG	ATTCTCTTTA	AGGTGTCAGG	TCCCTTTCAC	600
ACCCTCTCC	TTGAGCCAGC	TAGCCAGAAA	CTAGCTGAAA	CTCTAGCTCA	GGTAAGTTTT	660
TCAGATTTTA	CTTGTCCTT	AGTCGGCAAT	ACAGAAGCTG	CTGTGATGCA	AAAAGAGGAC	720
ATTGCTCAGC	TCTTGACGCG	TCAGGTCAAG	GAACCCGTTT	GTTTCTATGA	AAGTATTGGG	780
GTCATGCAAG	AAGCAGGCAT	AAGCAACTTT	ATCGAGATTG	GACCGGGGAA	AGTCTTGTCA	840
GGTTTTGTTA	AAAAAATTGA	TCAAAGCTG	CACTTAGCTC	ATGTGGAAGA	TCAAGCGAGT	900
TTAGTAGCAC	TTTTAGAAAA	ATAG				924

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

TTCATGGCTA	AGGTGTTATT	AGGGTTTATG	GGGGCTGGAA	AATCGACTAT	TGCAAGAGGC	60
TTGGACACTA	ATTACCTTGA	TATGGATGCT	CTGATTGAGA	AGCGCCTAGG	TATGTCCATT	120
GCGAATTTTT	TCGCTGAAAA	GGGAGAAGAG	ACCTTTCGTC	AGGTAGAATC	AGAAGTCCTA	180
GCTGATTTAC	TACAAACAGA	CCAAGTCGTG	TCAACTGGAG	GAGGAGTGGT	TATTTCTCAG	240
AGAAATCGTG	ACTTACTCAA	GACTAATACA	GATAACATCT	ACCTGAAAGC	AGATTTTGAA	300
ACCCTCTACC	AACGTATCGC	AGCTGATAAG	GACAATCAGC	GACCGCTTTT	TCTAAATAAT	360
AGCAAGGAAG	AACTAGTAGC	TATTTTTCAT	GAAAGACAGG	CTTGGTATGA	GGAAGTGGCT	420
AGTCGGGTTT	TGGATGTGAC	CAAGCTAAGC	CCAGAGGAAA	TTATAGAGGA	ACTAAGATGA	480

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GCTCGGGCTA	AATCAGTCCA	CTGGACTGAT	TTACTACACC	AGGATAGCTT	CAAGCTCTGT	60
CAGAAACGAT	TCTATCAGCC	CACGTTTCGA	ATGCACTTAA	CCCATCGGGA	AGTACGAGAT	120
AAACTGCTTT	CTTACTCTGA	GGGATTACAG	GTTCACTACG	AACTCTATCA	ACTCCTGCTC	180
TTTCATTTTC	AAGAGAAGAA	TGCCGACCAT	TTCTTTGGAT	TGATTGAGCA	AGAACTGCCA	240
ACGGTTCATC	CGCTTTTTC	AACGGTCTTT	TGGACTTTTT	TAAGGGATAG	AGATAAGATT	300
ATCAACGCAC	TTAAGCTGCC	TTATTCCAAC	GCTAAACTTG	AAGCGACCAA	TAATTTGATT	360
AAGGTATCA	AGTGCAAAGC	CTTTGGTTTC	CGGAACTTTA	ACAATTTTAA	AAAACGGATT	420
TTGATGACTT	TGAACATCAA	AAAAGAGAGT	ACGAATTTTC	TACTCTCCAG	ATTGTAA	477

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

ATCTATTATA	ACAAAGGAAT	GAGAAATATG	AAGGCAAAAT	ATGCTGTTTG	GGTGGCTTTT	60
TTCTTAAATT	TGACTTATGC	CATTGTTGAG	TTTATTGCAG	GTGGAATATT	TGGTTCTAGC	120
GCTGTTCTTG	CTGACTCTGT	GCATGACTTG	GTAGATGCGA	TTGCAATTGG	AATATCAGCT	180
TTTCTAGAAA	CAATCTCCAA	TCGTGAAGAA	GACAATCAGT	ACACCTTGGG	CTATAAGCGG	240
TTTAGCCTGC	TAGGAGCCTT	GGTAACAGCT	GTGATTCTCG	TAACGGGCTC	TGTTCTAGTC	300
ATTTTGGAAT	ATGTCACGAA	GATTTTGCAT	CCGCAACCAG	TCAATGATGA	GGGGATTCTC	360
TGGTTAGGAA	TTATTGCGAT	TACTATCAAT	CTGTTAGCGA	GTCTGGTGGT	TGGTAAGGGA	420
AAGACAAAGA	ATGAGTCTAT	TCTGAATCTG	CATTTTCTGG	AAGATACGCT	AGGGTGGGTA	480
GCTGTTATCC	TGATGGCGAT	TGTTCTTCGA	TTTACGGACT	GGTATATCCT	AGATCCTCTT	540
TTGTCCCTTG	TCATTTCTTT	CTTTATTCTT	TCAAAAGCCC	TTTCACGTTT	TTGGTCTACA	600
CTCAAGATTT	TCTTGATGTC	TGTGCCAGAA	GGTCTTGATA	TCAAGCAAGT	AAAGAGTGGC	660

CTGGAACGAT	TGGATAATGT	GGCCAGCCTT	AATCAGCTTA	ATCTCTGGAC	TATGGATGCT	720
TTGGAAAAAA	ATGCCATTGT	CCATGTTTGT	CTAAAAGAAA	TGGAACATAT	GGAAACTTGT	780
AAAGAGTCTA	TTCGAATTTT	CCTAAAAGAT	TGTGGTTTTT	AAAATATTAC	CATTGAAATT	840
GATGCTGACC	TAGAAACTCA	CCAAACCCAT	AAGCGAAAGG	TGTGTGACTT	GGAACGGAGT	900
TATGAGCATC	AACATTAG					918

(2) INFORMATION FOR SEQ ID NO:798:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

AGACCCTATA	AAATTCCTTA	CCTTGAGACA	ACTGGTATGC	CTACTAGAAT	TCTCCTTAGA	60
AAGCGTCGCT	TTAAGTGCTA	TCACTGTTCA	AAAATGATGG	TCGCTGAAAC	TTCTATCGTC	120
AAGAAGAATC	ACCAAATCCC	TCGTATCATC	AACCAAAAGA	TTGCTCAAAA	GTTAATTGAA	180
AAGATTTCTA	TGACTGATAT	TGCCCATCAG	CTGGCCATTT	CAACTTCAAC	TGTCATTTCGC	240
AAGCTCAATG	ACTTTCACCT	TGAGTGTAAT	TTTAGAAATC	TGCCTAAGAT	TATGTCCTTGG	300
GACGTTGAAA	CAGTCCGGGG	AGTGACTGTT	TCAATCGGGA	GATGGAGATG	A	351

(2) INFORMATION FOR SEQ ID NO:799:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2040 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

AAATACTATA	AGTATGCTAA	AATAGGAATA	GCACATGGAG	AGAGGATTCT	TATGATCAAT	60
CACATTACAG	ATAATCAATT	TAAACTAGTA	TCAAAAATATC	AACCATCAGG	AGATCAACCC	120
CAAGCTATCG	AGCAGTTGGT	GGATAACATT	GAGGGGGGAG	AAAAAGCTCA	GATTCTGATG	180
GGGGCGACTG	GAACAGGGAA	GACCTATACT	ATGAGTCAGG	TCATTTCTAA	AGTCAATAAA	240
CCAACTCTGG	TTATTGCCCA	CAATAAAACT	CTGGCTGGTC	AGCTCTATGG	GGAGTTTAAG	300
GAATTTTTTC	CTGAAAATGC	AGTTGAGTAT	TTCGTATCCT	ACTATGATTA	TTACCAGCCA	360
GAGGCCTATG	TCCCTTCTAG	CGATACCTAT	ATTGAGAAGG	ATAGTTCTGT	CAATGACGAG	420
ATTGACAAGC	TTCGCCACTC	AGCTACCTCA	GCCCTTTTGG	AGCGTAATGA	TGTTATTGTC	480
GTGGCCTCAG	TCTCTTGAT	CTATGGTTTG	GGTTCGCCCA	AGGAATACGC	TGATAGTGTC	540
GTTAGTCTCC	GTCTTGGTCT	AGAGATTTCT	CGTGATAAAC	TCTTGAATGA	CTTGGTCGAT	600
ATTGAGTTTG	AACGCAATGA	TATTGATTTT	CAACGCGGAA	GATTTTCGCGT	TCGTGGGGAT	660
GTGGTAGAGA	TTTTCCCAGC	TTCCCGAGAT	GAACATGCCT	TTCGAGTAGA	ATTTTTTTGGA	720
GACGAAATTG	ACCGTATTCG	TGAAGTTGAG	GCTCTGACAG	GTCAGGTGTT	GGGAGAAGTG	780
GATCATTTAG	CGATTTTCCC	AGCGACACAC	TTTGTGACCA	ATGACGACCA	CATGGAAGTT	840
GCCATTGCAA	AGATTTCAGGC	CGAGTTGGAA	GAACAAATTA	CTGTCTTTGA	AAAGGAAGGT	900
AAACTGCTTG	AAGCCCAGCG	TTTGAACAG	CGGACAGAGT	ATGATATCGA	AATGTTGCGT	960
GAGATGGGCT	ATACCAATGG	GGTTGAAAAT	TATTCTCGCC	ACATGGATGG	ACGGAGCGAA	1020
GGAGAGCCTC	CTTATACGCT	TCTCGACTTC	TTCCAGATG	ATTTCTTGAT	TATGATTGAC	1080
GAGAGTCATA	TGACCATAGG	GCAAATCAAG	GGCATGTACA	ATGGAGACCG	TTCCGCTAAA	1140
GAAATGCTGG	TTAATTATGG	TTTCCGTTTG	CCGTCTGCTT	TGGACAATCG	TCCTCTACGT	1200
CGGGAGGAGT	TTGAGAGTCA	CGTTCATCAG	ATTGTTTACG	TTTCAGCGAC	ACCTGGTGAC	1260
TATGAAAAATG	AACAGACCGA	GACAGTGATT	GAGCAAATCA	TTCTGTTCAAC	GGGACTCTTG	1320
GATCCAGAGG	TGGAAAGTCCG	TCCGACTATG	GGACAGATTG	ATGACCTCTT	GGGTGAAATC	1380
AATGCCCGCG	TTGAAAAAAA	TGAGCGTACC	TTTATCACAA	CTTTGACCAA	GAAAAATGGCA	1440
GAGGACTTGA	CCGACTACTT	CAAGGAAATG	GGTATCAAGG	TCAAGTACAT	GCACTCGGAT	1500
ATCAAGACCT	TGGAACGGAC	GGAGATTATC	CGTGACCTGC	GCTTGGGTGT	CTTTGATGTC	1560
TTGGTTCGGAA	TTAACCTGCT	CCGTGAAGGA	ATTGACGTTT	CTGAAGTGAG	CCTCGTAGCT	1620
ATTCTCGATG	CTGACAAGGA	AGGTTTCCCT	CGCAACGAAC	GTGGACTCAT	CCAGACTATT	1680
GGACGTGCTG	CTCGTAACAG	TGAAGGCCAT	GTCATCATGT	ATGCAGACAC	GGTTACCCAG	1740
TCTATGCAAC	GTGCTATCGA	TGAAACTGCC	CGCCGTCGGA	AAATTCAGAT	GGCCTATAAT	1800
GAAGAGCATG	GTATCGTACC	ACAGACAATC	AAGAAAGAAA	TCCGTGACCT	GATTGCCGTG	1860
ACCAAGGCAG	TTGCTAAGGA	AGAGGACAAG	GAAGTCGACA	TCAATAGCCT	CAACAAACAA	1920
GAGCGCAAAG	AACTCGTCAA	GAAACTAGAA	AAACAAATGC	AAGAAGCCGT	CGAAGTGCTT	1980
GACTTTGAAC	TGGCGGCTCA	GATCCGTGAT	ATGATGTTGG	AAGTCAAGGC	CTTGGATTAG	2040

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

ATTTGCTATA	ATAGGACCAT	GGAAGAAGAA	CAATTATTAA	AATCAGGAGA	GCGCATTAAC	60
CAGCTCTTTT	CGACAGATAT	CAAAATCATT	CAAAATAGAG	AGGTTTTTTAG	CTATTCGGTG	120
GATAGTGTTT	TCTTATCACG	ATTTCCACGT	TTTCCTAAGA	AGGGGTTGAT	TGTGGATTTT	180
TGTGCTGGGA	ATGGAGCAGT	GGGGCTTTTT	GCTAGCACTC	GTACTCAAGC	ACAGATATTG	240
TCTGTTGAGA	TTTCAGGAGC	GTTTGGCGGA	TATGGCTGA			279

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

ATTTGCTATA	ACAATGTCTT	AGCCATCCTT	ACTCATCTC	CATTGATTAA	TCTAGCTTTT	60
TTAGCCTTGA	TTGTAATTAA	CCTTCTGGTT	GCTTATTTTC	AAATAGGACT	CCTCTTTTATT	120
GGTGCTCGTC	ATCTCCTCTA	TAATGAAAAG	CGAAGGCTAA	TTGAGTATAT	CCGCAAGGTT	180
TTCCATGAAA	GTTTTGGATT	TATGAAAAAG	CTAACTTGCG	CTAAAGCCTT	GTTTATCTTT	240
TTCTATATAG	CTATGCTGTT	TCCTTTTATA	CGGAAAATGC	TGAAGATTTA	TTATCTTAAT	300
AAAATCGTCA	TTCCAGAGTT	TATCCAAGCT	TATTTAGAAG	ATAGATATTG	GATGTGGTGG	360
CTGAGCATCC	TACTTCTATC	TCTTATCTTT	CTCTATGTCT	CTGTCAGATT	GATGTTTGCC	420
CTTCCGAAGA	TTGTATATGA	TCAGCTGACT	GTTTCGAGAAG	CAGTGATGTT	TAGCTTGGAG	480
AAAACCAAGA	AGAGAGTTAC	TTTTTATGCT	TGGAATTTAT	TTTACATCTT	GCTCAAAGCA	540
CATTTATTAT	TTTATCTTCC	TTTGATTCCCT	TTATTATTGG	CTCAAACCTT	GGTAGATGAT	600
ATCACTCAGA	GAGAGTCTCT	GATTCTTGGT	ATTTTGAATT	TTGTCGTGAT	TAAAAATCTC	660
TATTATATGG	CTCTGACTTA	TTCCCCGGTT	AAATTTGTTT	CATTTTTTGAC	AGGAAAGGAG	720
CTGGATATGC	TTCTTAGGAG	AGAAAAAGAT	CACATCGTGC	GATGGGGTGT	CATGACTTGT	780
GCCAGTCTTT	TCTTTGCCCT	AGAAGGTTAT	ATTTATCTGG	AGGCTCCCAT	GGTTCATCTA	840
CCTCAACTTA	TTTCTCACCG	AGGGGTTTCC	AATGCAAATG	GGATTCAAAA	TACAGTAGAG	900
TCCTTGGAAG	CTACAGCACA	ACTCAAACCA	GACTTGGTGG	AGACGGACGT	GCAGGAAACA	960
AAAGATGGGC	AGTTTGTCAT	GATGCATGAT	GCTAACTTGA	AAAATCTAGC	AGGTATCAAT	1020
AAAAGTCCTC	AAGACTTAAA	CTTGGAGGAG	CTTAAAGGGA	TTGATATTTT	TGAAAATGGC	1080
TACCAGACTA	AAATTTCAAG	CTTTGAAGAT	TATCTCAGTC	GAGCCAACGA	ACTTGGTCAA	1140
AAATTACTAA	TTGAAATPAA	AACCAGTAAA	AAAGATAGTC	CAGACATGAT	GAACCGCTTT	1200
TTAGCCCCGT	ATGCTGCAAT	GCTCAAGATT	TATGGACATC	AAATCCAGTC	TTTAGACTAC	1260
CATGTTGTCG	AAAAAGTAAG	ACAGTATGAT	GCCGAACTGC	CAGTTTATTT	CATCATGCCC	1320
TACAATTCTG	TCTTTCCTAA	AACAAGAGCG	ACAGGATATA	CTATGGAGTA	CTCAACCTTG	1380
GATGAATATT	TTGTAAGCAA	ACTATGGACA	ACGGATCAGA	AACTTTATGT	CTGGACTGTC	1440
AATGATTCAG	AAGCTATCAG	CAAATCTCTT	CACCTAGGAG	TAGATGGAGT	GATTACAGAT	1500

GATTTGGAAA AAGTTCAGCG GGAAATAGAA GTAGCCCAAG AAGATCCAGA ATATACGGAT	1560
TTGCTCTTGA AAAAAAGCATT GGAATTCTTT GAATTTTAG	1599

(2) INFORMATION FOR SEQ ID NO:802:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...726
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

CATTCATATA ACATAAAAAA GGGAGGAACT GTTATGGATG CAATCTTTGA CCTAATCGGA	60
AAGGTTTTCA ATCCCATCTT AGAAATGGGT GGACCTGTCA TCATGTTAAT CATTTTGACA	120
GTATTGGCTT TACTTTTTGG AGTGAAATTC TCCAAAGCGC TTGAAGGTGG TATCAAACCTT	180
GCCATCGCTC TTACAGGTAT CGGTGCTATC ATCGGTATGC TAAATGGTGC TTTCTCAGCA	240
TCACTTGCAA AATTCGTTGA AAACACTGGT ATACAATTGA GTATTACCGA CGTTGGTTGG	300
GCACCACTCG CAACAATCAC TTGGGGTTCT GCTTGGACAC TATACTTCTT GCTCATCATG	360
TTGATTGTCA ACGTAGTGAT GCTTGCTATG AAGAAAACCG ATACACTTGA TGTCGATATC	420
TTTGATATCT GGCACCTGTC TATCACAGGT CTCCTGATTA AATGGTATGC TGATAACAAT	480
GGTGTGAGTC AAGGGGTTTC ACTCTTTATT GCTACAGCAG CTATCGTCCT TGTCGGTGTG	540
TTGAAAATTA TCAACTCTGA CTTGATGAAA CCTACATTTG ATGACCCTTCT TAACGCCCCA	600
AGTTCATCAC CAATGACATC AACTCACATG AACTACATGA TGAACCCAGT TATCATGGTT	660
TTGATAAGA TTTTGTAAAA ATCTTCCCAG GCCTTGATAN ATATGACTTT GATGCTGCTA	720
AATTGA	726

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GTAAATATA	ATAATAAAGG	AGTTAAAACA	ATGACAGTAA	TTAATAAATT	TGTTTTAATG	60
GAGCAAGCAA	AAAAAGTTTT	AAAAAATGCT	TACTGTCCGT	ATTCCAAATT	TCCTGTAGGT	120
GCAGCAATTT	TATTTAAAGA	TGGTAAAGTA	ATTACAGGAG	CAAATATAGA	AAATGTATCG	180
TTTGGTGTA	CTAACTGTGC	AGAACGTAGT	GCTATTTTTT	ATGGGGCTTC	TCAAGGATAT	240
AGAAAAGGAG	ATATTCTTGC	GATTGCTGTT	GCAGGTGAAA	CTGAAGACTA	CTTACCACCA	300
TGCAACATTT	GTCGTCAAGT	TATGGTAGAA	TTTTGTGAGC	CTGATACCTT	AGTCTTTCTA	360
TTAAATGGTA	AGGGAAACAT	ACTTGAATTG	CGATTAGAGG	AATTAGTCCC	ATATTCGTTC	420
TCAAGTCTAG	AAATGTAA					438

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

AAAATGTATA	ACTACCCTAT	GCGCATTTCAT	TACCATCGTA	AGAATGGAGA	ATATGACACT	60
TGCTCCTTTG	TAAAAAGTCA	GGATCAACGA	ATTGATTTGC	TAACCTACAA	AGAAGATTAT	120
TTTGGAGCTT	TATTTAGCTT	TGAACACCCA	AGTTCACATG	TTATAGAAAAG	CTTGAATTTT	180
GTGGTTCATA	CAGGTCAAAC	TAGTAAAGAA	TATTCTATCC	GTTTTAATCA	CTATCCCCTA	240
TTAACAGAGG	TCTGGATTTT	GGAAGGCGAT	GATAGGATTT	ATTACTCTGA	AAATCCTGCT	300
ATTGCCAGTC	CTTTCTATAA	AAATCAAAAT	CCTTTTGCCT	TTGATAAGGC	CATTAACAGT	360
GCTAGTTTTG	ATCATCATTG	GGGTTACCAA	GGAGAATTGG	GTTGCCGTGT	AGAGGACAAT	420
CAGGCTCATT	TTTCCCTCTG	GTCACCTACA	GCGACAAAAG	TGCAAGTTGT	CGTTTATGAA	480
TCAGCTGCTA	ATGATGCACC	CGTTTGGAA	ACTTTTGAAG	TGAAAAGAGG	CAATAGCTAC	540
TCTTATAATC	ATAAGGACAA	TACAATCGGT	GTCTGGAGTT	TGGATGTTGA	AGAAGATTTG	600
GTAGGTAAGA	CTTATCAGTA	TCAAGTCCAA	TTCCCTCATC	ACCAAACACT	GACACGTGAT	660
CCTTATACAA	TCGCGACCAG	CCCTGATGGC	AAACGTTTCA	CTATTCTGAG	CCATGTAGAA	720
AAGCAAGTTG	AAAACCTTCGA	GGTTAAGCAC	GGTTCGGAGG	CTACTTGGCG	CTTGGAAAAT	780
CCATGTAAAG	CAGTTATCTG	TGAAATGCAC	ATTTCGTGATT	TGACTAAATC	ACCTACATCG	840
GGTGTAGATG	AACATCTTCG	AGGAACTTTC	TTGGGTGCTG	CTCAGGCTGG	AACAGTTAAC	900
CAATACGGCC	AGTCAACTGC	TTTTGATTAC	ATCAAGAAGC	TGGGCTACAA	TTATGTTCAA	960
TTGCAACCAA	TTGCAGACCG	TCATAAAGAA	TACGATGAGG	ATGGAAATGT	AACCTACAAC	1020
TGGGGTTATG	ATCCACAAAA	CTATAACGCG	CCAGAAACTA	GTTTTTCAAC	TAATCCAGAT	1080
GATCCAGCTC	AGGTCATTTC	TGATTTGAAG	GTGATGGTTC	AAGCTTATCA	CGATGCGGGT	1140

ATTGGAGTCA	TTATGGATGT	AGTCTATAAC	CATACCTTCT	CAGTTGTTGA	TGCACCATTC	1200
CAAACAACAG	TCCCTGATTA	CTATTATCGT	ATGAATCCAG	ATGGTACCTT	CCAGAATGGA	1260
ACGGGTGTTG	GAAATGAAAC	AGCCAGTGAA	CACGAAATGT	TTCGCAAGTA	TATGATTGAT	1320
TCTCTTCTAT	ACTGGGTGCA	GGAATATAAT	ATTGACGGCT	TCCGTTTTGA	CTTGATGGGG	1380
ATTCATGATG	TCAAGACCAT	GCAGATGATT	CGTCAAAGCT	TGGATGAAAT	CGACTCCAAC	1440
ATTATCCTCT	ATGGAGAAGG	ATGGGATATG	GGAACAGGTC	TTGCCCCCTTA	TGATAAGGCC	1500
AAGAAGGACA	ATGCCTACCA	GATGCCAAAT	ATTGGTTTTCT	TTAATGACAA	TCAGCGCGAT	1560
GCTGTCAAAG	GGGGAGAAAGT	TTATGGTGCT	ATCAAGTCAG	GTTTTGTCAG	TGGTGCTGCG	1620
ACAGAGCCAA	TTCTAGCTAA	AGCAATCCTA	GGAAGTCGTG	AATTAGGAAG	CTATACACAT	1680
CCAAATCAGG	TGCTTAACTA	TGTAGAAGCC	CATGACAAAT	ACAATCTTCA	CGATTTATTG	1740
GCAACCC TTC	ATCCAGACCA	AAGTTCAGAG	CAAATCATGC	GCAAGGTCGA	AACTGCCACA	1800
GCCATGAATC	TGCTCATGCA	GGGGATGGCC	TTTATGGAAA	TCGGTCAAGA	ATTTGGTCGT	1860
ACCAAAC TGG	TTGCGACTGG	TGAAAATGGT	GAGTTGACCC	ATGATGATAG	AGAGCGTGCG	1920
ATGAATAGCT	ATAATGCTCC	TGACAGTGTG	AACCAAGTGA	ACTGGAAC TT	GATTAATGAG	1980
CGTCAAGACA	GTATTGAGTT	TATCCGTCAA	GTCATCCGAT	TGAAGACAAA	AACTGGTGCC	2040
TTTTCTTACT	CTAGCTATGA	TGAAATTTAC	CATCATGTCT	TTGTGCATTC	TGCGATTGAA	2100
CATAGCGGCT	GCCTTATCTA	TGAAGTTCAC	GGCAAAGAAC	ACCTCTTGGT	AGTTGTGAAT	2160
GCTAAATCAG	AACCCTATCA	ATTTGAAAAAT	GCAGGAAAT T	TAGCTATGTT	GGTAACCAAC	2220
AGTCGCTCAA	AAGAAGATAA	TGTTTTAAAT	GATATTAGTC	TAGCTGTCTT	GAGTGTTTTA	2280
TAA						2283

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

AAATGGTATA	ATATAGTGAG	AAGGATAGAG	GAGAAGTGTA	AATTGATCGC	ACAAATAGAT	60
ACAAAAACAG	TCTATAGTTT	TATGGAAAGC	GTCATTT CGA	TCGAAAAGTA	TGTGAGAGCA	120
GCTAAAGAAT	ACGGCTACAC	TCATTTGGCT	ATGATGGATA	TTGACAATCT	TTATGGCGCT	180
TTCGACTTTC	TAGAGATTAC	AAAAAAATAC	GGCATTCATC	CTTTGCTAGG	GCTTGAAATG	240
ACAGTGT TTG	TAGATGATCA	GGGAGTAAAT	TTGCGCTTTT	TAGCTCTATC	TAGTGTGGGC	300
TATCAGCAGT	TGATGAAGCT	TTCGACAGCC	AAGATGCAGG	GGGAGAAAAC	TTGGTCAGTC	360
CTGTCCCAGT	ACCTGGAGGA	TATCGCGGTC	ATTGTGCC TT	ATTTTGATAG	AGTTGACTCG	420
TTAGAAGTAG	GTTTAAATAA	GCCTTACACC	AGCAAT			456

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

GTTATTCATA	AAAATTTCTC	TATCAAATAT	CATAATGCGT	CGTTTAAGGA	GATGGTTACA	60
ATGCAATATA	GTTGTGGAAA	AATAAATATT	AATATCCCTG	ATGGATATGG	AGACATTAAG	120
GATATAGTGT	TTTCGGCTCA	TATTATAGTT	AGGTATAATA	ATGGACATTG	TGGAGGTATA	180
GATCCGCATA	TAATTGGACT	TTGTAAAAAG	CAGATCAGAA	GGATGTCTCT	ATATCCTATT	240
TTGATAATCG	TATCTAGAGA	TTCAAAGGTT	ATTGATGATT	ATAAAAATTT	AGATATTGCC	300
TATGTTGATT	GTACTCAATG	TTCAAATAAT	TTTGAAACTG	CCTTACACGT	TAAAAATATT	360
TTAAAAATTAT	TAAAAATCCG	ACTTATACAC	TGTCATGGCT	ACTCAACTAA	TTATTTTTTA	420
TATATGTTAA	AAAAACTTGA	CAAGAATGGA	TTTGGAAAGG	TTAAGACAGT	GATAACATGC	480
CATGGATGGG	TTGAATATAA	CTTAAAAAAG	AAATTCCTGA	CTTATTTTGA	TTTTTGGACA	540
TATTCTATGG	GAGATGCTTT	TATTTGTGTA	TCTGAAACTA	TGAAAAAAG	ATTGGAGAGT	600
ATAATAAAAA	AATAA					615

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

GCGAATCATA	AAAAATTTCA	TTTTGATTTT	AAAACAGTTC	AAGAAAGTCA	AAAAATTATT	60
CTATTTGAAA	GAGAGGTGCC	GACTGTGAAA	GTCAATAAAA	TCCGTATGCG	GGAAACAGTG	120
ATTCCTACG	CTTCCTAGC	ACCAATATTA	TTCTTCTTTG	TCATCTTTGT	GTTGGCTCCG	180

ATGGTGATGG	GCTTCATTAC	AAGTTTCTTT	AACTACTCAA	TGACTAGATT	TGAGTTTGTA	240
GGCTTGGATA	ACTATATCCG	TATGTTTAAA	GATCCTGTCT	TTACAAAATC	TCTGATTAAC	300
ACAGTTATTT	TGGTTATTGG	ATCTGTACCA	GTTGTTGTTC	TATTCTCACT	CTTTGTAGCA	360
TCTCAGACCT	ATCATCAAAA	TGTCATTGCC	AGATCCTTCT	ACCGTTTCGT	CTTCTTCCTT	420
CCTGTTGTAA	CGGGTAGTGT	TGCCGTGACA	GTTGTTTGGA	AATGGATTTA	TGACCCGCTA	480
TCAGGGATTTC	TAAACTTTGT	CCTTAAGTCA	AGCCACATCA	TCAGCCAAAA	CATTTCTTGG	540
TTGGGAGATA	AAAAC TGGGC	ATTGATGGCG	ATTATGATTA	TTCTCTTGAC	CACTTCAGTT	600
GGTCAGCCCA	TCATCCTTTA	TATCGCTGCC	ATGGGGAATA	TTGACAATTC	ACTGGTTGAA	660
GCGGCGCGTG	TTGATGGTGC	AACTGAGTTT	CAAGTTTTTTT	GGAAGATTAA	ATGGCCAAGC	720
CTTCTTCCAA	CAACTCTTTA	TATTGCAATC	ATCACAACAA	TTAACTCATT	CCAGTGTTTC	780
GCCTTGATTTC	AGCTTTTGAC	ATCTGGTGGT	CCAACTACT	CAACAAGTAC	CTTGATGTAC	840
TACCTTTACG	AAAAAGCCTT	CCAATTGACA	GAATACGGCT	ATGCCAACAC	AATTGGTGTC	900
TTCTTGGCAG	TCATGATTGC	TATCGTAAGC	TTTGTTCAAT	TTAAAGTACT	TGGAAACGAC	960
GTAGAATACT	AA					972

(2) INFORMATION FOR SEQ ID NO:808:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

AGTAGTCATA	AGAAAATGAG	TACAGATAAA	AGGAGCAAAT	CAATGCCAAA	TTACAATATT	60
CCATTTTCAC	CGCCTGATAT	CACAGAAGCA	GAAATTGCTG	AAGTAGCGGA	TACCCTGCGT	120
TCTGGTTGGA	TCACAACAGG	TCCTAAAACA	AAAGAACTGG	AGCGCCGCTT	GTCTCTTTAC	180
ACACAGACAC	CTAAGACTGT	TTGTCTCAAC	TCTGCGACAG	CGCTCTGGAG	TTGA	234

(2) INFORMATION FOR SEQ ID NO:809:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

GATTGGCATA	AAATGGTTGA	ATCGTATAGT	AAGAATGCTA	ACCATAACAT	GCGTCGTCCT	60
GTCGTCAAAG	AAGAAATTGT	AGACTTGATG	CGTCAGCGTC	AAAAGCAGGT	CACAGGTTTC	120
TTGAAAGAAT	TGAAGACTT	TGCCCCGAAG	GAAAATATTC	CTATTATTCC	CCATGAAACG	180
GTTGCTTATT	TCCGTTTTCT	TATGGAAACC	ATGCAGCCTA	AAAATATTCT	GGAAATTGGG	240
ACGGCTATCG	GTTTTTCAGC	TCTCTTGATG	GCTGAACATG	CGCCAAATGC	TAAGATTACA	300
ACTATTGATC	GTAATCCAGA	AATGATTGGT	TTTGCCAAGG	AAAATTTTGC	CCAGTTTGAC	360
AGTCGCAAGC	AAATCACTCT	CCTAGAGGGA	GATGCGGTGG	ATGTCTTATC	TACACTGACA	420
GAGTCTTATG	ATTTCTGCTT	TATGGATTCT	GCCAAGTCTA	AATACATCGT	CTTTCTGCCA	480
GAAATCCTCA	AACATTTGGA	AGTTGGTGGT	GTGGTTGTCT	TGGATGATAT	TTTTCAAGGT	540
GGTGATGTTG	CCAAGGATAT	TATGGAAGTC	CGTCGTGGTC	AGCGAACCAT	TTATCGAGGC	600
CTTCAAAAAT	TATTTGATGC	AACCTTAGAC	AATCCAGAAC	TCACCGCAAC	ATTAGTGCCCT	660
TTAGGAGATG	GTATTCTCAT	GCTTCGTAAA	AATGTAGCAG	ATGTTCAACT	GTCTGAAAGC	720
GAATGA						726

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

ATGAAAAATA	AGCGTTATTT	TTTGGACACA	ATTTTAATAA	TTTACTGCT	TATAAGCACG	60
ATATTTTGTG	TCAGCCCAGT	ATTTATAAAA	TTGGACATCT	TAGGAACTCC	CTCTCATGCC	120
ATCTTAACCT	TTGTATTGGC	GATACCGTTA	TTCTATATTT	TGTCTCAATG	CTTACATACT	180
TTGCTATTAC	TAGTTTCCTC	AATCTTTTGT	AAATTAAGAC	CAATTTATTT	TTATTTTATA	240
TTTGTGATCA	TTATAGGAGC	GGATGAATTA	TAA			273

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...654
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

AAGGAAAATA	AGATGATTGA	TATTCAAGGA	TTGGAAAAGA	AATTTAATGA	CCGCGCGATT	60
TTCTCTGGTT	TGAATCTCAA	GCTGGAGAAAG	GGCAAGGTTT	ATGCCTTAAT	CGGAAAGAGT	120
GGAAGCGGAA	AGACGACGCT	GCTGAATATC	TTGGGAAAGC	TAGAAAAGAT	AGATGGAGGA	180
AGGGTTCTCT	ATCAGGGGAA	AGATTTAAAA	ACCATTCCCA	CTCGTGAGTA	TTTTCGAGAT	240
CAGATGGGCT	ATCTCTTTCA	AAATTTTGGC	CTCTTAGAAA	ACCAATCAAT	CAAAGAAAAT	300
TTGGATTGGG	GTTTTGTTGG	TCAGAAAATC	TCAAAAAGTAG	AACGTTTGGA	AAGGCAAGTG	360
GGGGCTTTAG	AAAAAGTTAA	TCTAGGGTAT	TTGGATTTAG	AACAAAAAAT	TTATACTTTA	420
TCTGGGGGAG	AGGCCCAACG	AGTTGCCCTT	GCAAAAACTA	TTTTGAAAAA	TCCACCCCTG	480
ATTTTGGCAG	ATGAACCAAC	AGCAGCTCTT	GATCCTGAAA	ATTCAGAGGA	GGTTATGAAT	540
CTCTTGGTGG	ATTTGAAAAG	TGAAAATCGA	ATTATCATCA	TTGCGACCCA	TAATCCCCTA	600
GTCTGGAATA	AGGCTGATGA	AATCATTGAT	ATGAGGAAAC	TTGCTCATGT	GTGA	654

(2) INFORMATION FOR SEQ ID NO:812:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1062 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1062
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

GGAAGAAATA	AAGAGAGGCT	TTTGGTTTTA	GTAATAGAGG	GAGTTAGTGA	GATGATTAAA	60
TTTGATAATA	TTCAAATTAA	ATATGGTGAT	TTTGTTGCAA	TTGATAATCT	GAATTTAGAT	120
ATACATGAAG	GGGAATTCTT	TACATTTCTT	GGGCCTTCAG	GATGTGGTAA	ATCAACTACT	180

TTGAGAGCAT	TGGTAGGTTT	TTTAGATCCA	TCATCAGGAA	GTATTGAAGT	TAATGGAACA	240
GATGTCACTC	ATTTGGAACC	TGAAAAGCGT	GGGATTGGTA	TTGTATTTC	ATCTTATGCG	300
CTATTTCCAA	CTATGACTGT	TTTTGATAAT	ATTGCATTTG	GTTTAAAAGT	TAAGAAGGTA	360
GCTCCAGATG	TTATTAAAGC	TAAAGTATCA	GCAGTGGCAG	CAAAAATTAA	GATCTCTGAT	420
CAACAGTTAC	AGCGTAATGT	ATCAGAAATTA	TCTGGGGGTC	AACAACAAAG	GGTAGCATTG	480
GCTCGTGCTC	TGGTTCTTGA	ACCTAAAATT	CTTTGTCTAG	ATGAACCATT	GTCAAACCTT	540
GACGCAAAAT	TACGTGTAGA	TTTGAGAAAA	GAGTTGAAAA	GACTTCAAAA	AGAGTTAGGT	600
ATTACTACTT	TATATGTTAC	TCATGATCAA	GAGGAAGCCT	TGACTTTATC	TGATAGAATT	660
GCAGTCTTTA	ACAATGGATA	CATCGAACAG	GTCGGTACAC	CAGTAGAGAT	TTATCATAAT	720
TCTCAAACCTG	AATTTGTATG	TGATTTTATT	GGAGATATTA	ATGTTTTGAC	CGATGAAACA	780
GTCCACGAAG	TATTATTGAA	AAATACAAGC	GTTTTCTTAG	AGGATAAAAA	AGGATACATT	840
CGATTAGAGA	AAGTTCGATT	CAATCGTGAA	ACTGAACAAG	ATTTTATTCT	AAAAGGGACA	900
ATTATTGATG	TTGAGTTTTC	TGGAGTTACA	ATTCACTATA	CAATAAAAGT	TTCTGAAAGT	960
CAGATTCTTA	ATGTAACAAG	TATTGATAGT	CAGGCTGCTA	TTAGATCTGT	CGGAGAAAGT	1020
GTGGAATTAT	TTATCACACC	ATCAGACGTT	CTGCAATTTT	AA		1062

(2) INFORMATION FOR SEQ ID NO:813:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GGAGGAAATA	AGTATGTTAA	AAGAAGTATT	AACCGTTGCA	AAAGTTGCCA	AAAAATCTTC	60
ATTATTTTTG	GGTGGTGTCG	CATTGGTACC	CTTGGTTTGA	AAATCTTAGC	AAGTAAGGAA	120
GCTAAAAAAG	GTTATTCTAA	AGCTTTGGCT	AAGGCTTACA	ATTTGAAAAA	CAAGCTAAAT	180
GCATCTGTTT	CTGTTGTGAA	GCAACATGGA	AACAATGTCT	TGCAAAATGC	CAAATATTTG	240
TACGAGCAAG	AGAAAAAAGA	AAAGCAATTA	GATAGCCTTA	TAGGTGAATA	A	291

(2) INFORMATION FOR SEQ ID NO:814:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

ACTATGAATA	ATCTTTCGCT	TGTCCTTATG	GATATATCTG	TTCAAAATCG	TCAAGAAGCC	60
TACAAAGAAT	TAGCAAATCA	AATCAGCCTT	CTTGTTTCTG	AAGATACAGA	AAAAATAGAA	120
GAGCTTCTAT	ATTACCGTGA	GAGACAGGGA	AGTATAGAGG	TTGCTAAAGG	TGTTCTTCTA	180
CCACATTGTG	AAGGAAACTT	TCAACATCAT	GTCTTAGTGA	TTACTAGATT	AAAATCACCT	240
ATCAGAGAAAT	GGTCGAAGGA	TATCCAGTGT	GTTGACCTTA	TTATCGGTTT	GGCCATTGCA	300
GTATCACAGG	ACAAGTCATG	TATTAAAAACA	TTGATGAGAA	GACTAGCAGA	TGAATCATTC	360
ATAAATCAAT	TAAAACAGTT	AACAAAAGAA	GAATTACGGG	AGATAATATA	TGGAAATCAA	420
AGATATTCTT	AA					432

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

AAAATGAATA	AAAGTATGAT	TCGTTACCTC	CTTTCAAAGT	TACTTTTGAT	TGAAGCTGTT	60
CTCCTCTTGG	TTCTGTGGC	TATCGCTGTC	TATTACCGTG	AATCGAGCCA	AGTCTTTACG	120
GCCCTCTTTT	CGACCATAGG	GATTCTCGTA	TTGTTAGGCG	G TTCAGGGAG	TTTACAGAAG	180
CCAAAAAATC	AACGGATTTA	TGCCAAGGAG	GGAGTCTTGA	TCGTTGCCCT	CTGTTGGATC	240
CTTTGGTCTT	TCTTTGGTGG	TCTCCCCCTT	GTCTTTTCTG	GGCAAATCCC	TAGCGTTATT	300
GATGCCTTTT	TTGAAATTAG	TTCTGGGTTT	ACAAC TACTG	GAGCAAGTAT	TTTGAACGAC	360
GTTTCGGTTC	TCAGCCGTTT	CCTCCTCTTC	TGGCGAAGTT	TTACCCACTT	GATTGGAGGG	420
ATGGGAGTGC	TTGTTTTTGC	ACTTGCTATT	ATGGACAATG	CCAAAAATAG	CCACCTAGAG	480
GTGATGAAGG	CTGAGGTTCC	AGGTCCTGTT	TTTGCCAAGG	TTGTATCCAA	ACTAAAAAAC	540
ACTGCCCAGA	TTCTCTATCT	CCTTTATCTA	GCTCTCTTCT	CCCTCTTTGT	CATCATCTAT	600
TATCTAGCTG	GTATGCCTCT	CTACGATAGT	TTTGTCATTG	CTATGGGGAC	AGCGGGA ACT	660
GGAGGCTTTA	CCGTCTATAA	CGACGGAATT	GCCCACTATG	GCAGCTCACT	GATTACCTAT	720

CTGGTCAGTA	TCGGAGTTCT	GATTTTTTGGG	GTAAATTTCA	ACCTCTACTA	CTACCTCATG	780
CTCCGTCGCA	TCAAGGCCCT	CTTTGGTGAC	GAAGAACTTC	GGGCTTACTT	GGTCATTGTA	840
CTGGTTTCTA	CAGGCTTGAT	TAGCCTCAAC	ACCTCTACC	TCTACCCAGG	GTTTTCAAAG	900
AGCTTTTGAAA	TGACCTTCTT	CCAGGTTTCC	AACATCATTA	CAACAACGG	TTTTGGATAT	960
GGAGATATTA	CCAACCTGGCC	CCTCTTCTCC	CAGTTTATCC	TCCTCTTCCT	CATGACAATC	1020
GGTGGTTCTG	CTGGATCAAC	TGCAGGTGGA	CTCAAGATTA	TTCGAGGCCT	CATCCTTTCA	1080
AAAATTGCCA	AAAATCAAAT	TTTGTCCATT	CTATCTCCCC	ACCGTGTTTT	GACTCTCCAT	1140
GTGAATAAAA	CGGTGATTGA	TAAGGATACC	CAGCATAAAA	TTCTCAAGTA	CTTTGTCATC	1200
TATGCTATGA	TTTTGCTATC	CCTTATCTTT	ATTGTCAGCC	TAGATAGCAA	TGATTTTCTG	1260
ATCGTGACCA	GCGCTGTCTT	TAGCTGTTTC	AATAATATCG	GGCCTATTCT	AGGAACCACT	1320
TCTAGTTTCT	CAATCTTTAG	TCCTATCTCA	AAAATTCTCC	TCTCCTTTGC	AATGATTGCA	1380
GGCCGCTTGG	AGATTTACCC	AATCCTACTT	CTCTTTATGA	AGAGAACTTG	GTCTAAGAGA	1440
TAA						1443

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

CGAATGAATA	ATCCAAAACC	ACAAGAATGG	AAAAGCGAGG	AACCTTAGTCA	AGGTCGTATC	60
ATTGACTACA	AGGCCTTTAA	CTTTGTGGAC	GGCGAAGGCG	TGCGTAACTC	TCTCTATGTA	120
TCAGGCTGTA	TGTTTCACTG	CGAGGGATGT	TATAATGTTG	CGACTTGGTC	TTTTAATGCT	180
GGCATTCCCCT	ATACAGCAGA	ATTAGAAGAG	CAGATCATGG	CAGATCTTGC	TCAGCCCTAT	240
GTTCAAGGTT	TGACTTTGTT	GGGAGGGGAG	CCTTTTCTTA	ATACTGGGAT	TCTCTTGCCA	300
CTTGTTAAGC	GGATTTCGAA	GGAATTGCCA	GACAAGGACA	TCTGGTCCTG	GACCGGCTAC	360
ACTTGGGAAG	AAATGATGTT	GGAAACTCCA	GATAAACTGG	AATTCTTGTC	ACTG	414

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

TTTCTTGATA	AAATAGAGGT	TATGACGAGA	TATAAAGCAA	CTATTTCCCTA	TGATGGTTAT	60
GCCTTTGATG	GCTTTCAGCG	CCAGCCTCAT	GCGCGTAGCG	TTCAGGAAGA	AATTGAAAAA	120
ACCTTGACCA	GATTAAATAA	AGGGCAAACC	ATTACTGTTC	ACGGTGCTGG	TAGGACAGAT	180
AGTGGGGTTC	ATGCCCTGGG	ACAGGTCATT	CATTTTGACC	TGCCTTATCA	GATGGATGAG	240
GAGAACTCC	GTTTTGCCCT	GGATACCCAG	TCTCCTGAAG	ATATTGATGT	GATTTTCGATT	300
GAGCTTGTTG	CAGATGATTT	TCATTGCCGT	TATGCCAAAC	ATAGCAAGAC	CTATGAGTTT	360
ATTGTGGATA	GAGGACGTCC	CAAAAATCCT	ATGCGCCGTC	ACTATGCCAC	CCACTTTCCC	420
TACCACTCG	ATGTGGAACG	AATGCAGATT	GCAATCAAAA	AGCTAGAGGG	AACCCATGAT	480
TTTACCGGTT	TTACAGCCTC	TGGGACTAGT	GTAGAGGATA	AGGTTTCGCAC	CATCACAGAA	540
GCTAGTTTAA	TAGTCGATGA	GACAGGACAA	TTTTTGACCT	TTACCTTTTC	AGGAAATGGT	600
TTCTTGATATA	AACAGATTTCG	CAATATGGTG	GGGACTCTTC	TCAAAAATCGG	TAACAACCGC	660
ATGCCAGTAG	AGCAGATTGC	TCTCATCTTG	GAGAAGAAGG	ACAGGCAACT	TGCAGGTCCC	720
ACTGCAGCAC	CAAAATGGTTT	GTATTTAAAG	GAGATTCGTT	ATGAAGAATA	A	771

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GCCCTTGATA	ACCACTGTCA	GCCAAGCTTT	CACAAGCTTA	TCCAGATGAT	TATCTTTTAT	60
TCGTTATGGA	CAATGCTAAT	GGACAATGCT	ATATGGCATA	AATCAAGTGC	CTTAAAGATT	120
CCGACTAATA	TTGGCTTTGC	ATTTATTCCT	CCATACACAC	CAGAAATGAA	CCCCATTGAA	180
TAA						183

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2001 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

TCTGCTGATA	AAAAATCAAT	GCTTAGAAAC	TATGAAATAA	TAAAAAAGGA	GAACATCATG	60
ATTAACATTA	CTTTCTCAGA	TGGCGCTGTT	CGTGAATTCG	AATCTGGCGT	AACAACTTTT	120
GAAATTGCC	AATCTATCAG	CAATTCCCTA	GCTAAAAAAG	CCTTGGCTGG	TAAATTCAAC	180
GGCAAACCTCA	TCGACACTAC	TCGCGCTATC	ACTGAAGATG	GAAGCATCGA	AATTGTGACA	240
CCTGATCACG	AAGATGCCCT	TCCAATCTTG	CGTCACTCAG	CAGCTCACTT	GTTGCGCCAA	300
GCAGCTCGTC	GTCTTTTCCC	AGACATTAC	TTGGGAGTTG	GTCCAGCCAT	CGAAGATGGT	360
TTCTACTACG	ATACTGACAA	CACAGCTGGT	CAAACTCTCTA	ACGAAGACCT	TCCTCGTATC	420
GAAGAAGAAA	TGCAAAAAAT	CGTCAAAGAA	AACCTCCCCT	CTATTCGTGA	AGAAGTGACT	480
AAAGACGAGG	CACGTGAAAT	CTTCAAAAAAT	GACCCTTACA	AGTTGGAATT	GATTGAAGAA	540
CACTCAGAAG	ACGAAGGCGG	TTTGACTATC	TATCGTCAGG	GTGAATATGT	AGACCTCTGC	600
CGTGGACCTC	ACGTTCCATC	AACAGGTCGT	ATCCAAATCT	TCCACCTTCT	CCATGTAGCT	660
GGTGCGTACT	GGCGTGAAA	CAGCGACAAC	GCTATGATGC	AACGTATCTA	CGGTACAGCT	720
TGGTTTGACA	AGAAAGACTT	GAAAAACTAC	CTTCAAATGC	GTGAAGAAGC	TAAGGAACGT	780
GACCACCGTA	AACCTGGTAA	AGAGCTTGAC	CTCTTTATGA	TTTCACAAGA	AGTGGGACAA	840
GGTTTGCCAT	TCTGGTTGCC	AAATGGTGCG	ACTATCCGTC	GTGAATTGGA	ACGCTACATC	900
GTAAACAAAAG	AGTTGGCTTC	TGGCTACCAA	CACGTCTACA	CTCCACCACT	TGCTTCTGTT	960
GAGCTTTACA	AGACTTCTGG	TCACTGGGAT	CATTACCAAG	AAGACATGTT	CCCAACCATG	1020
GACATGGGTG	ACGGGGAAGA	ATTTGTCCCT	CGTCCAATGA	ACTGTCCGCA	CCACATCCAA	1080
GTTTTTAAAC	ACCATGTTCA	CTCTTACCGT	GAATTGCCAA	TCCGTATCGC	TGAAATCGGT	1140
ATGATGCACC	GTTACGAAA	ATCTGGTGCC	CTCACTGGCC	TTCAACGTGT	ACGTGAAATG	1200
TCACTCAACG	ACGGTCACCT	ATTCGTTACT	CCAGAACAAA	TCCAAGAAGA	ATTCCAACGT	1260
GCCCTTCAGT	TGATTATCGA	TGTTTATGAA	GACTTCAACT	TGACTGACTA	CCGCTTCCGC	1320
CTCTCTCTTC	GTGACCCTCA	AGATACTCAT	AAGTACTTTG	ATAACGATGA	GATGTGGGAA	1380
AATGCCCAAA	CCATGCTTCG	TGCAGCTCTT	GATGAAATGG	GCGTGGACTA	CTTTGAAGCC	1440
GAAGGTGAAG	CAGCCTTCTA	CGGACCAAAA	TTGGATATCC	AGATTAAAAAC	TGCCCTTGGA	1500
AAAGAAGAAA	CCCTTTCTAC	TATCCAACCT	GATTTTTTGT	TACCAGAACG	CTTCGACCTC	1560
AAATACATCG	GAGCTGATGG	CGAAGATCAC	CGTCCAGTCA	TGATCCACCG	TGGAGTTATC	1620
TCAACTATGG	AACGCTTCAC	AGCTATCTTG	ATTGAGAACT	ACAAGGGGGC	CTTCCCAACA	1680
TGGCTGGCAC	CACACCAAGT	AACCCTCATC	CCAGTATCTA	ACGAAAAACA	CGTGGACTAC	1740
GCTTGGGAAG	TGGCCAAGAA	ACTCCGTGAC	CGCGGTGTCC	GTGCAGACGT	AGATGAGCGC	1800
AATGAAAAAA	TGCAGTTCAA	GATCCGTGCT	TCACAAACCA	GCAAGATTCC	TTACCAATTA	1860
ATTGTTGGAG	ACAAAGAAAT	GGAAGACGAA	ACAGTCAACG	TTCGTCGCTA	CGGCCAAAAA	1920
GAAACACAAA	CTGTCTCAGT	TGATAATTTT	GTTCAAAGCTA	TCCTAGCTGA	TATCGCCAAC	1980
AAATCACGCG	TTGAGAAATA	A				2001

(2) INFORMATION FOR SEQ ID NO:820:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...719
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

CAGCTGATAA	AAAATCAGAA	GCCTTGTATC	TAGTGCAGGA	CTCTGTTGCT	GGTTTGGATG	60
ACTATATCAC	TGGTAAAACA	AGCGACTTTT	CAACTGTCGG	TGTCAAGGCA	CTTGATGACC	120
AAACGGTTCA	ATATACTTTG	GTAAACCAG	AACTTTACTG	GAATTCAAA	ACACTTGCAA	180
CGATACTTTT	TCCTGTTAAT	GCAGATTTCC	TGAAATCAAA	AGGGGATGAT	TTTGGGAAAAG	240
CGGATCCATC	TAGTATTTTG	TACAATGGAC	CTTTCTTGAT	GAAAGCACTT	GTCTCAAAAT	300
CTGCTATTGA	ATATAAGAAA	AACCCTAATT	ACTGGGATGC	TAAGAATGTC	TTTGTAGACG	360
ATGTGAAATT	GACCTACTAT	GATGGTAGCG	ACCAAGAATC	ACTGGAACGT	AATTTTACAG	420
CTGGTGCTTA	TACTACGGCT	CGTCTTTTTT	CTAACAGCTC	CAGCTATGAA	GGGATTAAAG	480
AAAAATACAA	AAACAATATC	ATCTATAGTA	TGCAAAATTC	AAC TTCATAT	TTCTTTAATT	540
TTAACCTAGA	TAGGAAGTCT	TACAATTATA	CTTCTAAAAC	AAGTGACATT	GAAAAGAAAT	600
CGACTCAGGA	AGCAGTTCTC	AATAAAAAC	TCCGTCAGGC	TATCAATTTT	GCTTTTGACA	660
GAACATCTTA	TGGGGCTCAG	TCTGAAGGGA	AAAGAAGGTG	CAACAAAGAT	TTTGCCTAA	719

(2) INFORMATION FOR SEQ ID NO:821:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1734 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1734
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

AATTGTGATA	AAATAGTAGA	AAAGTCCAAA	AAGGAGCTCT	TAATGAATAC	AAAAGAATTG	60
ATTGCTAGCA	AATTATCTAG	CATCATTGAT	AGCCTGGACC	AAGAGGCTAT	TTTAAAGTTA	120
CTGGAAACCC	CTAAAAACTC	AGAAATGGGA	GACATTGCTT	TCCCTGCTTT	TTCTCTTGCA	180
AAAGTCGAAC	GTAAGCACC	ACAAATGATT	GCGGCTGAAC	TGGCTGAAAA	AATGAACAGC	240
CAAGCCTTTG	AAAAAGTTGT	CGCAACAGGA	CCTTACGTTA	ACTTTTTCCT	TGATAAATCT	300
GCCATTTCTG	CTCAAGTATT	GCAAGCTGTT	ACCACTGAAA	AAGAACACTA	TGCTGACCAG	360
AATATTGGTA	AACAAGAAAA	TGTTGTTTATC	GACATGTCTA	GTCCGAATAT	CGCTAAACCA	420
TTTTCTATTG	GCCACCTGCG	TTCAACTGTT	ATCGGAGATA	GCTTGTCCAA	TATTTTCCAA	480
AAAATCGGTT	ATCAAACGGT	CAAGGTCAAC	CATTTGGGAG	ACTGGGGTAA	ACAATTTGGG	540
ATGTTGATTG	TTGCCTACAA	AAAATGGGGC	GACGAAGAAG	CTGTAAAAGC	TCATCCAATC	600
GATGAACTCC	TTAAACTCTA	TGTCCGCATC	AACGCTGAAG	CTGAAAATGA	CCCTAGCTTG	660
GATGAAGAAG	CGCGCGAATG	GTTCCGTAAA	CTTGAAAATG	GAGATGAGGA	AGCTCTCGCT	720
CTTTGGCAAT	GGTTCGCGA	TGAAAGTTTA	GTGGAATTTA	ACCGCCTTTA	CAATGAATTG	780
AAGGTTGAAT	TTGACAGCTA	TAACGGAGAA	GCCTTCTACA	ATGATAAGAT	GGATGCAGTT	840
GTAGACATTC	TTTCTGAAAA	AGGACTACTT	CTTGAAATCAG	AAGGTGCCCA	AGTTGTGAAT	900
CTTGAGAAAAT	ACGGAATTGA	ACATCCAGCC	CTCATCAAGA	AGTCTGATGG	TGCAACTCTC	960
TATATCACAC	GTGACTTGGC	TGCAGCCCTC	TACCGTAAAA	ATGAATACCA	ATTTGCTAAA	1020
TCTATCTACG	TCGTTGGTCA	AGAACAATCT	GCCCCCTTTA	AACAGCTCAA	AGCTGTCTTG	1080
CAAGAGATGG	GCTACGATTG	GAGTGACGAC	ATTACCCACG	TTCTTTTGG	TCTGGTTACA	1140
AAAGAAGGGA	AGAAGCTCTC	TACTCGTAAA	GGGAATGTCA	TCTTGCTAGA	GCCTACTATT	1200
GCAGAGGCTG	TTAGCCGTGC	CAAGGTCCAA	ATCGAGGCTA	AAAATCCTGA	ACTAGAAAAC	1260
AAAGACCAAG	TAGCACATGC	TGTTGGGGTT	GGAGCCATTA	AATTCTATGA	CCTCAAAACC	1320
GACCGTACAA	ATGGATACGA	CTTCGACCTA	GAAGCTATGG	TATCCTTCGA	GGGTGAAACT	1380
GGACCTTACG	TTCAATATGC	CTACGCTCGT	ATCCAATCTA	TCTTACGCAA	AGCCGATTTT	1440
AAACCAGAAA	CATCTGGCAA	CTATAGCTTG	AATGATACTG	AAAGCTGGGA	AATCATTAATA	1500
CTCATTTCAAG	ACTTCCCACG	TATTATCAAC	CGTGCGGCAG	ATAACTTTGA	ACCTTCTATC	1560
ATTGCTAAAAT	TTGCAATTAG	CCTGGCTCAA	TCCTTTAACA	AATACTATGC	ACATACACGT	1620
ATCTTGGATG	AAAGCCCAGA	ACGCGACAGC	CGTCTAGCCC	TCAGCTACGC	AACCGCAGTC	1680
GTTCTCAAAG	AAGCCCTTCG	CTTGCTTGGA	GTAAGAAGCG	CAGAGAAGAT	GTAA	1734

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

AAACGTGATA	AAGGAGAAAAT	AAAGATGGCA	GAAATTTATC	TAGCAGGTGG	TTGTTTTTTGG	60
GGCCTAGAGG	AATATTTTTTC	ACGCATTTCT	GGAGTGCTAG	AAACCAGTGT	TGGCTACGCT	120
AATGGTCAAG	TCGAAACGAC	CAATTACCAG	TTGATCAAGG	AAACAGACCA	TGCAGAAACG	180

GTCCAAGTGA TTTACGATGA GAAGGAAGTG TCACTCAGAG AGATTTTACT TTATTATTTTC	240
CGAGTTATCG ATCCTCTCAT CTATCAATCA ACAAGGGAAT GA	282

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

ATGTCAGATA ATTTTTTTGG AAAAAACTTT GCAGTGC GTA AGATTGATGC TATACCAGGA	60
CTGCTAGAGT TTGACATTCC CGTTCATGGA GACAATCGTG GTTGGTTTAA GGAAAACTTC	120
CAGAAGGAAA AGATGGAGCC ACTTGGCTTT CCTGAAAGCT TCTTTGCTGC AGGGAAATTG	180
CAAAACAACG TCAGCTTTTC TCGCAAAAAT GTTCTTCGAG GATTGCATGC AGAACCTTGG	240
GACAAGTATA TCTCTGTTGC AGACGATGGG AAGGTTTTAG GATCTTGGGT TGATCTACGC	300
GAGGGTGAAA CCTTTGGGAA TACCTATCAG ACAGTGATTG ATGCGAGTAA GGAATCTTT	360
GTTCCTCGAG GCGTAGCTAA TGGCTTCCAA GTTTTATCAG ATACAGTGTC ATATAGCTAT	420
CTGGTCAATG ATTA CTGGG C TCTTGA ACTC AAACCCAAGT ATGCCCTTTGT GAACTACGCT	480
GATCCAAGCC TTGGTATTGA ATGGGAAAAAT ATTGCAGAAG CAGAGGTTTC AGAAGCAGAT	540
AAAAATCATC CACTACTTAA GGATGTAAAA CCTTTGAAAA AAGAAGATTT GGAATAA	597

(2) INFORMATION FOR SEQ ID NO:824:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GATAAAGATA	AAACCCTATT	TAGCGCTAAC	CTTTTAGTAA	CCAACGGAAC	TAAAAGACTC	60
GCAACAAAAG	AGGATATTCC	TATTAAGATA	GGAAGTAGTG	ATGTGGCAAT	TACTGATTTT	120
GAAATAATGT	ATATGTTAGC	AATGATTGTT	ACTCTAAAGA	AAATATCTGC	TAAATTTGCA	180
AATAATTGA						189

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GCCGAGGATA	ATCTAATGGC	TCGACTCTTT	ACCCTTTCAG	AATCAAAGTA	CTACCTGATG	60
GCGCTGGATG	CAGGCACCGG	AAGTATTCGG	GCTGTGATAT	TCGACCTGGA	AGGCAATCAA	120
ATAGCAGTGG	GACAGGCGGA	GTGGCGGCAT	CTGGCAGTAC	CGGACGTTCC	TGGTTCATG	180
GAATTTGATC	TCAACAAAAA	CTGGCAACTG	GCGTGTGAGT	GTATGCGCCA	GGCGCTGCAC	240
AACGCCGGCA	TAGCCCCGGA	GTATATCGCT	GCCGTTTCGG	CATGTTCGAT	GCGTGAAGGC	300
ATTGTTTTAT	ATAATAATGA	AGGAGCCCCG	ATCTGGGCCT	GCGCCAATGT	GGATGCCAGA	360
GCGGCACGCG	AAGTTAGCGA	ACTTAAAGAA	CTGCACAACA	ATACCTTTGA	AAACGAAGTT	420
TATCGCGCGA	CCGACAAAC	ACTGGCTTTA	AGTGCCATCC	CCAGATTACT	TTGGCTGGCG	480
CACCATCGTT	CCGATATTTA	CCGTCAGGCA	TCAACCATCA	CCATGATCAG	CGACTGGCTG	540
GCCTATATGC	TCAGCGGCGA	ACTGGCGGTG	GAT			573

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

AACTTTTGTA	ATAGAAAAGG	AATTGAAATG	AAAATAGGAA	TTATTGCTGC	TATGCCAGAA	60
GAAGTGGCTT	ATCTGGTCCA	GCATTTAGAT	AATACCCAGG	AGCAAGTTGT	TTTGAGGAAT	120
ACCTATCATA	CAGGAACCAT	TGCTTCTCAT	GAAGTCGTTT	TTGTAGAAAG	TGGAATTGGT	180
AAGGTCATGT	CTGCTATGAG	TGTGGCGATT	TTGGCTGATC	ATTTCCAGGT	GGATGCCCTT	240
ATTAATACGG	GTTTCAGCTGG	GGCAGTAGCA	GAAGGTATCG	CTGTTGGGGA	TGTCGTGATT	300
GCTGACAAAT	TAGCCTATCA	TGACGTGGAT	GTCACAGCTT	TTGGCTATGC	TTATGGACAA	360
ATGGCGCAAC	AACCGCTTTA	TTTCGAATCA	GACAAAACCT	TTGTTGCTCA	AATCCAAGAG	420
AGTTTATCTC	AATTGGACCA	AAACTGGCAT	CTTGTTTTGA	TTGCTACAGG	AGATAGTTTT	480
GTTGCAGGAA	ATGACAAGAT	AGAAGCGATT	AAGTCCCATT	TCCCAGAAGT	TTAGCCCGTG	540
GAGATGGAGG	GGGCAGCTAT	TGCTCAAGCA	GCGCATGCCC	TCAATCTCCC	AGTCTTAGTC	600
ATCAGAGCTA	TGAGTGACAA	TGCCAACCCAC	GAAGCAAACA	TCTTTTTTTGA	TGAGTTTATT	660
ATCGAAGCTG	GACGTCGCTC	TGCCCCAAGTC	TTGTTGACCT	TTTTGAAGGC	TTTAGATTAA	720

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

CAAGATTGTA	AAAGGAAGGG	AAGTCTGATG	GCAGAAAGTAG	AAGAGTTACG	AGTACAACCT	60
CAAGATATCT	TAGCTGAGCA	ATCCGTTTTA	GGGGCTATCT	TTATTGATGA	GAGTAAACTT	120
GTTTTTGTGC	GAGAATACAT	TGAGTCTCGG	GACTTTTTTA	AGTATGCCCA	TCGTTTGATT	180
TTCCAAGCCA	TGGTCGATTT	ATCCGATCGT	GGTGATGCCA	TAGATGCAAC	AACGGTTCCG	240
TACTATCCTT	GA					252

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1404 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GACTACTGTA	ATGGAATAAA	ATATGGTATA	ATTGATAAGA	TAGATAGAAT	CGAGGATGTT	60
ATGTCATTTA	CGAAATTTCA	ATTTAAAAAC	TATATTAGAG	AAGCCTTGAA	GGAGTTAAAA	120
TTTACAACCTC	CAACAGAGGT	GCAAGACAAG	TTGATTCCCTA	TTGTTTTGGC	AGGTCGTGAC	180
CTAGTAGGAG	AATCAAAAAC	AGGTTTCAGGT	AAGACTCATA	CTTTCTTGTT	ACCGATTTTC	240
CAGCAATTAG	ATGAAGCTAG	CGATAGTGTG	CAAGCAGTGA	TTACTGCACC	GAGTCGTGAG	300
TTGGCTACTC	AAATTTACCA	AGTAGCGCGT	CAGATTTTCAG	CTCACTCAGA	TGTCGAAGTT	360
CGTGTGGTTA	ATTATGTGGG	TGGTACGGAT	AAGGCTCGCC	AGATTGAGAA	ATTGGCAAGC	420
AATCAGCCTC	ATATTGTTAT	TGGAACACCA	GGCCGTATCT	ACGACTTGGT	TAAATCTGGT	480
GATTTAGCTA	TTCATAAAGC	CAAGACATTT	GTTGTTGATG	AAGCAGATAT	GACCTTGGAT	540
ATGGGATTCT	TGGAAACTGT	TGATAAGATT	GCTGGCAGTC	TTCCAAAAGA	CTTGCAATTC	600
ATGGTCTTCT	CAGCGACTAT	CCCACAAAAA	CTGCAACCAT	TCTTGAAAAA	ATACTTATCA	660
AATCCTGTTA	TGGAGAAAAA	TAAGACCAAA	ACGGTTATTT	CTGACACCAT	TGATAATTGG	720
TTGATTTCTGA	CCAAGGGACA	TGATAAGAAT	GCTCAAATTT	ACCAGTTGAC	TCAGTTGATG	780
CAGCCGTATT	TGGCAATGAT	TTTTGTTAAC	ACTAAAACGC	GTGCTGATGA	ATTGCATTCA	840
TATCTGACTG	CTCAAGGCTT	GAAGGTTGCA	AAAATCCATG	GCGATATTGC	CCCTCGTGAA	900
CGCAAGCGAA	TCATGAATCA	GGTGCAAAAT	CTGGATTTTG	AGTATATTGT	CGCAACAGAT	960
TTGGCAGCAC	GTGGGATTGA	CATTGAAGGT	GTCAGCCATG	TCATCAATGA	TGCCATTCCG	1020
CAAGACTTAT	CTTTTTTTGT	TCACCGTGTT	GGTCGTACTG	GACGAAATGG	CCTACCAGGT	1080
ACAGCTATTA	CCCTTTATCA	GCCAAGTGAT	GACTCGGATA	TCCGTGAGTT	GGAGAAATTG	1140
GGAATCAAGT	TTAGTCCTAA	GATGGTCAAA	GACGGGGAAT	TTCAAGATAC	CTATGACCGT	1200
GATCGTCGTG	CCAACCGTGA	GAAAAAACAA	GATAAACTTG	ATATCGAAAT	GATTGGTTTG	1260
GTTAAAAAGA	AAAAGAAAAA	AGTCAAACCG	GGTTATAAGA	AGAAAAATTCA	ATGGGCGGTT	1320
GATGAAAAGC	GCCGTAAAAC	CAAGCGTGCT	GAAAATCGCG	CTCGCGGTCG	TGCAGAGCGT	1380
AAAGCTAAAC	GTCAAACATT	TTAA				1404

(2) INFORMATION FOR SEQ ID NO:829:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 918 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

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GGACACTGTA AAATTATGAT ACGTAAACTA ATTGTTTTCT TACTAATGCT CCCTCTTTTT 60
GTCTTGTTGGC TAGAGTTGCA TGTCCTAGTG AATAACTTAC TATTGAATCT AGAATCTCCC 120
CTTGATTTTG TGATTAGTAT GAGTCTTGCT TTCTGTAGTT TGATTTTATC AAAAATAGTT 180
TTAGACATAC TATACGCATT GAAAGATTG TACAAGAAAG AAGCTCTTAT TACGATTTTT 240
CCTTTTATTT TTATAGGCAG GAAGAAAGTA AATGTGAGGT TCTCGCCCTA TTTTTCATTC 300
CATCGTAAAA GTTTGTCGCC TGATGATTTA AGATCTAGGA TTATATGGAG TTTTATTCTT 360
GAAATTGCTA TTATCCTAGT ATTTATTTTA AAAATTCCTT TTGCAATCAT CATGCTTACT 420
ACAATATTTT TCTGGACTAT AATGGATATC AATCATCTCG TTTTAAATAA GACGGAATTT 480
CTTTTTAATC AAAATAAATG GGAAAAAGAA GATTCGTTTG AAAGCGATTT GACGAAAACG 540
TTAAAGGATA AAATACAAAA ATCAGAGCTA AGTTATTCTG ACTTAATGTC CCTTCTTCTC 600
TATGATGCGA TGAACCAATC CACCTTTTTA ACGGATAGTG AACTTTTTGA GGATATTTTG 660
AAAAAAATCG AAGATTCTCA TAACACCCTT CTGTGTACAG GTTTTGTCGA GTTACTGCTG 720
TATGAAATGT CTATTAGTAA CAATAACAAC TGGTCCAACA AGGTTGATAA AATTAGAATA 780
CACCTCATCA GAATAAATCA ATTAGATTTT TTCTATTATA CAAGTTGGTT AAGGCAAAAT 840
TTTGATTCTT GTATGAATAG AGAGTATCAT AAAATGAAAT CTCGGAAAT ATTACTGAGT 900
AATAAAAAGA TAGTTTAA 918
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(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

```
AGAAAATGTA AAGGAAAAAA CATGACAAAA AACTTATTAG TAGAACTCGG TCTTGAAGAA 60
TTACCAGCCT ATGTTGTGAC ACCAAGTGAA AAACAACCTAG GCGAAAAAAT GGCAGCCTTC 120
CTCAAGGAAA ACCGCCTGTC TTTTGAAGCC ATTCAAACCT TCTCAACACC ACGTCGTTTG 180
GCTGTTTCGTG TGACTGGTTT ATCAGACAAA CAGTCTGATT TGACAGAAGA TTTCAGGGGA 240
CCAGCAAAGA AAATTGCCTT GGATAGTGAT GGAAACTTCA CCAAGCAGC TCAAGGATTT 300
GTCCGTGGGA AAGGTTTGAC TGTTGAAGAT ATCGAATTCC GTGAAATCAA GGGTGAAGAA 360
TATGTCTATG TACTAAGGA AGAAGTTGGT CAATCAGTTG AAGCCATTGT TCCTGGTGTT 420
GTAGATGTCT TGAAGTCATT GACTTCCCT GTCAGCATGC ACTGGGCTGG AAATAGCTTT 480
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GAATACATCC	GCCCTGTCCA	CACTTTAACT	GTTCTCTTGG	ATGAGCAAGA	GTTTGACTTG	540
GATTTCCCTTG	ATATCAAGGG	AAGTCGTGTG	AGCCGTGGCC	ATCGTTTCTT	GGGGAAAGAA	600
ACCAAAATTC	AGTCAGCATT	GAGCTATGAA	GAAGACCTTC	GTAAGCAGTT	TGTAATCGCA	660
GATCCATGTG	AACGTGAGCA	AATGATTGTT	GACCAAATCA	AGGAAATTGA	GGCAAAACAT	720
GGTGTAAGTA	TCGAAATTGA	TGCGGATTTG	CTGAATGAAG	TCTTGAATTT	GGTTGAATAC	780
CCAACCTGCCT	TCATGGGAAG	TTTTGATGCT	AAATACCTTG	AAGTTCCAGA	AGAAGTCTTG	840
GTGACTTCTA	TGAAGGAACA	CCAGCGTTAC	TTTGTTGTTC	GTGATCAAGA	TGGAAAACCTC	900
TTGCCAAACT	TCATTTCTGT	TCGTAACGGA	AACGCAGAGC	GTTTGAAAAA	TGTCATCAAA	960
GGAAATGAAA	AAGTCTTGGT	AGCCCGCTTG	GAAGACGGAG	AATTCCTCTG	GCGTGAAGAC	1020
CAAAAATTGG	TGATTTTCTA	TCTTGTTGAA	AAATTTAAACA	ATGTCACCTT	CCATGAGAAG	1080
ATTGGTTCCC	TTCGTGAACA	CATGATTTCG	ACGGGTCAAA	TCACTGTACT	TTTGGCAGAA	1140
AAAGCTGGTT	TGTCAGTGGA	TGAAACAGTT	GACCTTGCTC	GTGCAGCAGC	CATTTACAAG	1200
TTTGACTTGT	TGACAGGTAT	GGTTGGTGAA	TTTGACGAAC	TCCAAGGAAT	TATGGGTGAA	1260
AAATACACCC	TTCTTGCTGG	TGAAACTCCA	GCGGTGGCAG	CTGCTATTCTG	TGAACACTAC	1320
ATGCCTACAT	CAGCTGAAGG	AGAACTTCCA	GAGAGCAAGG	TCGGCGCAGT	TCTAGCCATT	1380
GCAGACAAAT	TGGATACGAT	TTTGAGTTTC	TTCTCAGTAG	GATTGATTCC	ATCAGGTTCT	1440
AATGACCCTT	ATGCCCTTCG	TCGTGCAACT	CAAGGTGTGG	TTCGTATCTT	GGATGCCTTT	1500
GGTTGGCACA	TTGCTATGGA	TGAGCTGATT	GATAGCCTTT	ATGCATTGAA	ATTTGACAGT	1560
TTGACTTATG	AAAAATAAGC	AGAGGTTATG	GACTTTTATCA	AGGCTCGTGT	TGATAAGATG	1620
ATGGGCTCTA	CTCCAAAAGA	TATCAAAGAA	GCAGTTCTTG	CAGGTTCAAA	CTTTGTTGTG	1680
GCAGATATGT	TGGAAGCAGC	AAGTGCTCTC	GTAGAAGTAA	GCAAGGAAGA	AGATTTTAAA	1740
CCATCTGTTG	AATCACTTTC	TCGTGCCTTT	AACCTGGCTG	AGAAGGCAGA	AGGGGTTGCT	1800
ACGGTTGATT	CAGCACTATT	TGAGAATGAC	CAAGAAAAAG	CTTTGGCAGA	AGCAGTAGAA	1860
ACACTCGTTT	TATCAGGACC	TGCAAGTCAG	CAATTGAAAC	AACTCTTTGC	GCTTAGCCCA	1920
GTCATTGATG	CTTTCTTTGA	AAATACTATG	GTAATGGCTG	AAGATCAGGC	TGTCCGTCAA	1980
AATCGTTTGG	CAATCTTGTC	ACAACATAAC	AAGAAAGCAG	CTAAGTTTGC	TTGTTTTAAC	2040
CAAATTAACA	CTAAATAA					2058

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

ACCTATCGTA	ACGGTTGTTT	TACCTCTCCT	AGTTCCAACC	TTACTAGCAG	CTCCTTGCTT	60
GTATTTATGA	GAGCATTCTC	AGACTTTGGA	ACGCCTATGT	TGATTGGCGA	AGGATATCGG	120
ACTTTCCCTG	TCCTGATTTA	TACCCAATTT	ATTAGCGAAG	TTGAAGGAAA	TTCTGCCTTT	180
GCAATTATGG	CGATTATCAT	TGCCTTGGCA	ATTTTCCTTA	TCCAAAAACA	CATTGCAAAC	240
CGCTACAGTT	TCAGCATGAA	TCTGATCCAT	CCAATTGAGC	CTAAAAAAAC	TACAAAAGGA	300
AAAATGGCTG	CCATTTATGC	AACAGTCTAC	GGAATTATCT	TTATCTCTGT	TTTACCTCAA	360

ATCTACTTAA	TTTATACCTC	TTTCCTAAAA	ACATCAGGTA	TGGTATTTGT	TAAAGGTTAT	420
TCTCCAAACA	GTTACAAGCT	AGCTTTCAAT	CGTATGGGAT	CTGCTATTTT	CAATACCATT	480
CGTATCCCTT	TGATTGCCTT	AGTTCTAGTT	GTTCTATTTG	CGACATTTAT	CTCCTACCTA	540
GCCGTTAGAA	AACGGAATTT	GTTTACAAAC	TTAATTGACA	ACCTCAGTAT	GGTACCTTAT	600
ATTGTACCAG	GAACCGTTCT	AGGGATTGCC	TTCATTTCTT	CCTTCAATAC	TGGTCTATTT	660
GGAAGTGGAT	TTCTTATGAT	TACAGGGACT	GCTTTCATCT	TGATTATGTC	TCTATCTGTC	720
AGAAGATTAC	CTTATACTAT	TCGCTCATCT	GTTGCTAGCT	TACAACAAAT	AGCACCAAGT	780
ATTGAAGAAG	CTGCTGAAAAG	CTTAGGAAGT	AGTCGTCTCA	ATACCTTTGC	TAAGATTACA	840
ACTCCAATGA	TGCTATCTGG	TATCATTTCT	GGAGCCATCT	TATCTTGGGT	CACACTGATT	900
TCAGAACTCT	CTACTTCTAT	CCTCTATCCT	CCTCTACAAT	GTCAAAAACAA	GAACAATGAC	960
TGTAGCTATT	TATACAGAGG	TTCTCAGAGG	AAATTACGGT	GTAGCCGCAG	CCTTGTCAAC	1020
TATCCTGACT	GTTCTAACAG	TAGGTTCCCT	GCTCTTGTTC	ATGAAAATCT	CTAA	1074

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GCAACTAGTA	AATCCGCCAG	CTCGGTAGCG	CTCCATAGGA	GTGCAAGCCG	CTGTGGTACA	60
ACATTTAAAG	GAGAAAATAT	AAAAATGGGA	CGCAGTCTTA	AAAAAGGACC	TTTCGTCGAT	120
GAGCATTTGA	TGAAAAAAGT	TGAAGCTCAA	GCTAACGACG	AAAAGAAAAA	AGTTATTAAA	180
ACTTGGTCAC	GTCGTTCAAC	GATCTTCCCA	AGTTTCATTG	GTTACACTAT	TGCAGTTTAT	240
GACGGACGTA	AACACGTACC	TGTTTACATC	CAAGAAGACA	TGGTAGGCCA	CAAAC TTGGT	300
GAATTTGCAC	CAACTCGTAC	TTACAAAGGT	CACGCTGCAG	ACGACAAGAA	AACACGTAGA	360
AAATAA						366

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GATTTAAGTA	AAGAAAAGCT	AGAAAACGTT	TCAGAGGATA	TTATGAGTAT	TGAAATGACC	60
GTCAGTGAGA	TTGCAGAGGT	CTTAGGATTA	TCTCGCCAAG	CAATCAATAA	CCGTGTCAAA	120
GAATTACCAG	AAGAAGACAC	AGATAAAAAAT	GACAAAGGGG	TAACAGTTGT	TACCAGAAGT	180
GGCTTGATTA	AGCTAGAAGA	AATCTATAAA	AAAACGATTT	TTGAAGATGA	GCCTGTCAGT	240
GAAGATGTCA	AACAACGTGA	ACTGATGGAG	ATTCTAGTGG	ATGAGAAGAA	TGCAGCAATC	300
TTGTCTTTAG	AACAATGCCA	CACAAGGCTC	CGAATTTGTA	GAT		343

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

AAAGCGAGTA	AATTTATGTC	CCGTTCCCAA	TTAACGATTT	TAACAAATAT	TTGTCTGATT	60
GAAGACCTTG	AAACTCAGTG	CGTGGTTATG	CAGTACCGTG	CTCCTGAAAC	CAATCGCTGG	120
TCTGGTTATG	CCTTTCCTGG	AGGTCATGTA	GAAAATGGTG	AGGCTTTTGC	GGAGTCTGTC	180
ATTCGTGAAA	TTTACGAAGA	AACAGGATTG	ACTATCCAAA	ATCCGCAACT	GGTAGGTGTT	240
AAAAATTGGC	CTTTGGATAC	AGGGGGGCGC	TACATTGTCT	TTTGTTACAA	GGCGACCGAG	300
TTTACTGGAA	CTCTTCAATC	TTCAGACGAG	GGAGAAGTTT	CTTGGGTGCA	AAAAGACCAG	360
ATTCCAAACT	TGAATCTGGC	CTATGATATG	CTACCATTGA	TGGAAATGAT	GGAAGCTCCC	420
GACAAGTCAG	AGTTTTTCTA	CCCTCGCCGT	ACAGAAGACG	ATTGGGAAAA	GAAAATCTTC	480
TAG						483

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

CTTCAGAGTA ATGATCAAAC TCCTACCAGA ACAGAGCAAG GCAATCTCTT TAAATTAACC	60
GCTCTTGCAA AACTATCTAA CGAGGATAGT AAACATCATCC AATATGGCTT ACAAGGTCGC	120
GTCAC TAGTG TAACTACAAA GAAAACATAT TTTGATTATT TCAAAGATAA AATTTTAACC	180
CATTCTGATT AA	192

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

ATAATAGGTA ATCCAAAAAT TAATGGTTCA TTAATATTAA ATAAGGCTGG AACTACAGAT	60
GCTCGTCCTA TTGCTTTAAG CTGTTTCAGAT TTAGAGGCAA AAGCAATATA TAAACATAGT	120
CCTAAAGTTG CACCAGAAC ACCTGCAATT ACAAACATAT TAGAAAAATTC ACCTGCAACA	180
GCGAAGTGCC CGCCAGCAGC ATTTTCAGCC ATGTTGGCAA GAGCAATTGG ACTAACAAAT	240
GCAAAAAACAA TGTTCCGACC GTGGATACCT ACAATCCAAA GTAGTTGA	288

(2) INFORMATION FOR SEQ ID NO:837:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

AAGCGAGGTA ATCTCATGGA ACAATTTTTA GATAACATCA AAGACCTTGA AGTCACTACA	60
GTTGTGCGTG CGCAAGAAGC TCTTGATAAA AAAGAACTG CAACCTTCTT TATCGGTCGC	120
AAACTTGCC CTTACTGCCG TAAATTTGCA GGTACATTGT CAGGTGTCGT AGCTGAAACC	180
AAAGCTCACA TTTACTTCAT CAATAGTGAA GAACCAAGCC AACTCAATGA TTTGCAAGCA	240
TTCCGCTCAC GCTATGGAAT CCCAACTGTA CCAGGTTTTG TTCATATTAC AGATGGACAA	300
ATCAACGTCC GTTGCGACTC TTCAATGTCA GCACAAGAAA TCAAAGATTT CGCAGGATTG	360
TAA	363

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

TTAGTGGGTA AGAAAAGGAG ATTTATTATG TCAAAGATGG ATGTTGAGAA AATCATTGCA	60
CCGATGATGA AGTTTGTGAA TATGCGTGGC ATTATAGCTC TAAAAGATGG GATGTTAGCA	120
ATTTTGCCAT TGACAGTAGT TGGTAGTTTG TTCTTGATTA TGGGACAATT GCCGTTTCGTA	180
GGATTAAATA AAAACATTGC TAGTGTTTTT GGAGCTAATT GGACAGAGCC GTTTATGCAA	240
GTATATTCAG GAACTTTTGC TATTATGGGT CTAATTTCTT GTTTTCAAT TGCCTATTCT	300

TATGCTAAGA	ATAGCGGAGT	AGAGGCTTTA	CCAGCTGGAG	TTCTATCTGT	ATCTGCATTC	360
TTTATTTTGC	TAAGATCATC	TTATATCCCT	AAACAAGGTG	AGGCGATTGG	GGACGCTATT	420
AGTAAAGTTT	GGTTTGGAGG	CCAAGGAATT	ATCGGTGCTA	TCATTATAGG	TTTGGTAGTA	480
GGAAGTATTT	ATACCTTCTT	TATAAAGAGA	AAAATTGTTA	TTAAGATGCC	AGAACAAGTT	540
CCACAAGCTA	TTGCCAAACA	GTTTGAAGCA	ATGATTCCAG	CATTTGTAAT	TTTCTTATCT	600
TCTATGATTG	TATATATTTT	AGCGAAGTCA	TTGACTAATG	GCGGAACATT	CATAGAAAATG	660
ATTTATTCTG	CTATTCAAGT	TCCGTTGCAA	GGTTTAACTG	GATCTTTGTA	TGGTGCTATT	720
GGAATTGCAT	TCTTTATATC	ATTTTGTGG	TGGTTTGGTG	TTCATGGGCA	ATCGGTAGTA	780
AATGGAGTAG	TGACAGCTCT	GCTTTTATCT	AATCTTGATG	CTAATAAAGC	TATGTTAGCC	840
TCTGCTAATC	TATCATTAGA	AAATGGTGCA	CATATTGTTA	CTCAACAATT	TTTAGATTCA	900
TTTTTAATTC	TATCAGGTTT	AGGGATTACG	TTTGGTCTTG	TAGTTGCCAT	GCTTTTTGCA	960
GCAAAATCAA	AACAATACCA	AGCCTTAGGA	AAAGTTGCAG	CTTTTCCAGC	AATATTTAAC	1020
GTAATGAGC	CAGTTGTATT	TGGATTTCCG	ATTGTCATGA	ATCCAGTTAT	GTTTGTACCT	1080
TTCAATCTTG	TTCTGTACT	TGCAGCTGTG	ATAGTATATG	GAGCTATTGC	AACAGGTTTC	1140
ATGCAGCCAT	TCTCAGGGGT	AACATTGCCT	TGGAGTACAC	CAGCTATTTT	ATCAGGATTT	1200
TTGGTGGGTG	GATGGCAAGG	AGTTATTACT	CAGCTGGTGA	TATTAGCGAT	GTCTACATTG	1260
GTTTATTTTC	CATTCTTTAA	AGTACAGGAT	CGTTTAGCTT	ACCAAAATGA	AATCAAACAA	1320
TCTTAG						1326

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

TTTTGGGGTA	AGACAAATGAA	TAGCAGAGTA	GAATTTTCGGA	TTTTCACTAT	TGTTGATTTG	60
GACAAGGAAG	AAGAATATTT	ACATGAGATG	CATTTGAAAG	GTTGGAGGTA	TAGAACGAGT	120
CGTTTTGGTT	TGTTCTATTT	TGACCAATGT	CAACCAGACG	ATGTCATCTA	CCGTATCTAT	180
GATTCTAGAT	TTCTTAAAAA	ATATAAGCAT	GAAC TGCAAG	ATTTTAGAGA	TAGAGGTTGG	240
GAATTGATAG	GAGCAGGTTT	TTGTTTCGAT	CTTCGTAAAT	CGTCTTCTGA	TTTACTTCCA	300
GAGGATCAAG	TCTATATGAG	TAAGGGGCTC	AAATGGGAAG	TTATGCGATC	TAGACTTCGT	360
TCCTGTACAA	CTACTTTCTT	AGGTGGTCTT	GTTGTTTGTA	CGAGTTTGTT	TAGAGAGGAT	420
CTTTCTATGT	CTTTCTTTCT	TATTTTGTGTT	TTATATGCTT	TTCTGATTTT	TTATCTAATT	480
CATGGTTATT	TCAGACTAAA	AAGGAAATAC	CGAGTAGATG	AATAG		525

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...861
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

TTTATCTGTT	TGGGTTGCGA	TTGTTTTGGT	TCGATTTTTTA	GGAGAAAAC	TAGTGCGTTT	60
TCTGGCGATG	ATAGGATGAA	TAAAGGGATT	TATCAGCATT	TCTCCATAGA	AGATCGTCCA	120
TTTCTTGACA	AGGGAATGGA	ATGGATAAAG	AAGGTAGAAG	ATAGCTATGC	TCCTTTTTTA	180
ACTCCTTTTA	TCAATCCTCA	TCAGGAGAAG	CTATTAAAGA	TTTTGGCAAA	AACCTATGGT	240
CTTGCTTGTA	GCACTAGTGG	GGAATTCGTC	TCGAGTGAGT	ATGTTTCGAGT	TTTATTATAC	300
CCAGATTATT	TCCAACCAGA	GTTTTTCAGAT	TTTGAAATAT	CTCTTCAGGA	AATTGTGTAT	360
TCCAATAAAT	TTGAACATTT	AACGCATGCT	AAGATTTTAG	GGACAGTCAT	CAATCAATTA	420
GGGATTGAAC	GGAAACTTTT	TGGAGATATC	CTAGTAGATG	AAGAACGGGC	GCAGATTATG	480
ATTAATCAGC	AGTTTCTTCT	TCTCTTTCAA	GATGGACTAA	AGAAAATTGG	TCGTATACCT	540
GTTTCGCTGG	AGGAACGTCC	TTTCACCGAG	AAAATAGATA	AGCTAGAACA	GTATCGAGAA	600
CTGGATTTAT	CTGTGTCTAG	TTTTTCGATTA	GATGTTCTTT	TATCAAATGT	TTTGAAACTA	660
TTTAGGAATC	AAGCAAACCA	GTTGATTGAA	AAGAACTTG	TCCAAGTAAA	TTATCATGTG	720
GTAGACAAAT	CAGATTACAC	TGTTCAAGTT	GGAGACTTGA	TTAGTGTGAG	AAAATTTGGT	780
CGCTTGAGAT	TACTTCAAGA	TAAGGGACAA	ACGAAAAAAG	AGAAGAAAAA	AATAACCGTC	840
CAGTTATTAT	TAAGTAAGTG	A				861

- (2) INFORMATION FOR SEQ ID NO:841:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...723
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

TTTTCATCC	TTCTCACGAA	TAATAAAGTG	AGGAGGATTT	TTATGTACAG	TATTTTCATTC	60
CAAGAAGATT	CACTATTACC	AAGAGAAAGG	CTGGCCAAGG	AAGGAGTTGA	AGCGCTTAGT	120
AACCAAGAGT	TGCTAGCTAT	TTTACTCAGG	ACAGGAACAG	GTCAAAGTTAG	CGTTTTTGAA	180
ATTGCCCAAA	AAGTCTTGAA	CAATCTTTCA	AGCCTAACGG	ATTTGAAAAA	AATGACCCTG	240
CAGGAATTGC	AGAGTTTGGC	TGGTATTGGG	CGTGTTAAGG	CCATAGAATT	ACAAGCTATG	300
ATTGAACTGG	GGCATCGTAT	TCACAAACAC	GAGACTCTTG	AAATGGAAAG	TATTCTCAGC	360
AGTCAAAAGT	TGGCCAAGAA	GATGCAGCAG	GAATTAGGGG	ATAAAAAACA	AGAGCACCTG	420
GTGGCACTCT	ATCTCAATAC	TCAAAATCAA	ATCATCCATC	AGCAGACCAT	TTTTATCGGT	480
TCTGTAACTC	GTAATATCGC	TGAACCGCGA	GAGATTCTTC	ACTATGCAAT	CAAGCATATG	540
GCGACTTCTC	TTATCTTGGT	CCACAATCAT	CCTTCAGGAG	CGGTAGCGCC	TAGCCAAAAT	600
GATGATCATG	TCATAAACT	TGTTAAAGAA	GCCTGCGAAC	TGATGGGAAT	TGTTCTCTTG	660
GACCATTTGA	TTGTCTCTCA	TTCTAATTAC	TTTAGTTATC	GTGAAAAGAC	AGATTTAATC	720
TAA						723

(2) INFORMATION FOR SEQ ID NO:842:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...828
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GAAACCATCC	TCAAGAAAAA	TCTTCCTTTC	ACGGGAAATA	TTGCCTACAC	AACGAGAGAG	60
TTACCTATG	ATAATCCCCT	CATGCAGTTG	GTCCGTCACA	CTATTGAATA	CATTAAGAAT	120
CAGAAAAGCA	TTGGTCAAGG	GGTACTAGAT	AATCTCTCAA	CTAGTCGTGA	AAACGTATCT	180
GAAATCGTGC	GTGTAACGCC	CTCTTATAAA	CTAGCTGATC	GTGCTAAGAT	TATTCGGGGA	240
AATCAATCTA	AACCTATACG	TCATGCATAC	TTTCACGAGT	ACAGAAATTT	ACAAGAACTT	300
TGTCTGATGA	TCCTAAACCA	AGAAAAGCAC	GGTTTAGGGT	ATCAAGATCA	AAAAATCTAT	360
GGTATTCTCT	TTGATGTTGC	CTGGCTTTGG	GAAGAGTATG	TTTACACCTT	GTTGCCAAAA	420
GGTTTTGTAC	ATCCAGAAAA	TAAGGATAAG	ACGGATGGAA	TTTCAGTATT	TTCTGTTGGG	480
AAACGAAAAG	TATATCCAGA	TTTTTATGAC	AGAGAACGAA	AGATTGTTCT	AGATGCAAAA	540
TATAAAAAAC	TGGAATTGAC	TGAAAAAGGA	ATCAACCGTG	AGGACTTATT	CCAGCTGATT	600
TCCTATTCTT	ATATTTTAAA	AGCTGAGAAG	GCTGGACTGA	TTTTTCCTAG	TATGGAGCAG	660
TCAGTAAATA	GTGAAATAGG	AAAAGTAGCT	GGCTATGGAG	CTCAATTGAA	GAAGTGGTCT	720
ATTCGAATCC	CTCAGAATGC	CTCATCCTAT	AGTGCATTTT	GTAAAATGAT	GGAAAATTCA	780
GAAGAAAATT	TTAAAGCGAT	TATTGATGAA	GAAGTGGGGA	GAAAAATAA		828

(2) INFORMATION FOR SEQ ID NO:843:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

AACGTTTTCA	AGGAAGGTAA	CGATATGTCT	GAAGAAACAA	TTGATTATGG	ACAAGTGACA	60
GGAATGGTGC	ATTTCGACAGA	AAGCTTTGGG	TCAGTAGATG	GGCCTGGTAT	TCGCTTTATT	120
GTCTTTTTGC	AGGGCTGTCA	CATGCGTTGC	CAGTATTGCC	ACAACCCAGA	CACTTGGGCT	180
ATGGAGTCCA	ATAAGTCACG	TGAACGGACG	GTAGATGATG	TCTTGACAGA	GGCCTTGCGC	240
TACCGTGGTT	TCTGGGGAAA	TAAGGGTGGG	ATTACAGTCA	GTGGAGGAGA	AGCTCTCTTG	300
CAGATTGATT	TCCTGATTGC	TCTCTTCACC	AAGGCTAAGG	AACAAGGAAT	CCACTGTACC	360
TTGGATACCT	GTGCTCTTCC	TTTCCGTAAT	AAACCACGTT	ACCTTGAGAA	GTTTGACAAA	420
CTCATGGCTG	TCACTGACTT	GGTTCCTTTG	GATATCAAGG	AAATCAACGA	AGAACAGCAC	480
AAGATTGTCA	CTAGCCAAAC	TAATAAAAAT	ATCTTGGCTT	GTGCCCAGTA	TCTATCAGAT	540
ATTGGAAAAC	CTGTCTGGAT	TCGCCACGTG	CTAGTTCCAG	GATTGACAGA	CAGAGATGAT	600
GACTTGATTG	AAC TTGGTAA	GTTCGTCAAG	ACCCTCAAAA	ATGTTGATAA	GTTTGAAATT	660
CTACCTTATC	ACACCATGGG	TGAGTTCAAG	TGGCGTGAAC	TTGGAATTCC	ATATTCCCTC	720
GAAGGAGTCA	AACCACCAAC	AGCAGATCGC	GTCAAGAACG	CTAAAAAACT	CATGGATACC	780
GAAAGTTATC	AAGATTATAT	GAAACGTGTA	CATGGATAG			819

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

ACCTATTTCA	ACCCCATTTAT	CTATAGGCGT	ATTTTTACGC	CTTTTTTATAT	ACTTGAAGCA	60
CATAAGAAAC	ATTATGGGAA	GTTTGCTGAT	GGAAGTACTC	AAGAAATTGA	TGTTCCCTTAT	120
GATATTCCTG	ATACTTGGGA	GTGGGTGAGG	TTTACTACAT	TGGTTAAAAT	TGTCAAAAGT	180
GGCTCTTCCT	GA					192

(2) INFORMATION FOR SEQ ID NO:845:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GCTCATTTC	AAATTACGTT	AACTTTTTTC	ACGAAAAGGA	GAAAATTATG	CGTTATGATT	60
ATGGATAGCG	CTTTCAAATT	TTTAAACTCT	ATCCCATCCT	TTTATCTATA	TTATGAGCGA	120
AAATATAATA	ACTGTCAAGT	AACTAAAGTG	AATTTTATAA	AAAAATTACA	AGCCAAATTT	180
GTAAAGTTTA	CACTAAGCCG	CTAG				204

(2) INFORMATION FOR SEQ ID NO:846:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1188 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

TTGGA	CTTCA	ACCCCTGTGG	TAGAAGACAG	ACTGGTGATG	TTGTTAGTGC	TGAAGTATTG	60
ACAGT	TGATG	CGACTCAAGC	TAACGTTGCA	ATCTCTGGAA	CTGGTGTGTA	AGGTGTCTTG	120
ACTCT	TCGCG	AATTGACAAA	CGATCGTGAT	GCAGATATCA	ATGACTTTGT	TAAAGTAGGA	180
GAAGT	TATTGG	ATGTTCTTGT	ACTTCGTCAA	GTAGTTGGTA	AAGATACTGA	TACAGTTACA	240
TACCT	TGTAT	CTAAAAAACG	CCTTGAAGCT	CGCAAAGCAT	GGGACAAACT	TGTTGGTCGC	300
GAAGA	AAGAAG	TTGTTACTGT	TAAAGGAACG	CGTGCCGTTA	AAGGTGGACT	TTCAGTAGAA	360
TTTGA	AGGTG	TTCGTGGATT	TATCCCAGCT	TCAATGTTGG	ATACTCGTTT	CGTACGTAAC	420
GCTGA	GC GTT	TTGTAGGTCA	AGAATTTGAT	ACTAAAATCA	AAGAAGTTAA	CGCTAAAGAA	480
AACCG	CTTCA	TCCTTTACAG	TCGTGAAGTT	GTTGAAGCAG	CTACTGCAGC	AGCTCGCGCT	540
GAAGT	ATTTCG	GTAAATTGGC	TGTTGGTGAT	GTTGTAAC TG	GTAAAGTTGC	TCGTATCACA	600
AGCTT	CGGCG	CTTTCATCGA	CCTTGGTGGT	GTTGACGGAT	TGGTTCAC TT	GA CTGAATTG	660
TCACAT	GAAC	GTAACGTATC	ACCAAAATCA	GTTGTAAC TG	TTGGTGAAGA	AATTGAAGTG	720
AAAAT	CC TTG	ATCTTAACGA	AGAAGAAGGA	CGTGTATCAC	TTTCACTTAA	AGCAACAGTA	780
CCAGG	ACCAT	GGGATGGCGT	TGAGCAAAAA	TTGGCTAAAG	GTGATGTAGT	AGAAGGAACA	840
GTTAA	ACGTT	TGACTGACTT	CGGTGCATTT	GTTGAAGTAT	TGCCAGGTAT	CGATGGACTT	900
GTTCA	CGTAT	CACAAA TTTC	ACACAAACGG	ATTGAAAATC	CAAAAGAAGC	TCTTAAAGTT	960
GGTCA	AAGAAG	TTCAAGTTAA	AGTTC TTGAA	GTTAACGCAG	ATGCAGAACG	CGTGTCAC TT	1020
TCTAT	TAAAG	CTCTTGAAGA	ACGTCCAGCC	CAAGAAGAAG	GACAAAAAGA	AGAAAAACGT	1080
GCTGT	CTCGTC	CACGTCTGCC	AAGACGTCAA	GAAAAGCGTG	ATTTTCGAAC T	TCCAGAAACA	1140
CAAAC	AGGAT	TTTCAATGGC	TGATTTGTTT	GGTGATATCG	AACTTTTAA		1188

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

AGGAG	CTTCA	ATATGGAGTA	TGAATTGCTC	ATTAGGGAAG	CAGAGCCCAA	AGATGCAGCT	60
GAATT	AGTGG	CCTTTT TAAA	TCGTGTGAGT	TTGGAGACAG	ACTTTACCAG	CCTAGACGGA	120
GATGG	TATTC	TCTTGACTAG	TGAGGAGATG	GAAATATTCC	TCAACAAGCA	AGCTAGTTTCG	180
GACAAT	CAGA	TAACCTTACT	TGCATTCTTA	AATGGCAAAA	TTGCTGGTAT	TGTAAATATT	240
ACAGCT	GATC	AGCGTAAGAG	AGTCCGTCAT	ATTGGAGATC	TCTTCATTGT	GATTGGAAAA	300
AGATAT	TGGA	ATAATGGCTT	GGGAAGTTTG	TTGCTAGAAG	AAGCGATAGA	GTGGGCACAA	360
GCAAGT	GGCA	TTCTGCGTCG	TCTCCAACTG	ACTGTCCAAA	CTCGTAATCA	AGCAGCAGTC	420
CATCTT	TATC	AAAAGCATGG	CTTTGTCA TT	GAAGGTAGCC	AAGAGCGTGG	GGCATATATA	480
GAAGA	AGGGA	AATTTATCGA	TGTTTACTTG	ATGGGTAAAC	TGATAGGTTA	G	531

(2) INFORMATION FOR SEQ ID NO:848:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...435
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

TCTTCATTCA	AAATTTCTGT	CTCGAAAAGA	GTTTTCCTT	GTAAGTCACA	TAGACTGAGA	60
AAGATACCTA	GGACGTTTAT	TTCAATACCT	CCAACAACAT	ACGGAATATT	ATCTGTGATA	120
GAAATAGTTT	TTCTACGTCT	TCCAGATCCG	GAAAACTCGC	TAAATTCATC	ACCAGTTTCG	180
TATATGAGGG	ACTGTTTCGCT	TAGTTCTTTT	ATGATGTTAG	TCGTTGTTGC	TGGAGTAAGT	240
CCTGTTTCAT	TAACAATATC	TGTACGGGAT	GTTGCTGGAT	TTCGATATAG	AAACTCCAGT	300
ATAGTGGCTC	TATTTTGTA	AAAGNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	360
CGCGGGGNNN	NAAAANNANN	ANNANNAANN	AANAAAAAAC	NCNNACAAAA	ACCCCCACCT	420
TCATTTTCAA	GTTAA					435

(2) INFORMATION FOR SEQ ID NO:849:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...828
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

ATAAGATTCA	AGCTATCAAG	GAGGTGCTCC	ATGTTAGCAA	GTGAAGTGAT	CCAAGCTTAT	60
GAAGCCTTTT	GCCCTCAGGA	ATTTTCTATG	GAGGGAGACA	GCCGTGGTCT	GCAAATTGGC	120
ACTTTAGACA	AGGGTATCCA	AAGGGTCATG	GTTGCCCTCG	ATATTCGTGA	AGAGACGGTG	180
GCAGAGGCCA	TTGAAAAGGG	TGTGGACTTG	ATTATCGTCA	AGCACGCGCC	TATCTTTCGT	240

CCTATCAAGG	ACTTGCTTGC	CAGCCGTCCG	CAAAATCAGA	TTTACATCGA	CCTGATTAAG	300
CATGATATCG	CAGTTTATGT	CAGCCATACC	AATATTGATA	TCGTTGAAAA	TGGGCTCAAT	360
GACTGGTTTT	GTCAGATGCT	AGGAATCGAG	GAGACGACTT	ATCTGCAGGA	AACAGGTCCA	420
GAACGTGGAA	TTGGACGTAT	TGGGAATATT	CAGCCTCAGA	CATTTTGGGA	ATTGGCCCAA	480
CAGGTCAAGC	AAGTCTTTGA	CCTAGATAGC	CTTCGAATGG	TGCATTATCA	AGAGAATGAT	540
TTGCAGAAGC	CTATTTCAAG	AGTAGCAATT	TGTGGTGGAA	GCGGGCAGTC	TTTCTATAAG	600
GATGCTTTGG	CAAAGGGGGC	AGATGTCTAT	ATCACTGGCG	ACATCTACTA	CCATACTGCT	660
CAGGATATGC	TGTCTGATGG	CTTGTTAGCA	TTGGATCCAG	GTCACTATAT	CGAAGTGCTT	720
TTTGTGGAAA	AAATCGCAGC	ACTCCTTACT	CAATGGAAAAG	AGAAAAAAGG	CTGGGAACTA	780
GAGATTTTAC	CTAGTCAAGC	ATCGACCAAT	CCTTTCGGTC	ATATCTAG		828

(2) INFORMATION FOR SEQ ID NO:850:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 960 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...960
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

ATGGATATCA	AAATAAAAAAG	GGAGGAAATT	ATGAAAAAGT	TTTCAAAAAC	ATTGAGAGAC	60
AACTGGATCT	TTCTCTTGAT	GGTTTTGCCA	GGGGCACTCT	GGTTGATTCT	ATTCTTTTAC	120
ATTCCAGTAT	TTGGGAACGT	GGTTGCCTTC	AAAGACTACC	ACATGACCAG	TAATGGTTTC	180
ATAGATAGTA	TCATAAATAG	TAAATGGGTC	GGACTCGATA	ATTTTCAGATT	CTTATTTAGT	240
TCAAGAGACG	CCTTTATTAT	CACACGAAAT	ACTGTCCTCT	ACAATCTTGG	CTTTATCTTT	300
CTAGGTTTGA	TTGTATCTGT	AGGGATTGCC	ATTATCCTCA	GCGAGCTCCG	TTCTAAGAGA	360
ATGGTGAAGA	TTTTTCAAAC	TTCTATGTTG	TTCCCTTACT	TCTTGTCTTG	GGTTATCATC	420
AGTTTCTTTA	CAGATGCCTT	CCTAAATATT	GATAAAGGGG	TGTTCAATCA	TCTATTGGAA	480
AGTCTTGGTC	TCAAAGAAGT	CAATTTCTAC	GCTGACCTGG	GCATCTGGCC	CTATCTCCTA	540
CTTTTCCTAG	GTATTTGGAA	AGGTTTTGGA	TATAGCAGTG	TCATGTACTA	TGCGACGATC	600
ATGGGAATTG	ATCCAACCTA	CTACGAAGCA	GCGACAGTGG	ACGGAGCTAG	CAAGTGGCAA	660
CGTATTCGCA	ACGTAACCAT	TCCTCAGTTG	ACTCCGCTTG	TAACTGTATT	GACCATCCTT	720
GCAGTCGGAA	ATATCTTCCG	CGCAGACTTC	GGTCTCTTCT	ATCAAATCCC	ACACAATGCT	780
GGTCAGCTTT	ACAATGTAAC	CAACGTTTTG	GACGTATATG	TTTTTAATGG	TTTGAATCAG	840
ACAGCAGATA	TCGGTATGGC	TGCAGCAGCC	GGTCTTTACC	AATCCGTTGT	TGGTTTGATT	900
CTGGTTATCC	TATCAAACCT	GCTTGCAAGA	CGAGTCGATC	CAAACCTCAG	TTTGTTCTAG	960

(2) INFORMATION FOR SEQ ID NO:851:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

AGGAGTATCA	ATATGAAACA	AACAGTTAAA	AAATTAGCTC	TTGTAGCGAG	CATTGCAGCA	60
ACATTAGGTG	GAAGTGTAGC	AGTTGCCTCT	GCAGCCGTTT	AATACCCAGA	AGGTGGTGTT	120
TGGACTTATG	GTTTCAGGTAA	CGGTGGTGCT	TACTCAAAC	ACTATCACCC	TTCAAAATAC	180
CATAGTTCAA	CAGTTGTTAG	CAGAAAAACT	GGTTCATCTG	ACAAGGGATA	TGCTGGTGCT	240
GGAGGGACTT	CTCGTGCATG	GATTCGTACT	TCTTGGGGAG	AGAAAGTTGC	ATTCTACTAT	300
AATGTTTAG						309

(2) INFORMATION FOR SEQ ID NO:852:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

GTCGCCATCA	AAATAGTTGT	TCCTTGTAGG	TTAATCCGTT	CCAAGAGATT	CATAATTTCC	60
CATGAATTAT	CCGGATCCAG	ATTTCTGTGT	GGCTCATCAG	CTATCAATAC	TTTGGGATTA	120
TTTACAATTG	CACGCGCAAT	CGCAATCCGC	TGTTGCTCCC	CACCTGAGAG	TTTATTTGGG	180
AAAGAACGAA	CCTTATGCTT	CAATCCAACC	AGGTCCAAAA	CTTCCATCAC	TCGTCTTTTG	240
ATATTACGGC	GATTTTCCCC	GATTACTTCC	ATAGCGTAA			279

(2) INFORMATION FOR SEQ ID NO:853:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

CACATGATCA	ACC GTTACTC	TCGCCCTGAG	ATGGCGAATA	TTTGGAGTGA	AGAAAATAAA	60
TACCGTGCTT	GGCTTGAGGT	GGAAATCCTC	TCTGACGAGG	CATGGGCTGA	GTTGGGGGAA	120
ATCCCTAAGG	AAGATGTGGC	TTTGATTTCG	AAGAAGGCGG	ACTTTGACAT	CGACCGTATT	180
TTGGAAATTG	AGCAGGAGAC	GCGCCACGAT	GTGGTGGCTT	TCACGCGTGC	GGTTTCTGAG	240
ACTCTTGGTG	AAGAGCGCAA	GTGGGTTCAC	TATGGGTAA	CTTCTACCGA	CGTGGTGGAT	300
ACTGCTTATG	GTTACCTCTA	CAAGCAGGCC	AACGACATCA	TCCGTCGTGA	CCTTGAAAAC	360
TTCATAATA	TCATCGCTGA	CAAGGCCAAG	GAGCACAAGT	TCACCATCAT	GATGGGGCGT	420
ACTCATGGTG	TGCACGCTGA	GCCGACAACC	TTTGGTCTTA	AATTGGCAAC	TTGGTACAGC	480
GAAATGAAAC	GCAATATCGA	GCGTTTCGAG	CATGCAGCTG	CTGGTGTAGA	AGCTGGTAAG	540
ATTTCTGGTG	CGGTTGGGAA	CTTTGCCAAT	ATCCCACCAT	TTGTAGAGGA	GTATGTCTGC	600
GATAAACTTG	GCATCCGTGC	CCAAGAAATC	TCTACACAAG	TCCTTCCTCG	TGACCTTCAC	660
GCTGAGTACT	TTGCGGTTCT	TGCCAGCATT	GCGACTTCAA	TCGAACGTAT	GGCGACTGAG	720
ATTCTGTGGT	TACAAAAATC	TGAGCAACGC	GAAGTAGAAG	AGTTCCTTGC	TAAAGGGCAA	780
AAAGGATCTT	CAGCAATGCC	TCACAAACGC	AACCCAATCG	GTTCTGAAAA	TATGACTGGT	840
CTGGCGCGTG	TCATTCGTGG	TCACATGATT	ACGGCTTATG	AAAACGTCGC	TCTCTGGCAC	900
GAACGCGATA	TTTCCCACTC	ATCAGCTGAG	CGTATCATCA	CACCAGATAC	GACCATTTTG	960
ATTGACTACA	TGCTCAACCG	TTTTGGAAAT	ATCGTCAAGA	ACTTGACAGT	CTTCCCAGAA	1020
AATATGATCC	GAAACATGAA	CTCGACTTTT	GGTCTTATCT	TTAGCCAACG	GGCTATGTTG	1080
ACATTGATTG	AAAAAGGCAT	GACCCGTGAG	CAAGCCTATG	ACTTGGTGCA	ACCAAAAACA	1140
GCCTACTCTT	GGGACAACCA	AGTAGACTTT	AAACCACTTC	TTGAGGCAGA	TTCAGAAGTA	1200
ACATCACGTC	TCATCAAGA	AGAAATCGAT	GAAATCTTCA	ACCCAGTTTA	TTACACCAAA	1260
CGAGTGGATG	ATATCTTTGA	ACGTCTTGA	CTAGGTGATT	AA		1302

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

ATATTTGTCA	AATGTTTTAT	ATTACATTTT	TATTACAAAT	TTCTATATCA	TAAGCTTCTA	60
CTCCAAAAAG	ATAAAGACAC	TACTTTTGCC	CTTTTCGATT	CTCTTTTAA	ACATAGCATC	120
ATCTTCCTTC	ATTCCATATA	AAACACTTCC	GATGAGAGAG	CTTGTTTTTT	AATTTCTGTTA	180
AACAACAAAA	AACGCAAGCT	TAAGCCTGCG	GACAATCTTT	ATAGCCATTT	CATTTCTTTC	240
ACATCTGTTT	TACGAACTTT	AGCATATTTT	TTAGCGCTTG	TAAAATGTAG	AGTAACTGGT	300
TTAAATACTC	CGCTTTTGTC	TCTTCGTAAA	CCTAAAACGT	CGGATCTTTT	ATTTTTATCC	360
TCAAAAAATA	TGACGTCCAA	TTTCATAGTA	TTTTTAGATA	AATCGCTAGC	TACGATGCAA	420
CAACTTATTA	TTTTAGAATA	G				441

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

GGGCATGTCA	AGAATACCTT	GATGGACCAT	CCCGTTAATG	GAGAAATTGA	AACCTTGCTT	60
AAACTGTCTT	GTCGCAGAGA	TGTGCAACAT	TTTCTAGAAC	AAGTCGAGCA	TTCTGACTTT	120
AGACCTCTAT	CTGAATTGAC	AGATGGCATC	CATTACCACC	TAGTCGAAGC	CGAAACACAA	180
CAAGACCTCC	ACTATATCGA	GGAAGCCTTG	GATCAGCTAG	GTTATTTAGT	AAAAGACTAG	240

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

CAAAGTGTCA	AGGAGGAAAC	TGATGAACTG	GACAAAAAAC	AAGCCTACAT	CGTCAGCTGC	60
CACAGTGGTT	TGCGCAGCTA	TATCGCAGAG	CCTATCCTCA	AGCAAGCAGG	ATTTACCGCC	120
CAAAACCTTG	ACGGCGCTTA	TTCAC'TATAC	AAAATGGT'TA	ACCCANAAAG	AGTAAATAT	180
GGAAACTAG						189

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 882 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

ATATCAGTCA	AACTATACGG	CCCAGGAACT	TGTTTATATT	TACAAAGAGG	AGAAAAAACC	60
ATGCCGTCGA	TGAAAGAATA	CGCATTACAG	TACCAAAAAGT	TAGGGTTCTC	AGTCATTCCA	120
ATCAATCCTA	AAAACAAGAT	GCCTTTTAATC	GAATTTGCTG	ATAAACCAGC	CATGACTCCA	180
TCTGAGATTG	AAAAC'TTTTG	GGACGGCTAC	CCTAATGCAA	ACATTGCCCT	AAAGACTACC	240
AACTTCTTTG	TCATTGATAT	TGACAAACAC	GGCAAATCGA	ACGGT'TTTGA	ATCGCTAAAA	300
AAATGGAAAC	ATCTAAATTT	AATCGAACCG	ACACTGCAAG	CTAAGACGGC	TAGTGGCGGT	360
AAACATCTAT	TCTACTTCAA	ACGAGAAGAT	GAGCCGATCA	CTCAGATGAT	TGGATTCTTG	420
CCTGGTGTTG	ATATTAAGGC	TCACGAAAAT	AATTATGTGT	TAGTCGCACC	CTCTGCCACA	480
GATAAAGGGC	AGTATGAGTG	GGATCTGGAA	AAGTCTAAGG	AAGGTGGCAC	GATGGTCACT	540
CCTTCAAAAT	ATTTAATCCA	GTCTATAAAA	AAACAGTATG	GCGAAACTCA	CGGTTATAAG	600
TATGATGGTA	AGGACGGTCT	TAGGGATTTA	GTTAGACGTT	CACATACTAG	AGACCGAACA	660
CAGACTACAG	ATCTCTTTGA	AACCATCGCC	CTTGGTTTTG	GTGATGAAGG	TGGACGAAAT	720
GACAAACTAG	CAAAATTCGT	AGGTGGTCTC	TTATATCGTG	CGGTCGACGA	TGGTGTAGTT	780
GTTCAACTTG	CAAGATTAGC	AAATGCAAAT	AGTCCAACCC	CTTTGCCTGA	AAAGGAAATG	840
ATGCGTACTA	TTGAAAGTAT	GATTAAAAAA	GATAGGAGGT	GA		882

(2) INFORMATION FOR SEQ ID NO:858:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

ACACCAGTCA AACCTTCTGC AGCAACACGG TCAGCTTTCT TAGCTGCCTT AGCCATACCT	60
TTTTCACGAA GCAATTCAAT CGCTTTTTCG ATGTCACCGT CTGTTTCTAC AAGCGCTTTT	120
TTAGCGTCCA TAACACCGGC ACCAGATTTT TCACGCAACT CTTTACAAG TTTAGCTGTA	180
ATTCTGCCA TTTTAATTCT CCTATATTTT TTGAAAATAG GAGAGCCGGG CTAA	234

(2) INFORMATION FOR SEQ ID NO:859:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

CAGGTGGTCA AACTGACTAC CTGCTATTTT TGTGATTATG GCTCTTATTA TGGGAATATA	60
CCTATGAATT GGGTTGTTAT AAAAAATAAA GATATTTTTT CAATGAATAC AGGTCTTTCT	120
TACAAGAAGG GCGATTTAAG CATTAATAAT AAAGGTGTTA GAATTATACG TGGTGGTAAT	180
ATTAAGCCTT TAGAATTTTC TCTGTTGGAT AATGATTACT ACATTGATAC ACAATTCATC	240
TCCTCTGAAC AAGTTTATTT AAAACATAAT CAGCTAATAA CACCTGTATC AACCTCTTTA	300
GAACATATTG GAAAGTTTGC AAGAATCGAT AAAGACTATG ATGGTGTGTG GGCTGGTGGA	360
TTTATTTTCC AATTAACACC ATTCGAAAGT TCAGAGATTA TTTCAAAATT TCTATTATTT	420

AACTTGTCTT CTCCGTTATT TTATAAACAA TTGAAAGCAA TAACTAACT ATCAGGTCAA	480
GCTTTATATA ATATTCCCTAA AACTACACTG AGCGAGCTAT TAATTCCGTT AGCTCCTTTT	540
GAGGAACAGG AACTTATTAC TCAAAAAGTT GAGAACTTT TTGAAAAAGT AAATCAACTT	600
TGA	603

(2) INFORMATION FOR SEQ ID NO:860:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

CGCGCGGTCA ATGCGGTTCA AGCTGGGCAA GCCGACGCTA TCATGGCAGG GATGACAAAG	60
ACTAAAGAAC GTGAAAAAGT CTTCAACCATG TCTGATACTT ACTATGATAC AAAAGTTGTC	120
ATTGCTACTA CAAAGTCACA CAAAATTAGC AAGTACGACC AATTAACTGG CAAAACAGTT	180
TGTGTTAAAA ACGGAAGTGG CGCTCAACGT GTTCCTTGA	219

(2) INFORMATION FOR SEQ ID NO:861:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

TATCTTTCCA AGCATTGTAG TACAGCAGAT TTTTGCCCAA GGACTGAGCC TCCTTTAACA	60
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ACTCAA	ACTC	CCTTAC	ATTA	TATCGG	CCAG	CCCCAT	GGAA	AGATTAT	AGC	CAGACT	TAATC	120
AATAA	TATA	TACATA	CTAG	AATACAAA	AAT	ATTTTT	TAT	TCATACT	TTT	TCTCCT	TATCT	180
TTATTT	TCTA	CCTACA	TAGT	ACCTCT	TATT	AAGCTC	ATTT	CAAAATT	ACG	TTAA		234

(2) INFORMATION FOR SEQ ID NO:862:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GATTTCT	CCA	ATCGTTT	TAT	TTTGATT	TATA	CCATATT	TGA	AAGGGGG	TGA	GGAAAT	GAGA	60
CCAAGAC	GAT	ATCCGTAT	AG	TGGGAAAA	AAAA	GAGTCC	CACCT	TCGTAA	AGGC	AGACCCT	GAG	120
TTAATGT	TGA	ATATCAAT	AAT	GATTGAT	GTT	GGAAAT	AATAC	AAGCGAAA	AAAA	TATATT	TGGA	180
AAAATT	TAA											189

(2) INFORMATION FOR SEQ ID NO:863:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...999
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

TCAGACT	CCA	AGTCATA	CAA	GAAAAGA	AATA	CTCTCA	AATAC	CAACTAG	TAA	GAAAGG	CAAC	60
ATTATGA	AAT	CCTACCA	AGC	TGTCTAC	CAA	ATCCTAT	CTA	AAGAAACC	G	CTATAT	CAGC	120

GGAGAAAAAA	TCGCAGAAAA	ACTATCCCTA	AGCCGAACAG	CAATTTGGAA	AGCCATCAAG	180
CGACTAGAAC	AAGAAGGCAT	TGAAATTGAT	AGTATCAAAA	ATAGAGGATA	TAAACTGATG	240
AATGGTGACC	TTATTCCTCC	AGAGATTCTA	GAAGAAAAATC	TTCCAATTAA	AGTCAGCTTT	300
AAACCCGAAA	CAAAATCAAC	ACAAC TAGAT	GCAAAAAGAA	CAATTGATTT	AGGCCATGAA	360
GCAAATACCC	TCTATCTAGC	TTCCCTATCAA	ACAGCAGGCC	GAGGCCGTTT	TCAACGTTCC	420
TTCTACTCAC	CACAAGGTGG	TATTTATATG	ACACTCCATC	TTAAACCAAA	TCTCCCCTAT	480
GACAGATTAC	CATCCTACAC	ACTACTTGTA	GCTGGAGCTG	TCTACAAAGC	CATTAAGAAC	540
CTAACTTTAA	TAGATGTCGA	CATAAAATGG	GTCAATGATA	TCTATCTAAA	CAATCATAAA	600
ATTGGAGGAA	TCCTTACTGA	AGCAATGACC	TCTGTAGAAA	CTGGCTTAGT	CACAGATATC	660
ATTATTGGAG	TAGGTATCAA	TTTCACTATT	AAAGACTTCC	CTCAGGAATT	AAAAGAAAAA	720
GCTGCCAGCT	TATTTAAAGC	TACAGCTCCT	ATAACAAGGA	ATGAATTGAT	CATAGAAATC	780
TGGCGTGCTT	TCTTCGAAAC	ACCAGCAGAA	GAGCTATTAT	ACCTATACAA	AAAACAGTCA	840
TTCATTCTAG	GAAAAGAAGT	CACTTTCACA	CTAGAGCAAA	AAGACTACAA	GGGACTTGCT	900
AAAGACATCT	CAGAAAATGG	AAAAC TTTTA	GTTCAATGTG	ATAACGGAAA	AGAAATCTGG	960
CTAAATAGTG	GCGAAATTC	TCTCAATAGT	TGGAAGTAA			999

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

CAATTATCCA	ATCTGCAATA	TTGGACCAGT	TTGTTTGCAA	GTCCATGGAC	GATAGCTATC	60
AATCTGATTG	ATATTTTGAT	TGTTGCTTAT	ATTTTATACC	ATTTTACAAA	AGGTATTGCA	120
GGAACCAAGA	TTATGATTTT	GGTACGTGGA	GTTTTGGTAT	TTATTTTTTAG	CTCAAATCCT	180
TGCAAATATG	ATTGGTTTGA	CTACGATTTA	TTGGTTATTC	AATCAAATTA	TTACTTATGG	240
GGTTATTGCG	GCGGTTGTTA	TCTTCTCTCC	AGAGATTCGG	ACTGGTTTGG	AACGTTTGGG	300
AAGAGCGACA	GATTTCTTTT	CCAATGCCCC	TATTAG			336

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

ACGATTCCCA ATCCCAGTAA CCGTCGTTAT GATCGAGTTG AACTCAGCCA TCAAGTCATT	60
GACACATGTT TCCGCCTTGT CAATGAGCCT CTTGTAATGT TTGATGTTTT CATTACACGA	120
GATAAAACGT TTATGCGTTA TCAAATCAT GACCAATTGA AACAAAAAGC TGTGGTTAGA	180
TCCTTTCGGA AATTGTCAAG CGATTGGAGG AAATGA	216

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

AATTCTCCCA AAGTCAGAGT TTTATTTCTA ACTTTTGAGA GAACTTCATT TTTGATTCAG	60
ACTTTTTCTA CTGCTATTCC TTACGCTATG AAATCAGATA AATTCTTTTT TATCACTTCT	120
CCACTTGGCA ATCTTAATTC AATCGTTCCA TCCATATTGA ATATAACACT ATCTAAGCCT	180
AATCCGTAA	189

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

ATCGTTACCA	AAGAGCTGTT	AAAGGTTTGG	CTTCTTATGG	AGGATCAGAT	GAAAAGTAAA	60
AACGGAGTTC	CTTTTGGCCT	TCTCTCAGGT	ATTTTCTGGG	GCTTGGGTCT	AACGGTTAGT	120
GCTTATATCT	TTTCGATTTT	TACAGATTTG	TCACCCTTTG	TGGTGGCTGC	AGCTCATGAT	180
TTTTTGAGCA	TCTTTATCTT	ACTAGCTTTT	CTCTTGGTAA	AAGAAGGGAA	AGTTCGCCTC	240
TCAATTTTCT	TAAATATTCG	CAATGTCAGT	GTTATCATCG	GAGCCTTGCT	AGCAGGCCCT	300
ATCGGTATGC	AGGCCAATCT	TTATGCAGTT	AAGTATATCG	GAAGTTCCTT	AGCTTCATCT	360
GTATCGGCTA	TTTACCCTGC	GATTTTCAGT	CTATTGGCTT	TCTTCTTTT	GAAGCACAA	420
ATTTTCGAAA	ATACTGTATT	TGGGATTGTC	TTGATTATTG	GAGGGATTAT	TGCCCAGACC	480
TATAAGGTTG	AACAGGTTAA	TTCCCTTCTAC	ATTGGGATTG	TCTGTGCTTT	GGTTTGTGCT	540
ATTGCATGGG	GAAGTGAGAG	TGTTCTTAGC	TCCTTTGCTA	TGGAAAGTGA	ACTGAGTGAA	600
ATCGAAGCCC	TCTTAATCCG	TCAAGTGACT	TCGTCTTGT	CCTATCTTGT	GATTGTGCTC	660
TTCTCTCATC	AGTCATTTAC	TGCAGTAGTC	AATGGACAAT	TGCTAGGTCT	CATGATTGTT	720
TTTGACGCTT	TTGATATGAT	TTCTACTTGG	GCTTATTATA	TCGCTATCAA	TCGCTTGGCA	780
ACCAGCCAAG	GTTACAGGCT	TGAACGTGAG	CTATGTAGTA	TTGGACGGGT	CTTGTTTGGC	840
AATTGTTTTT	TTAGGGGTGC	ACCCGCTAGA	TATGCTGACC	ATTATGACGT	CACCTTGTCT	900
CATTGCTGGA	GTTTATATTA	TTATTAA				927

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GATTTACCA	ACATATGGTT	CATACTACCA	AAAGCAATCA	GAAGTATTAT	CGGTAATGAT	60
GATTTGATTA	AAATTGATAA	TACTTTACAG	TATCCGTATT	CGACTTCAGC	TATGGTTTTA	120
TCTAAGTATT	ATGGAGTAGC	CGATGGAATG	AATGTAGAAG	GGAGGGGAAG	TGCGAATTTT	180
ATTAAAGATA	ATGTGTTAAT	TACAGCGGCT	CACAACTACT	ACAGACATGA	CTATGGGAAA	240
GAAGCGGATG	ATATTTATGT	TCTTCCGGCT	GTTAGTCCAA	GTCAAGAACC	ATTTGGAAAG	300
ATCAAAGTAA	AGGAAGTTCG	TTATTTGAAG	GAATTTAGAA	ATTTAAATTC	TAAGGATGCA	360

AGGGAATATG	ACTTGGCTTT	ATTAATTCTA	GAAAAGCCCA	TTGGTGCAAA	ATTAGGGACT	420
TTGGGTCTTC	CTACTAGTCA	AAAAAATTTG	ACAGGAATAA	CTGTGACTAT	CACAGGCTAT	480
CCATCATATA	ATTTTAAAAAT	TTATCAAATG	TATACAGATA	AAAAACAAGT	TTTAAGTGAT	540
GATGGCATGT	TCTTGGATTA	CCAAGTTGAT	ACTTTAGAGG	GGTCTAGTGG	ATCTACAGTT	600
TATGATGCTA	GTCAACGTGT	AGTAGGAGTG	CATACTTTAG	GAGATGGAGC	TAATCAAATT	660
AACAGTGCAG	TTAAATTAAA	TGAACGAAAT	TTGTCATTTA	TTTATTTATT	CGGTTCTTAA	720

(2) INFORMATION FOR SEQ ID NO:869:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

TCAACCACCA	ACCTATTTTC	CAACTTTGTG	CATAGCACAC	GATTTAAAAC	TAAAGAGGTG	60
AAAACTGTGA	TTTCAAAC	AGATAAAAC	AAACTCCGCC	AAAAACGCCA	CCGTCGCGTT	120
CGCGGAAAAC	TCTCTGGAAC	TGCTGATCGC	CCACGTTTGA	ACGTATTCCG	TTCTAATACA	180
GGCATCTACG	CTCAAGTGAT	TGATGACGTA	GCGGGTGTA	CGCTCGCAAG	TGCTTCAACT	240
CTTGATAAAG	AAGTTTCAAA	AGGAACTAAA	ACTGAACAAG	CCGTTGCTGT	CGGTAAACTC	300
GTTGCAGAAC	GTGCAAACGC	TAAAGGTATT	TCAGAAGTGG	TGTTGACCG	CGGTGGATAT	360
CTATATCACG	GACGTGTGAA	AGCTTTGGCT	GATGCAGCTC	GTGAAAACGG	ATTGAAATTC	420
TAA						423

(2) INFORMATION FOR SEQ ID NO:870:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

AAAGCCACCA	AACCAGAAGC	ATCATTCAAG	AGTCCTTCGC	CCTTAAGAAT	ATTGGACACG	60
CGCTTAGGAA	AGCTAAAACG	CTCCGAAAAG	GAGGCAAAGG	CCACCAAGTC	CGTAGGACCA	120
AGGGCTGCAC	CAACAGCCAA	GCAAGCTGCC	AAGGGAAGGC	TGAACCAAAG	AAGATGGGCC	180
AAGCCACCCA	AACTCAGGGT	CGAGATAAAA	ATCACTGGAA	ATATGAGATA	A	231

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

TCCGTAACCA	AGACTCGCCA	TGGCGTTGTT	TCAATGTTCA	TGAGAATGGC	CAGGAGGTGG	60
GCCATGCTTA	GTTTATTATC	TTACGACTTT	ATACAACGCG	CCTTTTTGGC	GGTTATTGCT	120
ATGAGTCTTT	TCTCACCGGT	ATTGGGAACC	TTCCTCATCT	TGCGTCGTC	GAGTTTGATG	180
AGTGATACCC	TTAGCCACGT	CTCACTTTCA	GGTGTAGCCT	TTGGTCTGGT	TTTGGGGATT	240
TCTCCAACCTG	TTTCTACTAT	TGCCATTGTC	TTGATTGCGG	CGGTCTTTCT	GGAGTATCTC	300
CGTACGGTTT	ACAAGAGCTT	TATGGAAATC	GGGACAGCTA	TCCTCATGTC	AACAGGTCTG	360
GCTGTTTCTC	TGATTGTCAT	GAGCAAGGGT	AAAAGCTCGA	GTTCAATGAG	TTTGGACCAA	420
TATCTCTTTG	GTTTCGATCGT	GACTATCAGT	GAAGAACAGG	TCATTTCCCT	CTTTGTCATT	480
GCGGCGGTTG	TTTTGATTTT	GACCTTTCTC	TTTCTTCGTC	CTATGTATAT	CTTAACTTTT	540
GACGAAGATA	CGGCCTTTGT	GGATGGCTTG	CCAGTTCGTA	CCATGTCCAT	TCTTTTAAAC	600
ATGGTGACAG	GGGTGGCTAT	TGCCCTTATG	ATTCCCTGCAG	CAGGAGCTCT	TCTGGTATCG	660
ACCATTATGG	TCTTGCCAGC	TAGTATTGCC	CTGCGTCTGG	GGAAAACTT	TAAATCGGTT	720
ATGCTGCTTG	CCAGTGCGAT	TGGCTTTTTG	GGAATGGTAG	CAGGACTTTA	CATTTCCCTAC	780
TATGCAGAAA	CACCTGCAAG	TGCAAGTATT	ACCATTATTT	TTGTAACTGT	CTTTATACTA	840
ATCAGTTTAG	TAAGACGTTT	TATCAAATAG				870

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

GAAGCAACCA	AGTCTGCAGC	TAAGAATAAT	CAAAACGTGG	TTCAAGGTGT	TATGACCACT	60
CTGGCGGAAA	TCTTTACTCC	GATAATTCCA	GCCTTGATTG	TTGGTGGATT	GATCCTCGGT	120
TTCCGTAATG	TCTTGGAAGG	TGTCCATTGG	TCGATGTTGG	ATGGCAAGAC	CATCACAGAA	180
TCCTCTCAGT	TTTGGGCAGG	GGTTAATCAC	TTCCTCTGGT	TGCCTGGTGA	AGCTATCTTC	240
CAGTTCCTAC	CAGTTAGGGA	TTACTTGGTC	TGTTTCTCGT	AA		282

(2) INFORMATION FOR SEQ ID NO:873:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...552
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

AAAGCGACCA	AACAACTCAT	TAGAAAGATT	CATATGGAAC	AATTACATTT	TATCACAAAA	60
TTACTAGACA	TTAAAGACCC	TAATATCCAG	ATTTTAGACA	TCATCAATAA	GGATACACAC	120
AAGGAAATCA	TCGCCAAACT	GGACTACGAC	GCCCCATCTT	GCCCTGAGTG	CGGAAATCAA	180
TTGAAGAAAT	ATGACTTTCA	AAAACCTTCT	AAAATTCCTT	ATCTTGAAAC	GACTGGTATG	240
CCTACTAGAA	TTCTCCTTAG	AAAGCGTCGA	TTCAAGTGCT	ATCACTGTTC	AAAAATGATG	300
GTCGCTGAAA	CTTCTATCGT	CAAGAAAAAT	CACCAAATCC	CTCGTATCAT	CAACCAAAAG	360
ATTGCTCAAA	AGTTAATTGA	AAAGATTTCCT	ATGACTGATA	TTGCCCATCA	GCTTTTCATC	420
TCAACTTCAA	CTGTTATTTCG	TAAGCTCAAT	GATTTTCACT	TTAAACATGA	TTTTTCTTGT	480
CTTCCTGAGA	TTATGTCTTG	GGACGTTGAA	ACAGTCCGGG	TAGTGACTGT	TTCAATCGGG	540
AGATGGAGAT	GA					552

(2) INFORMATION FOR SEQ ID NO:874:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

ACTCTTGCCA	AGCAATTTTA	TCCAAATTTT	CCAATCAGAA	ATCATCAATA	TCGATTCCAT	60
CTCTCACCTC	AAGCTCACGC	CAAACGGTCT	GGTAGAAATT	TTCTTGAAAA	ACGAAAGCTT	120
CACCTACTCT	TCACGCCGTT	ATCTAAAAAC	CATCAAGGAG	AAATTAGAAC	TATGAAAAAA	180
CAAGTATTTT	ACGATGCAGC	TACCGGTGTT	CTTATCGGCC	TCATCCTCTC	TATCCTCTTT	240
TCACTCATTT	ATGCACCAAA	TACCTACGCA	CCACTAAATC	CCTACTCTCT	CATCGGCCAA	300
GTGATGGATC	AGCATCAGGT	TCACGGTGCC	CTGGTCTTGC	TCTACTGCAC	ACTTATCTGG	360
GCAACCATCG	GTATGCTCTT	CAACTTTGGC	AACCGCTTAT	TTAGCCGTGA	CTGGAGCATG	420
CTTCGTGCCA	CTCTGACTCA	TTTCTTCCTT	ATGCTGGCTG	GCTTTGTCCC	ACTAGCAACT	480
CTTGCTGGTT	GGTTCCCTTT	CCACTGGATT	TTCTACCTCC	AGCTCATTAT	CGAGTTTGCG	540
ATTGTCTATC	TCATCATCTG	GGCTATTCTC	TATAAAAGAG	AGGCTAAAAA	AGTAGATCAC	600
ATCAATCAAC	TCTTGGAGCA	TAGAAAATAG				630

(2) INFORMATION FOR SEQ ID NO:875:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

ATCTGTGCCA	AGATAGGTTG	GGTAGATAGC	CAAATGTTAA	GATTAGAAGA	TGGGAAAAAA	60
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GAAGGAAAAT	CAAATAGAGA	AATTGCCTCT	CTACTTGGAA	AAGCTCCTCA	AACTATCCAT	120
ACTGAAATCA	AGTATGGGAC	AGTCCGAAAA	TGTCTTGGAA	AAGGGCGCTT	CAAAGAGGTT	180
TATTCTGCCG	ACTATGCTCA	ACAGTCTTAT	GAAAATAATC	GCAAGCACTC	GGTCAAGAGA	240
TCAAGCTTGA	CCAAGGAAC	AAAGGAAAA	ATTCTCCACT	ATCATAACCA	AAAATTTTGT	300
CCTGAAATGA	TGGTGATGGC	TAAAGGGGTT	AACGTGGGAA	TTTCAACCAT	TTACTATTGG	360
ATTCATCATG	GAAAGTTGGG	GTTAAGCAAA	CAGGATTTGC	TTTATCCTAG	AAAAGGAAAA	420
TCTGTTAAGA	AACAAGTTAG	TCCCAATTTT	AAACCCGCTG	ATCAATCTAT	CGAATCATAA	480

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

AATCCAGCCA	AGTCTATTGT	GAAATCAATG	CATCCCAACA	TGGAAAGGAG	GACTAGAATG	60
AAACGACAAA	CTGTAAACCA	GACGCTCAAA	CGTTTAGCCG	TAGATTTAGC	AAGCCATCCT	120
TTCTCCTTT	TCCTAGCCTT	TCTAGGAACT	ATTGCTCAAG	TTGGCTTATC	AATTTACCTA	180
CCTATTCTGA	TTGGGCAGGT	CATTGACCAA	GTCCTAGTGG	CTGGTTTCATC	ACCAGTTTTT	240
TGGCAGATTT	TTCTCCAGAT	GCTCTTGGTG	GTAATAGGAA	ATACTCTGGT	ACAATGGGCC	300
AATCCTCTCC	TCTATAATCG	TCTAATCTTC	TCTTATACCA	GAGATTTACG	GGAGCGAATC	360
ATCCATAAGC	TCCATCGTTT	ACCGATTGCC	TTTGTAGATA	GGCAAGGTAG	TGGAGAGATG	420
GTTAGTCGTG	TAACCACGGA	CATCGAACAG	TTGGCAGCTG	GCTTGACCAT	GATTTTTAAC	480
CAATTTTTC	TTGGTGTTTT	GATGATTTTG	GTCAGTATTC	TAGCCATGCT	CCAAATTCAT	540
CTCCTCATGA	CTCTCTTAGT	CTTGCTGTTG	ACGCCACTGT	CCATGGTGAT	TTACACGCTTT	600
ATTGCCAAGA	AATCCTATCA	TCTCTTCCAG	AAGCAAACAG	AGACGAGGGG	AATTCAGACT	660
CAGTTGATTG	AAGAATCGCT	TAGTCAGCAG	ACTATAATCC	AGTCCTTCAA	TGCTCAAACA	720
GAATTTATCC	AAAGATTGCG	TGAGGCTCAT	GACAACTACT	CAGGCTATTC	TCAGTCAGCC	780
ATCTTTTATT	CTTCAACGGT	CAATCCTTCG	ACTCGCTTTG	TAAATGCACT	CATTTATGCC	840
CTTTTAGCTG	GAGTAGGAGC	TTATCGTATC	ATGATGGGTT	CAGCCTTGAC	CGTCGGTCGT	900
TTAGTGACTT	TTTTGAACTA	TGTTCAAGCA	TACACCAAGC	CCTTTAACGA	TATTTCTTCA	960
GTGCTAGCTG	AGTTGCAAAG	TGCTCTGGCT	TGCGTAGAGC	GTATCTATGG	AGTCTTAGAT	1020
AGCCCTGAAG	TGGCTGAAAC	AGGTAAGGAA	GTCTTGACGA	CCAGTGACCA	AGTTAAGGGA	1080
GCTATTTCC	TTAAACATGT	CTCTTTTGGC	TACCATCCTG	AAAAAATTTT	GATTAAGGAC	1140
TTGTCTATCG	ATATTCCAGC	TGGTAGTAAG	GTAGCCATCG	TTGGTCCGAC	AGGTGCTGGA	1200
AAATCAACTC	TTATCAATCT	CCTTATGCGT	TTTTATCCCA	TTAGCTCGGG	AGATATCTTG	1260
CTGGATGGGC	AATCCATTTA	TGATTATACA	CGAGTATCAT	TGAGACAGCA	GTTTGGTATG	1320
GTGCTTCAAG	AAACCTGGCT	CACACAAGGG	ACCATTCATG	ATAATATTGC	CTTTGGCAAT	1380
CCTGAAGCCA	GTCGAGAGCA	AGTAATTGCT	GCTGCCAAAG	CAGCTAATGC	AGACTTTTTTC	1440
ATCCAACAGT	TGCCACAGGG	ATACGATACC	AAGTTGGAAG	ATGCTGGAGA	ATCTCTCTCT	1500

GTCGGCCAAG CTCAGCTCTT GACCATAGCC CGAGTCTTTC TGGCTATTCC AAAGATTCTT	1560
ATCTTAGACG AGGCAACTTC TTCCATTGAT ACACGGACAG AAGTGCTGGT ACAGGATGCC	1620
TTTGCAAAAC NTCATGAAGG GCCGCACAAG TTTCATCATT GCTCACCGTT TGTCAACCAT	1680
TCAGGATGCG GATTTAATTC TTGTCTTAGT AGATGGTGA	1719

(2) INFORMATION FOR SEQ ID NO:877:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

GTTCAAGTCC TACAAGGTCC ATTTGAATAT TGGAGGATTA CCCAAGTCCG GCTGAAGGGA	60
ACGGTCTTGA AAACCGTCAG GCGTGTAATA GCGTGCGTGG GTTCGAATCC CACATCCTCC	120
TTTTATATTA TTAACGCGGG ATGGAGCAGC TCGGTAGCTC GTCGGGCTCA TAACCCGAAG	180
GTCGTAGGTT CAAATCCTGC TCCCGCAATA AGGCTCGGTA GCTCAGTTGG TAGAGCAATG	240
GATTGA	246

(2) INFORMATION FOR SEQ ID NO:878:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

TCGGAAGTCC TAGACTCACG CGGTAACCCA ACACTTGAAG TAGAGGTTTA CACTGAATCA	60
GGTGCTTTTCG GACGTGGTAT GGTTCATCA AGGAGCTTTC TACTGGTGAA CACGAAGCAG	120
TTGAACTTCG CGACGGTGAC AAATCTCGTT ACGGTGGTCT TGGTACACAA AAAGCTGTTG	180
ACAACGTAA	189

(2) INFORMATION FOR SEQ ID NO:879:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

ACGCAATACA AAAAGAGCCT GTTGCCAAGC TCTTTATACT CAATGAAAAT CAAAGAGCAA	60
ACTAGGAAAC TAGCCACAGG TTGCTCAAAA CACCGTTTTG AGGTAGTAGA TAAGACTGAC	120
GAAGTCAGCT CAAAACACTG TTTTGAGGTT GCAGATATAC GGCAAGGCGA CGCTGACGTG	180
GTTTGA	186

(2) INFORMATION FOR SEQ ID NO:880:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1083 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1083
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

TTACTGTACA	AAATATTCTT	TTTGTCTGT	ATCTGGTCAC	TATCTTTTAT	AAAACACATT	60
TCCGTGATCC	AAATTACCAT	AAATACGGAG	ATTTTTATGC	CCGTTACGAT	TAAAGACGTG	120
GCCAAGGCTG	CTGGTGTTC	GCCTTCAACC	GTAACCCGTG	TTATTCAAAA	TAAATCAACC	180
ATTAGCGACG	AAACAAAAAA	ACGCGTTCGC	AAGGCTATGA	AGGAACTCAA	CTACCACCCA	240
AACCTCAACG	CTCGTAGCTT	GGTAAGCAGC	TATACTCAGG	TTATCGGATT	GGTTCTTCCT	300
GATGACTCAG	ACGCCTTCTA	CCAGAATCCT	TTCTTTCCAT	CGGTTCTACG	TGGCATCTCT	360
CAAGTCGCAT	CTGAAAACCA	CTATGCCATT	CAGATAGCAA	CAGGGAAAGA	TGAGAAGGAG	420
CGTCTCAACG	CTATTTTACA	AATGGTCTAC	GGCAAGCGTG	TAGATGGGCT	AATCTTTCTC	480
TATGCCCCAAG	AAGAAGACCC	TCTCGTAAAA	CTCGTCGCAG	AAGAACAGTT	CCCCTTCCTT	540
ATCTTAGGTA	AATCTCTATC	TCCTTTCATC	CCACTTGTCG	ACAACGACAA	TGTTCAAGCT	600
GGTTTGTATG	CGACTGAATA	TTTCATCAAA	AAAGGCTGCA	AACGCATTGC	CTTTATCGGA	660
GGAAGTAAAA	AGCTCTTCGT	GACCAAAGAC	CGTTTAACAG	GCTATGAACA	GGCGCTTAAA	720
CATTACAAAC	TTACCACTGA	CAACAATCGC	ATCTACTTTG	CCGACGAGTT	TCTGGAAGAA	780
AAGGGCTATA	AATTTAGCAA	GCGATTATTC	AAGCACGATC	CACAAATTGA	CGCTATCATC	840
ACAACCGATA	GCCTCCTAGC	TGAAGGTGTT	TGTAACATA	TTGCCAAACA	CCAGCTGGAT	900
GTCCCTGTTT	TCAGCTTTGA	CTCGGTAAAT	CCCAAGCTCA	ACTTGGCAGC	CTATGTCGAT	960
ATCAATAGTT	TAGAGCTTGG	TCGTGTTTCC	CTTGAAACTA	TTCTCCAGAT	TATTAATGAT	1020
AATAAAAAACA	ATAAACAAAT	TTGTTACCGT	CAATTGATCG	CCCACAAAAT	TATCGAAAAA	1080
TAA						1083

(2) INFORMATION FOR SEQ ID NO:881:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...411
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

CAGTCGGTCC	TTATGCTCAC	ATTCGTCCAA	ATTCAAGTCT	GGGTGCCCCA	AGTTCATATT	60
GGTAACCTTT	TTGAGGTGAA	AGGATCTTCA	ATCGGTGAGA	ATACCAAGGC	TGGTCATTTG	120
ACTTATATCG	GAAACTGTGA	AGTGGGAAGC	AACGTTAATT	TCGGTGCTGG	AACTATTACA	180
GTCAACTATG	ACGGCAAAAA	CAAATACAAG	ACAGTCATTG	GAGTCAATGT	CTTTGTTGGT	240
TCAAAATCAA	CCATTATTGC	ACCAGTAGAA	CTTGGTGACA	ATTCCCTCGT	TGGTGCTGGT	300
TCAACTATTA	CTAAAGACGT	GCCAGCAGAT	GCTATTGCTA	TTGGTCGCGG	TCGTCAGATC	360
AATAAAGACG	AATATGCAAC	ACGTCTTCCT	CATCATCCTA	AGAACCAGTA	G	411

(2) INFORMATION FOR SEQ ID NO:882:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...366
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

ATTTTAAACA	AGCTTTTGAG	CTATTCACAA	GACTTGAAAC	ATCACTATCA	GCTCTATCAA	60
CTCTTGCTGT	TTCACCTTCA	GAATAAGGAA	CCGGAGAAAT	TTTTCGGACT	TATTGAGGAC	120
AATCTAAAGC	AGGCTCATCC	TCTTTTTCAG	ACTGTCTTTA	AAACCTTTCT	AAAGGACAAA	180
GAGAAAATCG	TCAACGCCCT	TCAACTACAC	TATTCTAACG	CCAAATTGGA	AGCGACCAAT	240
AATCTCATCA	AACTTATCAA	GCGCAATGCC	TTTGGTTTTC	GGAACCTTGA	AAACTTCAAA	300
AAACGGATTT	TTATCGCTTT	GAACATCAAA	AAAGAAAGGA	CGAAATTTGT	CCTTTCTCGA	360
GCTTAG						366

(2) INFORMATION FOR SEQ ID NO:883:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

CTGGTAAACA	AAATGTCAAA	GAATAGTATT	TTTCTCTTAA	AAAAGAGAAG	TCTAAAAGGA	60
AAGGAGTCAG	ATATGAGACA	GCTAGCAAAG	GATATCAATG	CTTTTTTGAA	TGAGGTGATT	120
TTGCAGGCGG	AAAATCAGCA	TGAAATCCTA	ATAGGTCATT	GCACTAGCGA	GGTGGCCCTG	180
ACCAATACTC	AGGAGCATAT	CCTTATGCTC	TTGTCAGAGG	AATCTTTAAC	AAATTCAGAA	240
TTGGCCCCGC	GTCTCAATGT	CAGTCAGGCG	GCAGTTACCA	AGGCCATTAA	GTCTTTGGTC	300
AAGGAAGGGA	TGTTGGAAAC	ATCTAAAGAT	TCTAAAGATG	CGCGTGTGAT	TTTTTATCAG	360
TTGACTGACT	TGGCTCGTCC	AATCGCTGAG	GAGCACCACC	ATCACCATGA	GCATACACTT	420
TTAACCTATG	AACAAGTGGC	GACTCAGTTT	ACTCCAAATG	AACAAAAAGT	GATTCAGCGG	480
TTTTTGACTG	CTTTAGTAGG	AGAAATCAAA	TAA			513

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

ATTATGAACA	ATACTGAATT	TTATGATCGT	CTGGGGGTAT	CCAAAAACGC	TTCGGCAGAC	60
GAAATCAAAA	AGGCTTATCG	TAAGCTTTCC	AAAAAATATC	ACCCAGATAT	CAACAAGGAG	120
CCTGGTGCTG	AGGACAAGTA	CAAGGAAGTT	CAAGAAGCCT	ATGAGACTTT	GAGTGACGAC	180
CAAAAACGTG	CTGCCATATGA	CCAGTATGGT	GCTGCAGGCG	CCAATGGTGG	TTTTGGTGGA	240
GCTGGTGGTT	TCGGCGGTTT	CAATGGGGCA	GGTGGCTTCG	GTGGTTTTGA	GGATATTTTC	300
TCAAGTTTCT	TCGGCGGAGG	CGGTTCTTCG	CGCAATCCAA	ACGCTCCTCG	CCAAGGAGAT	360
GATCTCCAGT	ATCGTGTCAA	TTTGACCTTT	GAAGAAGCTA	TCTTCGGAAC	TGAGAAGGAA	420
GTTAAGTATC	ATCGTGAAGC	TGGCTGTTCG	ACATGTAATG	GATCTGGTGC	TAAGCCAGGG	480
ACAAGTCCAG	TCACTTGTGG	ACGCTGTCAT	GGCGCTGGTG	TCATTAACGT	CGATACGCAG	540
ACTCCTCTTG	GTATGATGCG	TCGCCAAGTA	ACCTGTGATG	TCTGTCACGG	TCGAGGAAAA	600
GAAATCAAAT	ATCCATGTAC	AACCTGTCAT	GGAACAGGTC	ATGAGAAACA	AGCTCATAGC	660
GTACATGTGA	AAATCCCTGC	TGGTGTGGAA	ACAGGTCAAC	AAATTCGCCT	CGCTGGTCAA	720
GGTGAAGCAG	GCTTTAACGG	TGGACCTTAT	GGTGACTTGT	ATGTAGTAGT	TTCTGTGGAA	780
GCTAGTGACA	AGTTTGAACG	TGAAGGAACG	ACTATCTTCT	ACAATCTCAA	CCTCAACTTT	840
GTCCAAGCGG	CTCTTGGTGA	TACAGTAGAT	ATTCCAACCT	TTCACGGTGA	TGTTGAATTG	900
GTTATTCCAG	AGGGAACCTCA	GACTGGTAAG	AAATTCCGCC	TACGTAGTAA	GGGGGCACCG	960
AGCCTTTCGT	GCGGTGCAGT	TGGTGACCAA	TACGTTACTG	TTAATGTCGT	AACACCGACA	1020
GGCTTGAACG	ACCGCCAAAA	AGTAGCCTTG	AAAGAATTCT	CGGCTGCTGG	TGGCTTGAAA	1080
GTAAATCCAA	AGAAAAAAGG	CTTCTTTGAC	CATATTAAAG	ATGCCTTTGA	TGGAGAATGA	1140

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

TTATCGAACA	AGTTTTATGA	TAGCTACCTT	GTTGGGATGC	TCTTATTTTT	TATCAGACAA	60
AACAAAAGGA	TTAAGGGAGT	TAAATTCCTT	AATCCGATAG	TTCTTATTCT	TGACGTTGTC	120
CGAAATCTGC	AATCATCTGC	TCCATTTCTT	GTCGACTCGG	AGTGGTCAGC	ATATACAGGT	180
AATCTCCTTG	AAGTTCCGCG	AAGGCAGCTG	GCATGA			216

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

TATGAGAACA	AGGGAGAATA	TATGACCTTA	GAATGGGAAG	AATTTCTAGA	TCCTTACATT	60
CAAGCTGTTG	GTGAGTTAAA	GATTAAACTT	CGTGGTATTC	GTAAGCAATA	TCGTAAGCAA	120
AATAAGCATT	CTCCAATTGA	GTTTGTGACC	GGTCGAGTCA	AGCCAATTGA	GAGCATCAAA	180
GAAGAAATGG	CTCGTCGTGG	CATTACTTAT	GCGACCTTGG	AACACGATTT	GCAGGATATT	240
GCTGGCTTAC	GTGTGATGGT	TCAGTTTGTA	GATGACGTCA	AGGAAGTAGT	GGATATTTTG	300
CACAAGCGTC	AGGATATGCG	AATCATACAG	GAGCGAGATT	ACATTACTCA	TAGAAAAGCA	360
TCAGGCTATC	GTTCCATATCA	TGTGGTAGTA	GAATATACGG	TTGATACCAT	CAATGGAGCT	420
AAGACTATTT	TGGCAGAAAT	TCAAATTCGT	ACTTTGGCCA	TGAATTTCTG	GGCAACGATA	480
GAACATTCTC	TCAACTACAA	GTACCAAGGG	GATTCCCAG	TATGA		525

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1995 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1995
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GAGGTTGACA	AAATGAATCA	AACAGTTTTTA	GATGTAAGAAA	ACTTAAAAAC	TGAATTCATC	60
ACTGATAAAA	AAGCATTTTC	GATTATTAAA	GATGTAAGAA	TCACTTTGGA	AAGAGGGAAA	120
GTTTTAGGGA	TTGTTGGTGA	ATCTGGATGC	GGTAAGAGTG	TAACAGTGAA	TACAGTGTTA	180
AACTTATTAC	CTAAAAATGG	ACGCATTGCT	GAAGGTGAAA	TCACATATTT	CGATGAAGAT	240
AAGCCGATAG	AGCTTCAAAA	ATTAAAGCAA	TATGGTAAAG	AATTTTCGAA	GTTACGTGGT	300
GAACACATAT	CAATGATTTT	CCAAGATCCA	ATGTCTGCAT	TGAATCCAGT	ATATACAATT	360
GGTAATCAAA	TTACTGAAGT	CCTTCATGAA	CATTATGACA	TTTCTAAAGA	GGAGGCAAAT	420
AAACGTGCTA	TAGAAATGTT	AGAAAACTT	GGAATTCATA	ATGCTGCAGA	ACGCATGAAT	480
GACTATCCAC	ACCAATTTAG	TGGAGGGCAG	CGTCAAAGAA	TAGTCATAGC	GATTGCAATG	540
GTATGTAATC	CAGATATTCT	AATTGCAGAT	GAACCAACAA	CTGCCCTTGA	TGTAACAATC	600
CAAGCACAAA	TACTTGATTT	ACTTGATGAT	TTACGTAAAG	AGCATGGAAC	TTCTATTATC	660
TTAATTACTC	ACGATTTAGG	CGTTATTGCT	CAAAATGCGG	ATGAAGTTGC	AGTGATGTAT	720
GCTGGTGAA	TCGTTGAAGT	TGGAACTGTA	GCTCAGATCT	TTGATCAACC	TAAACACCCG	780
TATACTCGTT	CTCTATTAA	ATCTATTCC	AATCCTGAAA	ATATGGATAA	AAAGCTACAT	840
GTTATCCAGG	GGAGCGTACC	TTCAATTTCT	GAAATATCTG	AAAAAGGATG	CAGATTCGCA	900
AATCGTATTC	CATGGTTAGA	AAAAGAACAT	CATGAAGAAG	AACCTCAATT	GCATGATTTA	960
GGTGACGGAC	ATTTTGTAAG	GTGTTCTTGC	TATAAACATT	TCTTTTTTCG	AGATAAGGAA	1020
GAAGAAACAT	TAGCGGAAAA	ACATGTAGGT	AATGTTGTTT	TAGAAGTAAA	AAATATTAAA	1080
AAGTACTACT	ATCCTAAGAA	GCAACTATTC	AAGCCACTAG	GTTCTCCGTT	GAAAGCACTT	1140
GATGACGTAT	CTCTAGAGTT	AAGAAAAGGA	ACTACTATTG	GTATCGTAGG	AGAGTCTGGA	1200
AGCGGTAAGA	GTACGATTGC	GAAATCATT	ATGAAACTCC	ATGATATTAC	AGATGGTGAA	1260
ATCAATATTG	ATTTGAATGG	GAAAACTCAA	AATATTTATG	GAATTAAACG	TAAGGAAGAT	1320
TTGGATTTCC	GTAAGAAAGT	TCAAATGGTA	TTCCAAGATC	CTTATGCATC	ATTGAACCCA	1380
ACTAAGAAAA	TTTATAATTC	ATTTGATGAA	CCGATGATTG	TCCATAATAT	TGGAAACAAA	1440
GAGGAACGCT	TTGAACGTAT	GAAAGAAGCC	TTGAAGATGG	TAAACGTGCC	AGTTGAGTAC	1500
TTGGAGCGTT	ATCCTCATGA	ATTTTCAGGC	GGACAACGTC	AACGTTTATG	TATTGCTCGT	1560
GCCCTTTGTA	TGAAACCAGA	AATTTTAATT	TTAGATGAAC	CTGTTTCAGC	ATTAGATCTA	1620
TCTGTACAAG	CGCAAGTTTT	GAATTATCTT	GTTGAAATCC	AAAATAAAGA	AGATTTGACT	1680
TATGTATTTA	TTTCTCATGA	CCTAGGTGTT	GTGAAATACA	TGTGTGACTA	TCTATATGTT	1740
ATTCATAAAG	GACGTATTGT	AGAAGCTGGT	TCTCGAGAAG	ATATCTACAA	TAACCCAATG	1800
CATATTTACA	CTAAAAAACT	ATTAGCTGCT	ATTCCAGAAG	TTGATTATCA	CTTCAAAGAG	1860
GCATTGGCAA	CAAAACGTAA	AGAAAATGAA	GTTGAATTTA	AAGCACAGTA	CCATGAATTT	1920
TATGATGAAG	ATGGCCGTGC	TTATGATCTT	AAGCAGGTTT	CACCAACACA	TTTTGTAGCG	1980
TTAAAACCAG	AATAG					1995

(2) INFORMATION FOR SEQ ID NO:888:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

AATTATGACA AAACACATTC ACAAGAAGGC TACGACATTT TAAAAGGTGA GGGCGGATGT	60
ATCGTTTGCC CTAATAAGT TGGTTACATT ATCATGACCA GCAACAAGGC AGGACTTGAG	120
CGTAAGTTCG CAGCCAAAGA ACGTAAGCGT AACAAACCAG GTGTTGTTCT CTGCGGTAGC	180
ATGGATGAAC TTCGCGCTTT AGCGCAACTC AACCCAGAAA TTGAAGCATT CTACTAA	237

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

TCGCCTTGCA AGAAGGTCGC ACATCGTGTG GCTTTTTTTTG ATTATTCGAA GGGTGGTGAT	60
GGAAAATTGA GTGGATTGAG AATAAAACAA AAGAGATTTG CAGATGAGTA CATCATCTCA	120
GGTAATGCCA CGGAAGCCTA TAAGAAAGCA GGTATATCGTG TTTCTAGTGA TAGAGTGGCA	180
GGCGTTGAAG GACATAAGTT ACTAAAGAAT CCTAAGATTA AAAGCTATAT AGATGAACGA	240
CTGAAACAGC TTGATTCTGA AAAGATTGCG GATCAGCAAG AGGTCTTAGG TTATCTAACT	300
TCAGTCATGC GAGGAGAGAC GCAAGAACAG ACCTTGATAA GCATTGGAGA ACTAGGGCAG	360
ACGATTACGG ATATAGATGT AGGAGCTAAA GATAGAATCA AGGCGGCTGA ACTTCTTGGT	420
AAACGGCATA GGCTTTGGAC GGATAAGGTA GAGGCGGATG TTTCTGGAAC GGTGGTGT	480
GCAATGAGT CAGACATATC AGATTAA	507

(2) INFORMATION FOR SEQ ID NO:890:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

TGTGTCTGCA	AGGCTCGTCA	AAAAGGTTTT	GATGTGGTGG	TCGAAATTCT	TCACCATATC	60
TTGCAAGAAG	ATGTTTCAGAT	TGTTCTTTTG	GGAAGTGGCG	ATCCAGCCTT	TGAAGGAGCT	120
TTCTCATGGT	TTGCTCAGAT	TTACCCAGAC	AAGCTATCAG	CAAATATCAC	TTTTGATGTC	180
AAACTTGCTC	AGGAAATTTA	CGGTGCTTGT	GACCTCTTCC	TCATGCCAAG	TCGTTTTGAA	240
CCGTATGGTT	TGTCTTACAT	GTNG				264

(2) INFORMATION FOR SEQ ID NO:891:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GGATTATGCA	AGAGAAGTAT	AGGCTTTAAT	GAAGTTGAAG	AAAACATCAA	TCAAGGTACT	60
GGTCAAAATA	CTACTTTTAA	TCAATTAGGC	TTCAAGGGAT	ATTCAGATAA	GCCAGATGGT	120
TGGTATTTAC	CTAAAAATAT	GAATGATGTA	GCAATAATCC	TTGAAACAAA	ATCAGAAGAA	180
AGAGATATTA	GCAAACAAAT	TTTTATTGAT	GAGTTAATGA	AAAATATAGA	CATAATTTAA	240

(2) INFORMATION FOR SEQ ID NO:892:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...462
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GGAAATGCA ATGGCAAACC CAACTTTCGG AGAAAAAAG TGAATACAGA CTATATTGCT	60
CGCTATGGCG TATATGCAGT TATCCCTAAT CCTGAACAAA AACAAATTGT TCTTGTTCAA	120
GAACCAAATG GTGCTTGTTT CCTACCATGT GGAAAAATTG AAGCAGGTGA AAATCATCAG	180
GAAGCCCTAA AGCGTGAGTT GATTGAAGAG CTTGGTTTCA CAGCAGAAAT TGGTACCTAT	240
TACGGACAAG CTGACGAATA TTTCTATTCT CGTCATCGTG ATGCCTACTA CTACAATCCT	300
GCCTACCTCT ATGAAGCAAC TCCTTTCAAA GAAGTACAAA AGCCACTAGA AAACCTTAAT	360
CATATTGCCT GGTTCCTTAT TGACGAGGCT ATCAAAAACC TTAAACGTGG TAGCCATAAA	420
TGGGCCATTG AATCTTGAA AAAACAGCAT AAGATTGACT AA	462

(2) INFORMATION FOR SEQ ID NO:893:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

GCTTATCGCA AGGGAACAGT TTTTAGCTCT GCCAAGCCAC ATAGTGTGCT TACTACTATG	60
TGTCCATGTC ACCATGAATT GCCGAACGGT TTAACGAGAA AGTATAGTAG ATTGAAACAA	120

GATGTGAACA AATCGATTAG GAAAGTCAAA TTAATTTCTA GAAATATTTT AACAGTCATA	180
ACGGACTATT CCAGATTCAA TCTACTATAT TACTTTTAG	219

(2) INFORMATION FOR SEQ ID NO:894:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

TGCAGGCGCA AGGCTTCTAC CATCATCTAT TCAATAAATA AGGAGAATGT CATGAATCCT	60
AATCTTTTTA GAAGTGTCGA GTTTTATCAG AGACGTTACC ATAACATATGC GACAGTGTTT	120
ATTATACCTC TTTCATTACT ATTTACTTTC ATCTTGATTT TCTCCCTTGT TGCCACAAAA	180
GAAATTACTG TTAATTCCCA AGGAGAAATC GCCCCTACAA GTGTCATTGC ATCTATTTCAG	240
TCGACCAGTG ATAATCCTAT CCTTGCTAAT CATTAGTGG CAAATCAAGT AGTTGAGAAA	300
GGTGACTTAC TCATCAAATA CTCTGAAACA ATGGAAGAAA GTCAGAAAAC TGCCTTAGCA	360
ACTCAATTAC AAAGACTTGA GAAGCAAAAA GAAGGACTTG GAATCTTGAA ACAAAGCTTA	420
GAAAAAGCGA CTGATCTTTT TTCTAGCGAG GATGAGTTTG GCTACCATAA TACCTTTATG	480
AATTTTACTA AACAAATCCCA TGATATTGAA CTGGGTATCT CAAAGACTAA CACTGAAGTT	540
TCAAAATCAAG CTAATCTTAC CAATAGCAGT TCATCAGCCA TCGAACAAGA AATTACAAAA	600
GTTCAACAAC AAATTGGAGA ATATCAAGAG TTGAGAGATG CTATCATAAA TAACAGAGCA	660
CGCTTACCAA CTGGCAATCC GCACCAGTCA ATTTTAAATC GTTATCTTAT AGCCTCTCAA	720
GGACAAACAC AAGGAACGGC AGAGGAGCCA TTTTATCTC AAATTAATCA AAGTATTGCA	780
GGTCTGGAAT CATCTATCGC AAGCCTCAAA ATTCAGCAAG CTGGTATCGG AAGTGTAGCA	840
ACTTATGATA ATAGTTTAGC AACCAAAATT GAAGTACTCC GCACTCAGTT TTTACAAACA	900
GCCTCACAGC AACAATAAAC CGTGGAGAAT CAATTAACAG AATTAAAAAGT ACAACTAGAT	960
CAAGCGACAC AGCGCTTAGA AAATAATACC TTAACCGCTC CAAGTAAAGG TATCGTTCAT	1020
CTGAACAGCG AATTTGAAGG TAAAAATAGA ATTCCAAC TGACAGAAAT TGCTCAAATA	1080
TTCCCTGTCA TCACAGATAC AAGAGAAAGTA CTAATCACTT ACTACGTATC ATCTGACTAT	1140
CTCCCCTTAC TAGATAAAGG ACAAACCTGTA AGATTAAAAAC TGGAGAAGAA TGGAAATCAC	1200
GGCACCACCA TCATCGGCTA A	1221

(2) INFORMATION FOR SEQ ID NO:895:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

TTAAGGCGCA ATATACCTGA GGGTTATTTT GGGAAAATCA ATCAGTTTAT GGAGCAGGTC	60
TATTCTCAGG GGATTATTTA TCCACCCAAG GAAAAGGTTT TTCAGGCTCT CTTGACAACA	120
CTGCTTGAAG AAGTTAAGGT GGTAATTCTA GGCAAGACCC CTATCACGGA CCAGGTCAAG	180
CGCAGGGCTT GA	192

(2) INFORMATION FOR SEQ ID NO:896:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...921
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

CTCTTAAGCA AGGTCCAACC TATGCTAAAG ATTTTGACTA CGAATGAATT CCGTAACTAC	60
TTGGATGAGC TTGGGGATTCT TCTCCTCGTT GTTAACGATG ATGAAATTGT CAAAGTCCAT	120
GTTTCATACAG AAGATCCAGG ACTTGTTATG CAAGAAGGTC TCAAATATGG TAGCTTGGTC	180
AAGGTAAAAG TTGACAATAT GCGTAATCAA CACGAAGCAC AGGTTGAGAA AGAAGCTACT	240
CAAGTTATCA AGTCGGCTGA AGAAAAAGAG TATGCTTTGA TTGCTGTGGT GGCTGGTAAA	300
GGTCTAGCAG ATATCTTCTG TTCTCAAGGC GTGGATTATG TTATCGAAGG CCGTCAAACC	360
ATGAACCCTT CAACAGAAGA CTTTATCAAG GCTGTTGAAC AGGTCAATGC CCGTAACATC	420
ATCTTCTTGC CAAACAACAA GAACATCTTC ATGGCAGCTC AATCTGCGGC AGAAGTTTTG	480
GAGCAACCAG CAGTAGTGGT AGAGGCTCGC ACTCTTCCTC AAGGTATGAC AAGTCTTCTT	540
GCCTTTGATC CAAGCAAGTC CATTGAAGAA AACCAAGAGC GTATGACAGC TGCTCTTAGC	600
GATGTTGTTA GCGGAAGCGT CACAACAGCC GTGCGTGATA CAACGATCGA TGGCTTAGAA	660
ATCCATGAAA ACGATAATCT AGGTATGGTG GATGGAAAAA TTCTTGTGTC AAACCCTGAT	720
ATGCACCAA CATTGACTGA AACCTTGAAA CATATGTTGG ATGAAGACAG TGAAATCGTA	780
ACCTTCTATG TCGGTGAAGA CGGAAGCGAA GAACTTGCCA ATGAAATCGC TCAAGAAATC	840

GTAGAAGAAT TCGAAGACGT TGAAGTCGAG ATTCACCAAG GTCAACAACC TGTTTACCCA	900
TACCTATTTA GTGTGGAATA A	921

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

AAAAGGAGCA AACTCATGAA AAAAGAAACC TTCACTGAAA AACTGATCAA ACGCACATAC	60
GGTATTTCTG GTCCCTTGA CGAATACAAA CGGCGTGAGG CCGATAGTAT TGGGAACCAA	120
GTCTTTATCG TCCTCTTTTA TCTGATGATT TTCGGAAATC TTATTCCACT CCTTCTGGCC	180
TATAAATACC CTCAAGAAGT GGCTCTAATC TATCCTCCTC TGATTTTAGT GATTGCCCTC	240
ATCGCTGCTG GCTATGTCAC CTACCAAATG AAAAAAACA GGCATCACAG TCATTGA	297

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

GTTTTTTTAA ACTTTTTTTC ATCAAGTGTT CCAACCGCAA CATACCATAG TCCGTACGGG	60
ATTCGAACCC GTGTTACCGC CGTGAAAAGG CGGTGTCCTA ACCCCTTGAC CAACGGACCT	120

GAGTTGTTAT TTTCAACTCT TACTATTATA CAGTCTTTTC AAACCTTGTC AACTACTTTT	180
TCTAATTTTT TTCATTTTTT TTGCATGACT TACTAG	216

(2) INFORMATION FOR SEQ ID NO:899:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

GCTTTTTTAA ACTTTTTTTC ATCAAGTGTT CCAACCGCAA CATACCATAG TCCGTACGGG	60
ATTCGAACCC GTGTTACCGC CGTGAAAAGG CGGTGTCTTA ACCCCTTGAC CAACGGACCT	120
GAGTTGTTAT TTTCAACTCT TACTATTATA CAGTCTTTT ATGTTTTGTC AACTACTTTT	180
TCTAATTTTT TTTATTTTTT CAACTTATAG	210

(2) INFORMATION FOR SEQ ID NO:900:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

ATGAATTTAA ATCAATTAGA TATTATCGTT TCAAATGTTT CCCAAGTCTG TGCTGACTTG	60
GAGCATATTT TGGATAAAAA GGCAGATTAT GCTGATGATG GTTTTGCTCA GTTTACGATT	120
GGTAGTCACT GCCTTATGTT GTCACAAAAT CATTTGGTTC CTTTGAAAA CTTTCAGTCA	180

GGAATCATT	TTCATATCGA	GGTTGAGGAT	GTAGACCAGA	ACTACAAACG	GTTGAACGAG	240
CTTGGTATAA	AGGTTTAC	CGGACCAACT	GTAACCGATT	GGGGAACAGA	GTCCTTATTA	300
GTTCAAGGAC	CTGCTGGTCT	AGTGCTTGAT	TTTTATCGTA	TGAAATAG		348

(2) INFORMATION FOR SEQ ID NO:901:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

ATTGATTTAA	ATTCTCAAAT	CATATTATTC	AGTTCTTATT	TCATTTTGCT	CTACAATCCT	60
GTTGAGAAGA	CACGTGTTCA	TATCAAAAAG	GTATTGGCAA	GTTGCAATAC	CTTTTACGA	120
GGCTCTTTTA	TCTTATTTT	GTTTCAACTG	ACTATATCTC	CTATGGTTCT	AGTTCAGAAG	180
GCTAGGCTAT	AA					192

(2) INFORMATION FOR SEQ ID NO:902:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...804
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

CAAATTTCCC	TCAAATTAGC	TAGTAGCATT	GCCTGTTTGT	ACTGGCTAAA	AACAGGCTAT	60
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TTCAAATTCA	GTTTCAGACC	ATCTGGCATG	GAAAAATCTG	TTATAATAAT	AGAAAAGGAG	120
AAGCGCATGC	ACAAGATTTT	ATTAATAGAA	GATGATCAGG	TCATTTCGTCA	ACAGGTCGGG	180
AAAATGCTCT	CTGAATGGGG	ATTTGAAGTG	GTCCTGGTAG	AAGACTTTAT	GAAAGTTTTG	240
AGTCTATTTG	TTCAATCGGA	ACCTCATCTG	GTCTCATGG	ATATTGGTTT	GCCCTTGTTT	300
AATGGTTATC	ACTGGTGTCA	GGAAATCCGC	AAGATTTCCA	AGGTACCTAT	CATGTTTCTT	360
TCTTCGAGAG	ACCAGGCTAT	GGATATTGTC	ATGGCAATCA	ATATGGGGGC	GGATGACTTT	420
GTGACCAAGC	CTTTTGACCA	GCAGGTTCTT	TTAGCTAAGG	TTCAAGGGCTT	GTTGCGTCGT	480
TCCTATGAGT	TTGGGCGTGA	TGAGAGTTTG	CTGGAATATG	CTGGTGTTAT	CCTCAATACC	540
AAATCCATGG	ATTTACATTA	TCAAGGGCAA	GTCTTGAATT	TGACCAAGAA	TGAATTCCAG	600
ATTTTACGCG	TGTTATTTGA	GCATGCAGGC	AACATCGTAG	CACGTGACGA	CCTGATGCGG	660
GAACTTTGGA	ACAGTGACTT	TTTCATTGAT	GATAATACCC	TCTCTGTCAA	TGTGGCTCGT	720
TTGCGTAAAA	AGTTGGAGGA	GCAGGGATTG	GTAGGATTTA	TCGAGACCAA	GAAAGGAATA	780
GGGTACGGAT	TGAAGCATGC	TTGA				804

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

AAAAGCTTAA	AGACTATGTT	ACAGTGGATT	AAGAATTTCT	CTATTCCCCT	AATTTACCTG	60
AGTTTTCTGT	TACTTTGGCT	TTACTACGCT	ATTTTCTCAG	CATCCTATCT	TGCTTTGTTG	120
GGATTTGTTT	TTCTGTAGT	CTGTCTCTTT	TTCCAATTTT	CTTGGAATC	TGCTAGCAAA	180
GTTCTAGTGA	TTTGTGGAAT	CTTTGGATTT	TGGTTTGTTT	TTCAAAATTG	GCAACAGAGT	240
CAAGCGAGTC	AAAATCTGGC	GGATTCTGTT	GAAAGGGTAC	GGATTTTGCC	TGATACTATT	300
AAGGTCAATG	GTGATAGTCT	ATCCTTTTCGT	GGCAAGTCTA	ACGGTCGTGC	TTTCCAAGTC	360
TATTATAAAC	TCCAGTCCGA	GGAGGAGAAA	GAAGCCTTTC	AAGCTTTAAC	CGACCTGCAT	420
GAGATAGGAC	TAGAAGGGAA	GCTTTCGGAG	CCAGAAGGGC	AGAGAAATTT	TGGTGGCTTT	480
AATTACCAAG	CCTATCTGAA	GACTCAGGGA	ATTTACCAGA	CACTCAATAT	TAAAAGAATC	540
CAGTCACTCC	AAAAGGTTGG	CAGTTGGGAT	ATAGGTGAAA	AACTGTCCAG	TTTACGTCGA	600
AAGGCTGTGG	TTTGGAATTA	GATGCACTTC	CCAGACCTTA	TGCGCAATTA	CATGACAGGA	660
CTCTTGCTAG	GACATCTGGA	CACCGATTTT	GAGGAGATGA	ATGAGCTTTA	TTCCAGTTTA	720
GGAATTATT	ACTNTTTTGC	CTTGTCAGGT	ATGCAGGTAG	GGTTTTTCAT	GAATGGATTT	780
AAGAACTTTC	TCTTGCGATT	GGGCTTGACC	CAAGAAAAGT	TGAAATGGCT	GACTTATCCC	840
TTTTCCCTTA	TCTATGCGGG	ACTAACTGGA	TTTTTCAGCAT	CGGTTATTCG	CAGTCTCTTG	900
CAAAAGCTAC	TGGCTCAACA	TGGGGTTAAG	GGCTTGGATA	ATTTTGCCTT	GACGGTGCTT	960
GTCTCTTTTA	TTGTCATGCC	AAACTTTTTT	TTGACAGCAG	GAGGAGTCTT	GTCTGCGCT	1020
TATGCTTTTA	TCCTGACCAT	GACCATTAATA	GAAGGGAAGG	GGCTCAAGGC	TGTTGCTAGT	1080
GAAAGTCTAG	TCATCTCCTT	GGGCATATTG	CCCATTATAT	CCTTCTATTT	TGCGGAATTT	1140
CAACCTTGGT	CTATCCTTTT	GACCTTTGTC	TTTTCTTTTC	TATTTGACTT	GACCCTCTTA	1200

CCGCTCCTGT CTATTTTATT TGTCCCTTCC TTTCTCTATC CAGTCATTCA GCTGAACTTT	1260
ATCTTTGAAT GGTGGAGGG CATTATTCGC TTGGTCTCAC AGGTGACAAG TAGGCCTCTA	1320
GTCTTTGGAC AACCCAATGA ATGGCTTTTA ACCCTATTGT TAAATATTCT TTGGCTTTGG	1380
TCTATGATTT GA	1392

(2) INFORMATION FOR SEQ ID NO:904:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

AATCAATTAA AAAGTGAACA AATTTATTGG GAAATTCAAA TCACTTTCTT AAAATATTTT	60
AGGAACCGTA GTGTAATATT CCAGATTCAA TTCACTATAA AACTAGCCTT TCTCCTGCAA	120
AAGAAAAAGG AAAGACTTCC TTTCGTGCCT TTCCTCTTAC TTGCTACTTG TTTGATTATT	180
TTTGGTAAGC TACTGCTTGT CTGA	204

(2) INFORMATION FOR SEQ ID NO:905:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

AACAAATTAA	ATAAGGAGAA	AATCATGGTA	AAAGTAGCAG	TTATATTAGC	TCAGGGCTTT	60
GAAGAAATTG	AAGCCTTGAC	AGTTGTAGAT	GTCTTGCGTC	GAGCCAATAT	CACATGTGAT	120
ATGGTTGGTT	TTGAAGAGCA	AGTAACGGGT	TCGCATGCAA	TCCAAGTAAG	AGCAGATCAT	180
GTCTTTGATG	GAGATTTATC	AGACTATGAT	ATGATTGTTC	TTCTTGAGG	TATGCCTGGT	240
TCTGCACATT	TACGTGATAA	TCAGACCTTG	ATTCAAGAAT	TGCAAAGCTT	CGAGCAAGAA	300
GGGAAGAAAC	TAGCAGCCAT	TTGTGCGGCA	CCAATTGCC	TCAATCAAGC	AGAGATATTG	360
AAAAATAAGC	GATACACTTG	TTATGACGGC	GTTCAAGAGC	AAATCCTTGA	TGGTCACTAT	420
GTCAAGGAAA	CAGTAGTGGT	AGATGGTCAG	TTGACAACCA	GTCGGGGTCC	TTCAACAGCC	480
CTTGCCTTTG	CCTACGAGTT	GGTGGAGCAA	CTAGGAGGGG	ACGCAGAGAG	TTTACGAACA	540
GGAATGCTCT	ATCAAGATGT	CTTTGGTAAA	AATCAGTAA			579

(2) INFORMATION FOR SEQ ID NO:906:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...750
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

GAAAGATTAA	AATGTGAAAA	AAGGAGATTC	CTAATGGGAC	GTAAATGGGC	CAATATCGTA	60
GCTAAGAAAA	CGGCTAAAAG	TGGAGCCAAC	TCTAAAGTAT	ATGCAAAATT	TGGTGTAGAA	120
ATCTATGTAG	CAGCTAAAAA	AGGTGATCCA	GATCCAGAAT	CAAACTCAGC	TTTGAAATTC	180
GTTATCGACC	GTGCTAAACA	AGCCCAAGTG	CCAAAACACA	TTATCGATAA	AGCGATTGAT	240
AAAGCCAAAG	GAAACACAGA	CGAAACCTTT	ACAGAAGGAC	GTTACGAAGG	TTTTGGGCCA	300
AATGGCTCTA	TGCTAATTGT	GGATACTTTG	ACTTCTAACG	TCAACCGTAC	AGCAGCCAAT	360
GTCCGTGCAG	CCTTTGGTAA	AAACGGCGGA	AACATGGGCG	CTTCAGGTTT	TGTTTCTTAC	420
CTTTTTGACA	ACAAAGGTGT	TATTGTATTT	GGAGGTGAAG	ATGCGGACGC	AGTCTTTGAG	480
CAATTGCTCG	AAGCGGATGT	GGATGTGGAT	GACGTAGAAG	CACAAGAAGG	TACAATCACA	540
GTTTACACAG	CGCCAACTGA	CCTTCACAAG	GCTATCGTTG	CTCTCCGTGA	GTCTGGTATT	600
GAAGAATTCC	AAGTGACTGA	ATTGGAAATG	ATTCCTCAGT	CAGAAGTGGA	ATTGTCAGGC	660
GAAGACCTTG	AAACCTTTGA	AAAACTTTAC	AGCGTTCTTG	AAGACGACGA	AGACGTCCAA	720
AAGATTTATA	CGAACGTAGA	TGGGTTTTAA				750

(2) INFORMATION FOR SEQ ID NO:907:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

AATATGTTAA	AGGAAATAAA	AAGGAGAAAC	AGAATGAAAA	ATAAACGTTT	AATTGGAATT	60
ATTGCTGCAT	TAGCAGTCTT	AGTAGCAGGA	AGCTTGATTT	ATTCTTCAAT	GAATAAATCA	120
GAAGCTCAGA	ATAATAAGGA	TGAGAAGAAA	ATAACTAAGA	TTGGTGTGCT	TCAATTTGTG	180
AGCCATCCAT	CCCTTGATTT	GATTTATAAA	GGGATCCAAG	ATGGACTTGC	AGAAGAAAGA	240
TATAAAGATG	ATCAAGTTAA	AATTGATTTT	ATGAACTCAG	AAAGGTGA		288

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

ATAATGTTAA	AAATTGGTAC	AGCTTGTGGT	TCAGGATTAG	GTTCAAGTTT	TATGGTACAG	60
ATGAATATTG	AATCTGTATT	GAGTGATTTG	AATGTTTCGG	ATGTAGAAGT	TGAACATTAT	120
GATTTAGGTG	GAGCAGATCC	AAATGCAGCT	GATATTTGGA	TTGTTGGTCG	TGATCTAGCT	180
GATTCAGCTA	GTCATCTTGG	AGATGTTTCG	ATCTTAAATA	GTATTATTGA	TATGGACGAA	240
CTACGAGAAT	TAATTACTAA	AATTTGTGAA	GAAAAAGGAC	TTATATAG		288

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

AAGATGTTAA ATTTACAATT TGCAGAAACA ATGGAATTGA CAGAAGCTGA GTTGGAGACA	60
GTTTATGGAG GGGAAATTTGG GAATAATGCT GTTATCCCAG CCGGTGCTTG GGGAGGTTTA	120
GGAACGTCTT GGTCAATCAC TAATTTCTGG AAGAAATATT TTAACCATGA TTCTTCCACT	180
GTTAATCGTC GCCATTATTG A	201

(2) INFORMATION FOR SEQ ID NO:910:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

ATGGCGTTAA AATACACAAC TTGGAAAGTT ACTGACGAAA AAGAGTTGAA GCTACGTTTG	60
ACATCTCATC AAACCTGCAAC TGTGGAAGAA AAAATCGGCA TGAACCTGCT GAAGATTTTC	120
ATGCCTGAAG CTGGCGAAGA GTTCACTTTA CCGCCTTTGA AAGTTATGTT GTTGTTAGTT	180
CACGAGCCT TGCAGCAGTA TGAACATGGG TATTCTCTTG AGGATGTCTA TGATTTATAC	240
GATGAATACG TGGACAATGG CGGAGACCAA ACAACCTTCA TGACAGAGGT GTTGATGCCA	300
CTCTTTGAAG TATCGGTTT TACTCCACGA GGAAGCAAGG ACAAGAAAAC TTCCAAGAAG	360
AAAATGACAG TAGACAAGTA A	381

(2) INFORMATION FOR SEQ ID NO:911:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...345
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

AGAAAGTTAA	AAAAAGAGGA	AAACAAAATG	AATAAAACAA	CTGAAATGAT	CGTATTTTCGT	60
AGCCGTAAAA	CTGGAGAATT	TCTTAATTCT	TACAAGGACA	GAAGTTCTTT	AGCATTTTGCA	120
GCTGACTTTT	GCAGCTTGGA	ATATTGTTTG	AAGCTTCCTC	GTAAAAAATA	CGAAGACAAC	180
AAAAAGACTT	ACAAGGCTCT	TGCTGCAGCT	TTTGACTGTG	AAATTGTCGC	AGTTGAAGCG	240
GAATACAAAT	TGACCTATCC	GAATGGATCA	GAAGTTGAAC	CTATCAAGCG	TGACCGTTCA	300
TCAATTGAGG	ACATGATTAA	GGATATTATT	GGAGGGGTTC	TCTAA		345

(2) INFORMATION FOR SEQ ID NO:912:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1953 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1953
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

TTGCATTCCC	TAGTGATTTT	TGTTAAGATA	AATGCAAATA	CAAATGAAAG	CGAGAACAAG	60
ATGACACGTT	ATCAAGATGA	TTTTTATGAT	GCTATCAATG	GAGAATGGCA	ACAGACAGCT	120
GAAATCCCAG	CAGATAAGTC	TCAAACAGGA	GGTTTTGTTG	ATTTAGACCA	GGAAATTGAA	180
GACCTGATGT	TGGCGACAAC	AGACAAGTGG	TTAGCAGGTG	AAGAAGTGCC	TGAGGATGCT	240
ATCTTGGA	AACTTTGTCAA	ATACCACCGC	CTAGTTCGTG	ATTTTGACAA	GAGAGAAGCT	300
GACGGTATCA	CACCTGTCTT	ACCACTCCTT	AAAGAATTCC	AAGAATTGGA	AACTTTTGCG	360
GATTTTACAG	CTAAACTAGC	AGAGTTTGAG	CTTGCAGGAA	AACCAAACTT	CCTTCCTTTT	420
GGTGTATCGC	CAGACTTTAT	GGATGCTAGA	ATCAATGTTC	TATGGGCTAG	CGCTCCAAGC	480
ACAATCTTGC	CAGATACGAC	CTACTATGCA	GAAGAACATC	CTCAGCGCGA	AGAGCTCTTG	540

ACTCTTTGGA	AAGAAAGCAG	CGCAAATCTC	CTCAAGGCTT	ATGATTTCTC	TGATGAAGAA	600
ATTGAAGACT	TGCTAGAAAA	AAGACTTGAA	TTGGACCGCC	GAGTTGCGGC	AGTGGTGCTC	660
TCTAATGAAG	AAAGTTCAGA	ATATGCTAAA	CTCTATCATC	CATATTCTTA	CGAAGATTTC	720
AAGAAATTCG	CGCCTGCCCT	ACCTTTGGAT	GACTTCTTCA	AAGCAGTTAT	TGGGCAATTA	780
CCAGACAAGG	TTATTGTTAG	CGAGGAACGT	TTCTGGCAAG	CAGCAGAGCA	ATTCTACAGT	840
GAGGAAGCCT	GGTCTCTCCT	TAAAGCAACC	TTGATTTTGA	GTGTTGTCAA	TCTTTCAACC	900
AGCTATTTAA	CAGAGGATAT	CCGTGTTTTG	TCTGGTGCCT	ACAGCCGTAC	CCTTTCTGGA	960
GTTCCAGAGG	CAAAAAGATA	GGTCAAAAGCA	GCTTATCATC	TAGCACAGGA	ACCTTTCAAG	1020
CAAGCCCTGG	GTCTTTGGTA	CGCCCGTGAG	AAGTTCTCTC	CAGAAGCCAA	GGCGGATGTG	1080
GAGAAAAAAG	TGGCAACCAT	GATTGATGTC	TATAAGGAGC	GTCTGCTTAA	GAATGACTGG	1140
CTCACTCCAG	AAACCTGTAA	ACAGGCTATC	GTGAAGCTCA	ATGTGATCAA	ACCTTATATT	1200
GGCTATCCAG	AAGAATTGCC	TGCACGTTAC	AAGGATAAGG	TAGTGAATGA	AACTGCCAGT	1260
CTTTTTGAGA	ATGCTCTAGC	CTTTGCGCGT	GTGGAAATCA	AGCACAGTTG	GAGTAAGTGG	1320
AACCAGCCTG	TAAACTATAA	GGAATGGGGC	ATGCCTGCTC	ATATGGTCAA	TGCCTACTAC	1380
AATCCTCAGA	AGAACCTGAT	TGTCTTTCCA	GCGGCCATTT	TACAGGCGCC	TTTCTATGAC	1440
TTGCATCAGT	CATCTTCTGC	TAACTACGGT	GGTATTGGGG	CAGTGATTGC	CCATGAAATT	1500
TCCCACGCCCT	TTGATACTAA	CGGAGCTTCC	TTTGACGAAA	ATGGTAGCCT	CAAGGATTGG	1560
TGGACAGAGA	GCGACTATGC	TGCCTTCAAG	GAGAAAAACAC	AAAAAGTCAT	TGACCAATTT	1620
GATGGACAGG	ATTCTTATGG	AGCAACCATT	AACGGTAAAT	TGACTGTATC	AGAAAACGTG	1680
GCTGACTTGG	GAGGAATCGC	AGCAGCGCTT	GAAGCAGCTA	AGAGAGAAGC	AGACTTCTCA	1740
GCAGAAGAGT	TCTTCTACAA	CTTCGGTCGC	ATCTGGCGCA	TGAAAGGTCG	TCCAGAATTT	1800
ATGAAACTTT	TGGCTAGCGT	CGATGTGCAC	GCACCAGCCA	AACTCCGTGT	CAATGTGCAA	1860
GTACCAAAC	TCGACGATTT	CTTTACAACC	TATGATGTCA	AAGAAGGAGA	CGGAATGTGG	1920
CGTTCACCAG	AGGAGCGCGT	GATTATTTGG	TAA			1953

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

CCTTTACTAA	AAATTAAGGA	AAAACGAATG	AAAAAAGAAC	AAATTCCCAA	TCTCTTAACA	60
ATAGGTGCAA	TTCTCTTTAT	ACCTATTTTT	ATCTTTATTT	TAACGATAGG	AAATTCGATA	120
GAGAGTCATA	TAGTTGCAGC	TATTATCTTT	GCTGTTGCCA	GTATTACCGA	CTATTTAGAT	180
GGATATTTAG	CTCGTAAATG	GAATGTGGTC	AGTAATTTTG	GTAATTTTGC	AGATCCTATG	240
GCGGATAAGT	TACTAGTTAT	GTCGGCTTTT	ATTATGTTGA	TTGAGTTAGG	TATGGCTCCG	300
GCTTGGAATTG	TTGCAGTGAT	TATCTGTCGT	GAGTTAGCTG	TGACAGGTTT	AAGGCTTTTA	360
TTGGTTGAAA	CTGGTGGAAC	AATTTTAGCA	GCAGCAATGC	CTGGAAAAAT	TAAAACTTTT	420
AGTCAGATGT	TTGCCATTAT	TTTCTTGCTA	TTACATTGGA	CTTTGCTTGG	TCAAGTTCTA	480
CTTTATGTAG	CCTTATTTTT	CACTATCTAC	TCTGGCTATG	ACTATTTCAA	GGGTAGTGCC	540

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

CCTAAGCTAA	ATTTTAAAAA	GCGAGGGTGG	TTATTTTCTC	AAAGTTTGA	AGGAGCTAAA	60
GCAACAGCTA	TTATTATGAG	TTTGTTGGAA	ACAGCTAAAC	GTCATCAATT	AAATAGCGAG	120
AAATATCTAT	TCTATCTTCT	AGAATGTCTT	CCAAACGAGG	AAACTCTCGT	AAACAAAGAG	180
GTTTTAGAGG	CTTATTACC	ATGGACTAAA	GTTGTACAAG	AAAAGTGCAA	ATAA	234

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

AACAATATAA	ATAAGATGAA	AGAAATTGAA	AACAATCAGT	GGATTGCTAA	CTACCGGACG	60
GATCAACCGC	ATTTTGGCTT	GGAACGAATG	GTGGAAGTGT	TAGCTTTGCG	TGGCAATCCC	120
CATCTCAAAC	TCAAGGTCCT	CCATATCGGA	GGAACCTAACG	GCAAGGGCTC	GACTATTGCT	180

TTTTTGAAAA	AGATGCTAGA	AAAGCTAGGG	CTGAGAGTTG	GCGTGTTTAG	CTCGCCCTAT	240
CTCATTCATT	ACACAGACCA	GATTAGCATC	AATGGGGAAT	CGATCTCAGA	AGTGAGGCTA	300
GAAGCTCTCA	TGGCAGACTA	TCAGTCTTTG	CTGGAGGGAG	AAGCGGTCGC	CAATTTACAG	360
GGCACAACCG	AGTTTGAGAT	TATCACAGCC	CTAGCCTATG	ACTACTTTGC	CTCAGAGCAA	420
GTAGATGTGG	CTATCATGGA	AGTTGGCATG	GGTGGACTTT	TGGATAGTAC	CAATGTCTGT	480
CAGCCCATTT	TGACAGGAAT	TACAACTATT	GGCTTGGATC	ATGTGGCCCT	ACTTGGTGAC	540
ACCTTGAGAG	CCATAGCAGA	GCAGAAGGCA	GGTATTATCA	AACAAGGGAT	GCCCTTGGTA	600
ACAGGGCGTA	TTGCTCCAGA	AGCCTTGGCT	GTGATTGACC	GCATTGCGGA	AGGGAAAGAT	660
GCGCCGAGAC	TTGCCTACGG	GACAGATTAT	CAGGTTCTGC	ATCAAGAAAG	TGTGGTGACA	720
GGGGAAGTCT	TTGACTATAC	AAGTGCTGTC	AGACAAGGTC	GCTTCCAGAC	TAGCCTGCTT	780
GGTTTGTACC	AAATAGAGAA	TGCTGGGATG	GCCATAGCTT	TACTTGATAC	TTTTTGTCAA	840
GAAGATGGTC	GAGAGCTAGC	AAGCAATGAT	TTTCTTGGTC	AAGCCTTGA	AGAAACAAGT	900
TGGCCAGGGC	GTTTGGAAT	CGTGTCAAGA	GATCCCTTGA	TGATTTTGA	TGGAGCCAC	960
AATCCCCATG	CTATCAAGGC	CTTGTGGTA	ACCTTGCAAG	AACGTTTTGC	GGATTATCAT	1020
AAGGAAATCC	TCTTCACTTG	TATCAAAACC	AAGGCCCTGG	AGGATATGTT	GGACTTGCTG	1080
GGAGCCATGC	CAGATACCGA	GCTTACTCTA	ACACATTTTG	CGGATAGTCG	GGCGACGGAT	1140
GAAAACGTGC	TGAAAGAGGC	AGCTAAGTCT	AGAAATCTCA	GCTACCAAGA	TTGGCATGAT	1200
TTTCTAGAGC	AGAATTTGAC	AGATAAAAAA	GAAGAGAAAC	AAACAGTTAG	GATTGTCACA	1260
GGTTCCTTGT	ATTTCTTGAG	CCAAGTGAGG	GCCTATCTGA	TGGAGAGGAA	GAACGAGAAT	1320
GGATACACAA	AAGATTGA					1338

(2) INFORMATION FOR SEQ ID NO:916:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

ACCATCATAA	AGCTTAGCTT	TAACGTCAAC	CATTGGGTAA	CCTGCAAGAA	CACCGTTAGC	60
CATAGATTCT	ACCAAACCTT	TTTCAACCGC	TGGGATAAAT	TCACGAGGAA	CCACACCACC	120
GACGATTGCG	TTTTCGAATT	CGAATCCTTT	ACCTTCTTCG	TTTGGAGTAA	ATTCAATCCA	180
TACATCACCG	AATTGACCTT	TACCACCAGA	CTGACGTTTG	AAGAATCCAC	GTGCTTGAGT	240
AGAAGCGCGG	AATGTTTCAC	GGTAAGATAC	TTGAGGCGCA	CCTACGTTTC	CTTCAACTTT	300
GAACTCACGA	CGCATACGAT	CAACAAGGAC	GTCAAGGTGA	AGTTCACCCA	TACCTGA	357

(2) INFORMATION FOR SEQ ID NO:917:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

TACTCAATAA	AAATCAAAGA	GCAAAC TAGA	AAGCTAGCCG	CAGTCAGCTC	AAAACACTGT	60
TTTGAGGTTG	TGGATAGAAC	TGACGAAAGTC	AGCTCAAAAC	ACTGTTTTGA	GGTTGTGGAT	120
AGAACTGACG	AAGTCAGTAA	CCATATATAC	AGCAAGGCGA	AGCTGACGTG	GTTTGAAGAG	180
ATTTTCAAAG	AGTATAAGTT	ATACTTTTAC	AAC TTGAACC	TCGTCTTTAC	CGAGTAA	237

(2) INFORMATION FOR SEQ ID NO:918:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1056 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1056
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

AAGGCAATAA	ATAATAGAAA	AGAGAGAAAA	GCTATGACAG	TTCAAATGGA	ATATGAAAAA	60
GATGTTAAAG	TAGCAGCACT	TGACGGTAAA	AAAATCGCCG	TTATCGGTTA	TGGTTCACAA	120
GGGCATGCGC	ATGCTCAAAA	CTTGCGTGAT	TCAGGTCGTG	ACGTTATTAT	CGGTGTACGT	180
CCAGGTAAAT	CTTTTGATAA	AGCAAAAGAA	GATGGATT TG	ATACTTACAC	AGTAGCAGAA	240
GCTACTAAGT	TGGCTGATGT	TATCATGATC	TTGGCGCCAG	ACGAAATTCA	ACAAGAATTG	300
TACGAAGCAG	AAATCGCTCC	AAACTTGGAA	GCTGGAAACG	CAGTTGGATT	TGCCCCATGGT	360
TTCAACATCC	ACTTTGAATT	TATCAAAGTT	CCTGCGGATG	TAGATGTCTT	CATGTGTGCT	420
CCTAAAGGAC	CAGGACACTT	GGTACGTCGT	ACTTACGAAG	AAGGATTTGG	TGTTCCAGCT	480
CTTTATGCAG	TATACCAAGA	TGCAACAGGA	AATGCTAAAA	ACATTGCTAT	GGACTGGTGT	540
AAAGGTGTTG	GAGCGGCTCG	TGTAGGTCTT	CTTGAAACAA	CTTACAAAGA	AGAAACTGAA	600
GAAGATTTGT	TTGGTGAACA	AGCTGTACTT	TGTGGTGTT	TGACTGCCCT	TATCGAAGCA	660

GGTTTCGAAG TCTTGACAGA AGCAGGTTAC GCTCCAGAAT TGGCTTACTT TGAAGTTCTT	720
CACGAAATGA AATTGATCGT TGACTTGATC TACGAAGGTG GATTCAAGAA AATGCGTCAA	780
TCTATTTCAA ACACTGCTGA ATACGGTGAC TATGTATCAG GTCCACGTGT AATCACTGAA	840
CAAGTTAAAG AAAATATGAA GGCTGTCTTG GCAGACATCC AAAATGGTAA ATTTGCAAAT	900
GACTTTGTAA ATGACTATAA AGCTGGACGT CCAAAATTGA CTGCTTACCG TGAACAAGCA	960
GCTAACCTTG AAATTGAAAA AGTTGGTGCA GAATTGCGTA AAGCAATGCC ATTCGTTGGT	1020
AAAAACGACG ATGATGCATT CAAAATCTAT AACTAA	1056

(2) INFORMATION FOR SEQ ID NO:919:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

ATTAAAATAA ATCACTGTGA CTGCCTGTCC TCAGCAAATT TAAAATCAAT TCCGACTTAT	60
CTACTTTATA AACCAAAAGC CAATCTGGCT GGGTATGGCA TTCACGAACT CCTTGAAAAT	120
GCTTGGATGC CGTCAATGAA TGATCACGAT ATCTGGCAGG ATGTTCTTTT TCTTGAACCA	180
GAAAAATCAA AACTTCTTCT AATAATTCTG CCTTCAAACC ACGCTTCATA G	231

(2) INFORMATION FOR SEQ ID NO:920:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

GATAAAATAA	ATATAACAGG	AGAAATTATC	ATGTCAGTAG	AAGAAAAATT	AAATCAAGCT	60
AAAGGTTCTA	TTAAAGAAGG	TGTTGGGAAA	GCCATCGGTG	ATGAAAAAAT	GGAAAAAGAA	120
GGAGCAGCTG	AAAAAGTTGT	TTCTAAAGTA	AAAGAAGTTG	CCGAAGACGC	TAAAGACGCT	180
GTAAGAGGTG	CTGTAGAAGG	TGTTAAAAAC	ATGTTGAGTG	GCGACGATAA	ATAA	234

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GAAAAAATAA	AAGAGGTGGA	GGGCAGCATT	CCTTGTGCGC	CGTCCCTTCT	TTTAAATGGA	60
GACAGAAAGA	TGATGAATGA	ATTATTTGGA	GAAATTTCTAG	GGACTTTAAT	CCTGATTCTT	120
CTAGGAAATG	GTGTTGTTGC	AGGTGTGGTT	CTTCCTAAAA	CCAAGAGCAA	TAGCTCAGGT	180
TGGATTGTGA	TTACTATGGG	TTGGGGGATT	GCAGTTGCGG	TTGCAGTCTT	TGTATCTGGC	240
AAGCTCAGTC	CAGCTCATTT	AAACCCAGCT	GTGACCATCG	GTGTGGCCTT	AAAAGGTGGT	300
TTGCCTTGGG	CTTCCGTTTT	GCCTTATATC	TTAGCCCAGT	TCGCAGGGGC	CATGCTGGGT	360
CAGATTTTGG	TTTGTTTGCA	ATTCAAACCT	CACTATGAGG	CAGAAGAAAA	TGCAGGCAAT	420
ATCCTGGCAA	CCTTCAGTAC	TGGACCAGCC	ATCAAGGATA	CTGTATCAAA	CTTGATTAGC	480
GAAATCCTTG	GAACCTTTGT	TTTGGTGTTG	ACAACTTTTG	CTTTGGGTCT	TTACGATTTT	540
CAGGCAGGTA	TCGGAACCTT	TGCAGTGGGA	ACTTTGATTG	TCGGTATCGG	TCTATCACTA	600
GGTGGGACAA	CAGGTTATGC	CTTGAACCCA	GCTCGTGACC	TTGGACCTCG	TATCATGCAC	660
AGCATCTTGC	CAATTCCAAA	CAAGGGAGAC	GGAGACTGGT	CTTACGCTTG	GATTCCTGTT	720
GTAGGCCCTG	TTATCGGAGC	AGCCTTGGCC	GTGCTTGAT	TCTCACTTTT	CTAA	774

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GCTGAAATAA	ATGGTATTAT	AGCTGTTTTG	GCAGGAATTT	TGGTATATGG	AGGAGTTCAG	60
CTTATTGGTT	TAACGCTAA	TCATGAGATG	AGAATATTTA	TTCTCATCAT	CCTAACAAGT	120
TTAGTATTCA	TGCTATGGT	GACCACTTTA	GCAACGTGGA	ATAGCCGTAT	AGGAGCTTTT	180
TTCTCACTTA	TTTTGCTTTT	ACTACAGTTA	GCATCAAGTG	CAGGTACTTA	TCCACTTGCT	240
TTGACAAATG	ATTTCTTTAG	ATCTATTAAT	CCCTGGTTAC	CAATGAGCTA	TTCAGTTTCG	300
GGATTACGAC	AAACAATCTC	TATCAACAAG	TCATTTTCCT	AG		342

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

AAGGAAATAA	ACATGTTTGC	ATCAAAAAGC	GAAAGAAAAG	TACATTATTC	AATTCGTAAA	60
TTTAGTATTG	GAGTAGCTAG	TGTAGCTGTT	GCCAGTCTTG	TTATGGGAAG	TGTGGTTCAT	120
GCGACAGAGA	AGGAGGTAAC	TACCCAAGTA	GCCACTTCTT	CTAATAGGGC	AAATGAAAGT	180
CAGGCAGGAC	ATAGGAAAAGC	TGCTGAACAA	TTCGATGAAT	ATATAAAAAC	AATGATCCAA	240
TTAGATAGAA	GAAAACATAC	CCAAAATTTT	GCCTTAAACA	TAAAGTTGAG	CAGAATTAAA	300
ACGGAGTATT	TGCGTAAATT	AAATGTTTTA	GAAGAGAAGT	CGAAAGCTGA	GTTGCCGTCA	360
GAAACAAAAA	AAGAGATAGA	CGCAGCTTTT	GAGCAGTTTA	AAAAAGATAC	CAACAGAACC	420
AAAAAACCGG	TAGCAGAAGC	TGAGAAGAAG	GTTGAAGAAG	CTAAGAAAAA	AGCCAAGGCT	480
CAAAAAGAAG	AAGATCACCG	TAACACCCA	ACCAATACTT	ACAAAACGCT	TGAAC TTGAA	540
ATTGCTGAGT	CCGATGTGGA	AGTTAAAAAA	GCGAGCTTGG	AACTAGTAAA	AGAGGAAGCT	600
AAGGAATCTC	GAGACGATGA	AAAAATTAAG	CAAGCAGAAG	CGAAAGTTGA	GAGTAAAAAA	660
GCTGAGGCTA	CAAGGTTAGA	TAAACATCAA	GACAGATCGT	GA		702

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

TCTAGAATAA	ATGATAATAG	AAAAGAGAAA	ATTATGAAAA	TTCGTGGTTT	TGAATTGGTT	60
TCGAGTTTTA	CAGATGAAAA	TTTATTGCCC	AAGCGTGAGA	CAGCGCATGC	GGCTGGTTAC	120
GACTTAAAGG	TTGCTGTGCG	TACAGTTGTT	GCGCCAGGAG	AGATTGTCTT	GGTTCCGACA	180
GGGGTTAAGG	CTTATATGCA	GCCGACTGAG	GTTCTCTACC	TCTATGATCG	TTCTTCAAAT	240
CCTCGTAAGA	AGGGCTTGGT	TTTAATTAAC	TCAGTTGGGG	TCATTGATGG	GGATTATTAT	300
GGAAATCCTG	GAAATGAAGG	GCATATTTTT	GCGCAGATGA	AGAATATCAC	AGACCAAGAG	360
GTTGTTCTTG	AAGTTGGGGA	GCGTATTGTC	CAGGCTGTTT	TTGCTACTTT	CTTAATTGCA	420
GATGGAGATG	CGGCTGATGG	CGTTCGAACT	GGTGGATTTG	GATCGACAGG	GCACTAG	477

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1344 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

CTTATGATAA	AAAATCCTAA	ATTATTAACC	AAGTCCTTTT	TAAGAAGTTT	TGCAATTCTA	60
GGTGGTGTTG	GTCTAGTCAT	TCATATAGCT	ATTTATTTGA	CCTTTCCTTT	TTATTATATT	120
CAACTGGAGG	GGGAAAAGTT	TAATGAGAGC	GCAAGAGTGT	TTACGGAGTA	TTTAAAGACT	180
AAGACATCTG	ATGAAATTCC	AAGCTTACTC	CAGTCTTATT	CAAAGTCCTT	GACCATATCT	240
GCTCACCTTA	AAAGAGATAT	TGTAGATAAG	CGACTCCCTC	TTGTGCATGA	CTTGGATATT	300

AAAGATGGAA	AGCTATCAAA	TTATATCGTG	ATGTTAGATA	TGTCTGTTAG	TACAGCAGAT	360
GGTAAACAGG	TAACCGTGCA	ATTTGTTTAC	GGGGTGGATG	TTTACAAAGA	AGCAAAGAAT	420
ATTTTGCTTT	TGTATCTCCC	ATATACATTT	TTGGTTACAA	TTGCTTTTTT	CTTTGTTTTT	480
TCTTATTTTT	ATACTAAACG	CTTGCTCAAT	CCTCTTTTTT	ACATTTTACA	AGTGACTAGT	540
AAAATGCAAG	ATTTGGATGA	CAATATTGCT	TTTGATGAAA	GTAGGAAAGA	TGAAGTTGGT	600
GAAGTTGGAG	AAATTGGAAA	ACAGATTAAT	GGTATGTATG	AGCACTTGTT	GAAGGTTATT	660
CATGAGTTGG	AAAGTCGTAA	TGAGCAAATT	GTAATAATTG	AAAATCAAAA	GGTTTCCTTT	720
GTCCGTGGAG	CATCACATGA	GTTGAAAACC	CCTTTAGCCA	GTCTTAGAAT	TATCCTAGAG	780
AATATGCAGC	ATAATATTGG	AGATTACAAA	GATCATCCAA	AATATATTGC	AAAGAGTATA	840
AATAAGATTG	ACCAGATGAG	CCACTTATTG	GAAGAAGTAC	TGGAGTCTTC	TAAATTCCAA	900
GAGTGGACAG	AGTGTCGTGA	GACTTTGACT	GTTAAGCCAG	TTTTAGTAGA	TATTTTATCA	960
CGTTATCAAG	AATTAGCTCA	TTCAATAGGT	GTTACAATTG	AAAATCAATT	GACAGATGCT	1020
ACCAGGGTCG	TCATGAGTCT	TAGGGCATTG	GATAAGGTTT	TGACAAACCT	GATTAGTAAT	1080
GCAATTAAAT	ATTCAGATAA	AAATGGGCGC	GTAATCATAT	CCGAGCAAGA	TGGCTATCTC	1140
TCTATCAAAA	ATACATGTGC	GCCTCTAAGT	GACCAAGAAC	TAGAACATTT	ATTTGATATA	1200
TTCTATCATT	CTCAAATCGT	GACAGATAAG	GATGAAAGTT	CCGGTTTGGG	TCTTTACATT	1260
GTGAGTAATA	TTTTAGAAAAG	CTATCAAATG	GACTATAGTT	TTCTCCCTTA	TGAACACGGT	1320
ATGGAATTTA	AGATTAGCTT	GTAG				1344

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

ATGAATGTAA	AAGAAAATAC	AGAACTTGTT	TTTCGAGAAG	TTGCAGAGGC	TAGTCTGAGT	60
GCTAATCGAG	AGAGTGGTTC	GGTCTCTGTC	ATTGCAGTTA	CCAAGTATGT	AGATGTACCG	120
ACAGCGGAAG	CCTTGCTTCC	GCTAGGTGTT	CATCATATCG	GTGAAAATCG	TGTAGATAAG	180
TTTCTGGAAA	AATATGAAGC	TTTAAAAGAT	CGAGATGTGA	CTTGGCATT	GATTGGTACC	240
TTGCAAAGAC	GTAAGGTGAA	AGATGTCATT	CAATACGTTG	ATTATTTCCA	TGCATTGGAC	300
TCAGTAAAGC	TAGCAGGGGA	AATTCAAAAA	AGAAAGTACC	GAGTCATCAA	GTGTTTCCTT	360
CAAGTAAATA	TTTCTAAAGA	AGAAAGCAAA	CACGGTTTTT	CGAGAGAGGA	ACTGCTGGAA	420
ATCTTGCCAG	AGTTAGCCGG	ACTAGATAAG	ATTGAATATG	TTGGTTTAA	TGACGATGGCA	480
CCTTTTGAGG	CTAGCAGTGA	GCAGTTGAAA	GAGATTTTCA	AGGCGGCCCA	AGATTTACAA	540
AGAGAAAATC	AAGAGAAACA	AATTCCAAAT	ATACCTATGA	CCGAGTTAAG	TATGGGAATG	600
AGTCGTGATT	ATAAAGAAGC	GATTCAAATC	GGTCCACTT	TTGTTTCGTAT	AGGTACATCA	660
TTTTTTAAGT	AG					672

(2) INFORMATION FOR SEQ ID NO:927:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 741 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...741
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

AACGATGTAA	AGGTATTTTT	AAATGCTAGG	AAATACTATC	GAATTCTCTT	TCACCAACTA	60
ATGGGATTTA	GTCCAGGAAT	AGCAGTGTTT	TATAAGGAGA	GTCAAACAAC	TAAGAATCTG	120
TTTAAATTTT	ACTACTTCTT	GTACTTTACA	ACACTAATTT	CATACTATTT	TTTCTTTACT	180
TTTGTGTATG	ACAAACCGTT	GCTTTTGCCT	CTTATTCCAT	TTTCTATTAT	CATAGCATTA	240
GTACAAAAAC	TTTATAGAAT	TGAGAATCAA	CAATTATTTC	TGTTAAAATC	AAAGGTACTA	300
ACAATACTGG	AATCTAAGAA	GAATTGTGAG	TTTAATCTTC	AGGATTATCA	TGAAATTTGG	360
AAATTGCAAT	CAAAATCTGA	GTTGCCATGC	GTGGCTTTAT	CTTATATCAG	TTTGATCAAG	420
CCATATCTTT	CAGAGAGCGT	GCGTGAACAA	ATTGATTTAT	TAGAAGTTAA	GCGATTTAAA	480
AAAATAAATC	ATCCAATATC	ACTTTATGGT	ATGTTGGATG	TTATAAAATT	AAATCTATAT	540
TTACGGCATT	ATAATGAAAA	AAATAAATAT	GAATCAATGT	TAAAGAAAAT	TTTAGAGGTA	600
AGACCAGACT	TTGTTTAAAT	CGAGCAGAAT	ATTGATGATA	GTTTAAATAG	CTCGCAACCA	660
TTATCTTTAT	CTTTAGCCAT	TTCAGAAAATC	CAACTTTTGC	TTGAAGTGTA	TATGGGGATC	720
AAACATGTTT	CAACCAAGTG	A				741

(2) INFORMATION FOR SEQ ID NO:928:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

CAAATCGTAA	AGTCAATGAT	TAAGGCCTTT	ACCATGCTGG	AAAGTCTCTT	GGCTTTGAGT	60
CTTGTGAGTA	TCCTTGCCCTT	GGGCTTGTCC	GGCTCTGTTC	AGTCCACTTT	TGCGGCAGTA	120
GAGGAACAGA	TTTTCTTTAT	GGAGTTTGAA	GAACTCTATC	GGGAAACCCA	AAAACGCAGT	180
GTAGCCAGTC	AGCAAAAGAC	TAGTCTGAAC	TTAGATGGGC	AGACGATTAG	CAATGGCAGT	240
CAAAAGTTGC	CAGTCCCTAA	AGGAATTCAG	GCCCCATCAG	GCCAAAGTAT	TACATTTGAC	300
CGTGCTGGGG	GCAATTCGTC	CCTGGCTAAG	GTTGAATTTC	AGACCAGTAA	AGGAGCGATT	360
CGCTATCAAT	TATATCTAGG	AAATGGAAAA	ATTAAACGCA	TTAAGGAAAC	AAAAAATTAG	420

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

AGCCAAGTAA	AGAGAAACGA	GAAGCACATG	TATATTGAAA	TGGTAGATGA	AACTGGTCAA	60
GTTTCAAAAAG	AAATGTTGCA	ACAAACCCAA	GAAATTTTGG	AATTTGCAGC	CAAAAAATTA	120
GGAAAAGAAAG	ACAAGGAGAT	GGCAGTCACT	TTTGTGACCA	ATGAGCGTAG	TCATGAACTT	180
AATCTGGAGT	ACCGTGACAC	CGACCGTCCG	ACAGATGTCA	TCAGCCTTGA	GTATAAACCA	240
GAATTGGAAA	TTGCCTTTGA	CGAAGAGGAT	TTGCTTGAAA	ATCCAGAATT	GGCAGAGATG	300
ATGTCTGAGT	TTGATGCCTA	TATTGGGGAA	TTGTTTCATCT	CTATCGATAA	GGCTCATGAG	360
CAGGCCGAAG	AATATGGTCA	CAGCTTTGAG	CGTGAGATGG	GCTTCTTGGC	AGTACACGGC	420
TTTTTACATA	TTAACGGCTA	TGATCACTAT	ACTCCGGAAG	AAGAAGCGGA	GATGTTCCGT	480
TTACAAGAAG	AAATTTTGAC	AGCCTATGGA	CTCACAAGAC	AATAA		525

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

```
TCTCCTTCAA AAGTCGCCTG TATGGGTGGC TTTTATTTTA TCATTCATGA TATAATAGAA      60
GCAAACGGAG GACGGAAAAT GGTAAGTA CGATTGTATT TGGTACGTCA TGGCAAGACC      120
ATGTTTAAACA CGATTGGTCG CGCGCAAGGT TGGAGCGATA CTCCCTTAAC TGCTGAAGGT      180
GAACGAGGGA TTCAAGAGTT AGGAATCGGT TTGCGAGAAT CTGATCTACA GTTTGAGCGC      240
GCTTATTCGA GTGATTCTGG TCGTACCATT CAGACCATGG GAATTATACT TGAAGAACTT      300
GGCTTGCAGG GGAAAATCCC TTATCGCATG GACAAGCGTA TCAGAGAATG GTGTTTCGGT      360
AGTTTTGATG GAGCCTATGA TGGCGATCTT TTCATGGGCA TTATTCCTCG TATCTTTAAT      420
GTGGACCACG TTCACCAATT GTCTTATGCT GAACTGGCTG AGGGCTTGGT AGAGGTCGAT      480
ACAGCTGGTT GGGCTGAAGG TTGGGAAAAA CTCAGTGGCC GAATCAAGGA AGGCTTTGAA      540
ATAATTGCAA AAGAAATGGA AGATCAAGGT GGAGGTAACG CCCTTGTTGT CAGCCATGGA      600
ATGACTATTG GAACCATGTG TTATCTGATT AATGGCATGC ATCCGCATGG TCTAGATAAT      660
GGTAGCGTGA CGATTCTTGA ATATGAGGAC GGTCAGTTTA GGGTTGAAGT TGTCGGTGAC      720
CGTAGTTACC GAGAGCTAGG ACGTGAGAAG ATGGAAGAAG GCTCTATTTA A      771
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(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2571 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

```
GTACCTTCAA AGCAAAAGAT ATCACAGGGG AAGCTAAATT CCGCTTCTGG CCAATCACCC      60
GTATCGGAAC ATTTTAAGAA ACCTAAGAGG CCGAGAATCA CCAATCTCAG CCTCTTCTTC      120
TATCGTGAGA AAATGATTGG TAACTATCTA AACTTACCAG AACAGAAACA CCTCAACTCT      180
CACCTATTCA TGCAAAAGGAA TTTTATGGAA GTTTATTTTT CAGGAACTAT TGAACGGATT      240
ATTTTTGAAA ATCCCGACAA TTTTATCGCG ATCCTCCTCC TAGAAATCGA CGATACGGAC      300
GCAGAGGATT TTGATGATTT TGAAATCATT GTCACAGGAA CCATGGCTGA TGTAATTGAG      360
GGCGAAGACT ATACTTTTTG GGGGCAAATT GTCCAGCACT CCAAGTATGG AGAACAACTG      420
CAAATCAGTC GTTATGATCG CGCAAAACCA ACTAGTAAGG GCTTGGTCAA GTACTTTTCA      480
AGTAGCCATT TCAAGGGGAT TGGTCTCAAG ACAGCTCAGA AAATCGTGGA TACCTATGGC      540
GAAAATACCA TTGACGAAAT TTTGCAACAC CCAGAAAAGT TAGAAGGCAT CGCAGGACTC      600
```

TCTGCCAAAA	ATCGCGAGGC	TTTCGTCTCC	ACTCTCCGTC	TCAACTACGG	AACGGAGATG	660
ATTTTGGCCA	AAC TAGCCAA	CTACGGCATT	CCCAACAAAC	TAGCCTTTCA	GATTCAAGAC	720
TTTTACAAGG	AAGAAACCTT	TGATGTGGTT	GAAAATTATC	CCTACCAACT	GGTTGAGGAT	780
ATCAAGGGTT	TGGGCTTTAC	CATTGCTGAC	CAACTAGCTG	AGGAACTAGG	CATCGAAAGT	840
CAGGCTCCTG	AACGCTTCCG	CGCCGGTCTA	GTTCACAGTC	TTTTTCAGAC	CTGTATGGAA	900
ACAGGGGACA	CCTATGTTGA	AGCACGGGAT	TTGCTGGAAC	AAACCCTTAC	TCTCCTTGAG	960
TCTTCCCGTC	CCGTGGAACT	AGACCCAGC	CAAGTTGCCC	AAGAGCTCTC	CTACCTGATC	1020
GAAGAAGACA	AGGTTCAGCA	GATTGATACC	AAGATCTTTG	ACAACAGCCT	CTTTTTCGCT	1080
GAGGAAGGTA	TCCGCAGTCA	CTTGATTTCG	ATCCTTGAAA	AAGGAAAACA	GAAGAGCCAA	1140
GATTTAGAAA	CTATTCAAAA	GCATATCACT	ACTGTGCGAGC	AAGAACTGGG	GATTGAGTAT	1200
GATAACATTC	AAAAACAAGC	TATTTGTGAC	GCTATCCAGA	ACAAGGTCTT	TATCCTGACA	1260
GGTGGGCCTG	GTACTGGTAA	GACAACGTGT	ATCAATGGAA	TCATCGCTGT	TTATGCCCTT	1320
TTAGAAGGAC	TTGACTTCAG	GAAGAAAAAC	AATCTGCCCA	TTCTTCTTGC	TGCTCCAACT	1380
GGTCGAGCTG	CTCGTCGCAT	GAATGAATTG	ACAGGTTTGC	CTAGCGCGAC	CATACATCGC	1440
CAC TTGGGAA	TGACAGGTGA	CGATGATACC	AGTCATCTGG	AAGATTACCT	AGATGCTGAC	1500
TTTATCATCG	TGGATGAATT	CTCTATGGTG	GATACTTGGC	TGGCCAATCA	ACTCTTCTCC	1560
AATATCTCTT	CTAACAGTAA	GATCCTCATC	G TAGGTGACA	GTGATCAGCT	ACCTTCTGTC	1620
AGTCCTGGAC	AGGTTC TAGC	GGATCTGCTT	CATATTCCTT	TGATTCCTCA	GACTCGCTTG	1680
GAAAAAATTT	ATCGACAAAG	CAAAGAATCA	ACCATCGTCA	CCCTAGCTAG	TCAGATTCGA	1740
CAGGGCATCT	TGCCAGCTGA	TTTCACCCAA	AAAAAAGCTG	ACCGTTCCTA	CTTTGAAATT	1800
GCTAGTGGCC	ATATTCCTGC	CACCATTGAA	AAAATCTTAG	GTGCCGCCCT	CAGAAATGGT	1860
ATTCTTGCCC	GTGATATCCA	AGTTCTGGCT	CCTATGTACC	GAGGGACGGC	AGGGATTGAT	1920
GCTATCAATC	AGCTCATGCA	AGACCTGCTC	AATCCCCCAC	AAAAAGATCA	ACTCAGTTTTT	1980
GAAGCTCCTC	AGTGCCACTA	TCGTAAGAGA	GACAAGGTCA	TTCATTTGGT	TAACGATGCT	2040
GAAATCAATG	TCTTTAATGG	GGATTTAGGA	GCTATCACAG	ACCTGATTCC	TGGTAAATAC	2100
ACCGAATCGA	AACAAGACGA	GATTGTCATT	GATTTTGATG	GTAATGAAGT	CTCTTACCCC	2160
CGTAACGAAT	GGTACAAGAT	TCGCTTGGCC	TATGCCATGA	GTATTCATAA	GTCTCAGGGA	2220
AGTGAGTTCC	CAGTTGT CAT	CCTACCGATT	ACTAGTGCTA	GCCGACGTAT	GCTGGAGCGA	2280
AATCTCATCT	ACACAGCCAT	TACACGTGCC	AAAAGCAAAC	TCATCTTACT	AGGCGAATTA	2340
CAAGCCTTCG	ACTATGCTAC	CCAACACATC	GGAAGTCCCC	GAAAAACCTA	TCTGATTGAA	2400
CGCTTCAGTG	ATCTACTGGA	GAATGTTGAA	GAAAAGCAAC	AAGCTGTCTC	TGAAACAGTC	2460
ACATCAAGTG	CCTCTGAACA	ATCCTACATC	CTAACC GAAG	AAAAC TGGGA	CCGCATCCCA	2520
GCCATGATTG	GGATTACAGA	CACAGACCTC	AAAGAGATTT	TTGGAAAATA	G	2571

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

GTCTTCTCAA	AATTCGATAA	CCTTTCTGGT	CTTGCAGTTG	GTTCATTTGG	GCCGATTGAT	60
ATTGACAAAA	ACTCAAAAAC	TTATGGCTTT	ATCACGACGA	CTCCAAAACC	AAACTGGGCA	120
AATGTGGACT	TGCTTGGTGC	CTTTCGTGCG	GCCCTAAACG	TGCCAATGTA	CTTCACAACA	180
GACGTAAACA	GCTCTGCTTA	CGGTGAAATG	GTTGCCCGTA	ACAATGCTGG	TGGTCGTATC	240
GAAAAC TTGG	TTTACTACAC	AATCGGTACA	GGTATCGGTG	CAGGCGTCAT	CCAACGTGGT	300
GAGTTTATCG	GTGGTGTGGG	TCACCCTGAA	ATGGGTCAAT	ATTATGTTGC	TAGACACCCA	360
ATGGATATTG	AAAAAGAGTT	TAAGGGTGTT	TGTCCTTTCC	ATAAGGGATG	TCTAGAAGGT	420
TATGCAGCTG	GTCCAAGTTT	GGAAGCTCGT	ACAGGTGTAC	GTGGGGAAAA	TATTGAACTC	480
AACAACCTTG	TTTGGGATGT	TCAAGCCTAC	TATATCGCTC	AAGCTGCGGT	TAATGCGACA	540
GTGACTTTCC	CCCCAGACGT	GATTGTCTTT	GGTGGAGGGG	TCATGGCTCA	ACAACATATG	600
CTGGACCGTG	TCCGTGAGAA	ATTTACATCT	CTTCTTAATG	GTTACCTACC	AGTACCAGAT	660
GTGCGTGACT	ATATCGTGAC	GCCAGCAGTC	GCAGGAAATG	GTTCTGCCAC	ACTTGGAAC	720
TTTGTTCCTG	CAAAAGAAGT	TTCAAAATAA				750

(2) INFORMATION FOR SEQ ID NO:933:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

ATGATATCAA	AAATCTCTTG	GATGAAGATT	GGGGCAAGTC	CCATTGATGG	TTCATCTAAA	60
AGAAGAAGTT	TTGGTGTTGA	CATAAGAGCG	CGTCCCATGG	CAAGCATTTG	TTGTTCCCCCT	120
CCTGAAAGAG	TAGCTGCATC	TTGGTTCTTC	CGTTCTTCAA	GACGAGGAAA	GCGTGAGAAA	180
ACCTTCTTCA	AGTTAGCTTG	A				201

(2) INFORMATION FOR SEQ ID NO:934:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

ATACCATCAA	AGGAGAGGTT	TATGAATAGA	GAAGCGCTTA	GACTATATCT	GGTAACCAAT	60
CGCTATCAAG	ATTCCGTGGA	AAGCTTTCTT	GCAAAAAGTTG	AGACGGCCTG	CCGTTCAGGG	120
GTTACCATAG	TCCAATTGCG	AGAAAAAAAT	CTCACAACCA	ATCAATATTA	TCAACTGGCA	180
AAACAAGTCA	AGGAAATAAC	AGATGCTTAT	CAGGTCCCCT	TGATAATCGA	TGATCGGTTG	240
GATGTTTGTC	TTGCGGTTGA	TGCTGCTGGT	CTGCATATTG	GAGATGACGA	ACTCCCAGTT	300
TCGGTTGCC	GACAAGTCTT	GGGTCCTGAA	AAAATCCTCG	GTGTCACCGC	TAAAACGGTT	360
AAAAGAGCTC	TGGAAGCGGA	GAAATCAGGT	GCAGATTACT	TGGGGACAGG	AGCCATTTTT	420
CCGACAACCA	CCAAGGAAAA	TGCACCCATC	ACCCTGATTT	CAACCTTGAA	AACAATTTGC	480
CAAACGGTTG	CCATTCCAAT	AGTTGCTATT	GGCGGCTTGA	CTTCGGAGAA	TATTGATCAG	540
CTTATGGGCA	CTGGCATAGC	TGGTGTAGCT	GTTGTACGTG	ATTTGATGCA	AGCAGAAGAT	600
ATTGAGGCAA	AAACGCAAGC	CTTTTAAACA	AAGTTGCATG	ACATTCTTTC	CTAA	654

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

GTACCATCAA	ATCCTAGACC	TGTATACGGT	CTAGCCTCTT	TTAAAATTAT	TTTTTTCCCA	60
TCTTCTTTTA	GCCTAGCATT	ATATATCCCA	CCACTGTTTG	AAAATCTAAT	TGCATTATCT	120
ATAATAAAGG	GAAAGTCTCC	CTGTTTTTTA	TCTTCTTGT	CAAGCCATTT	ATTCAAAAAG	180
TCAGGGGGCA	CTATACCTTT	TGGAATTTTA	AATACTGGTA	AACGTTTCATC	TTTAACAAC	240
TCATCGCCAA	CAATTAATTC	ATCAATAGCA	ACCTTCTTTT	CATCATCCCT	TGACGGCCTA	300
AACACACCAT	ACCTCAGATA	TATTGGTGCT	TCATCCCAAC	GTTTATCGCT	TAAAATATAT	360
GGTCCATTAT	ATTGCTTTAA	GGCACTTTCT	AACCTTTGCA	AAACCGACTC	TAATTCATTT	420
TGA						423

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...699
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

AAGCCATCAA	ACTCTCAAGG	AGAGCAGGCA	CGTATTCAGG	AGCAAGGCTT	GTCCCTCGCT	60
TATCAGCAAA	CTAGTCAGCA	AGTTGAAGAA	CTGGAAACTC	TTTGAAACT	CCAAGAAGAG	120
GAAATAGATC	GTCTTTCTGA	GGGAGATTGG	CAAGCGGATA	AGGAAAAATG	TCAAGAGAGC	180
CTTGCTACTA	TCGCCAGTGA	CAAGCAAAAT	CTGGAAGCTG	AGATTGAAGA	AATTAAGTCT	240
AATAAAAACG	CCATCCAAGA	ACGCTATCAA	AATTTGCAGG	AAGAGGTGGC	GCAAGCTCGC	300
TTGCTTAAGA	CAAACTGCA	AGGGCAAAAA	CGTTATGAAG	TAGCTGATAT	TGAGCGTTTA	360
GGCAAGGAAT	TGGACAATCT	TAATATCGAA	CAAGAAGAAA	TTCAGCGCAT	GCTCCAAGAA	420
AAAAGTTGACA	ATCTTGAGAA	GGTTGATACA	GAATTGCTCA	GTCAACAGGC	GGAAGAATCC	480
AAAACTCAGA	AAACAAATCT	CCAACAAGGT	TTGATTTCGCA	AGCAGTTTGA	GTTGGATGAT	540
ATAGAAGGTC	AACTGGATGA	TATTGCCAGT	CACTTGGATC	AAGCTCGCCA	GCAGAAATGAG	600
GAGTGGATGC	CCAAGCAAAC	ACGTGCTGAA	GCCAAGAAAAG	AAAAGGTCAG	CGAGCGTGCG	660
CCATCTACAA	AATCAATTAA	CAGACCAGTA	CCAGATTAG			699

(2) INFORMATION FOR SEQ ID NO:937:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...786
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

AAGCAATCAA	AAAGGCTTGG	TCTAGCAGCC	CTTGCTACAG	TCGCAGGTTT	GGCTCTTGCA	60
GCTTGCGGAA	ACTCAGAAAA	GAAAGCAGAC	AATGCAACAA	CTATCAAAAT	CGCAACTGTT	120
AACCGTAGCG	GTTCTGAAGA	AAAACGTTGG	GACAAAATCC	AAGAATTGGT	TAAAAAAGAC	180

GGAATTACCT	TGGAATTTAC	AGAGTTCACA	GACTIONCTCAC	AACCAAACAA	AGCAACTGCT	240
GATGGCGAAG	TAGATTTGAA	CGCTTTCCAA	CACTATAACT	TCTTGAACAA	CTGGAACAAA	300
GAAAACGGAA	AAGACCTTGT	AGCGATTGCA	GATACTTACA	TCTCTCCAAT	CCGCCTTTAC	360
TCAGGTTTGA	ATGGAAGTGC	CAACAAGTAC	ACTAAAAGTAG	AAGACATCCC	AGCAAACGGA	420
GAAATCGCTG	TACCGAATGA	CGCTACAAAC	GAAAGCCGTG	CGCTTTATTT	GCTTCAATCA	480
GCTGGCTTGA	TTAAATTGGA	TGTTTCTGGA	ACTGCTCTTG	CAACAGTTGC	CAACATCAAA	540
GAAAAATCCAA	AGAACTTGAA	AATCACTGAA	TTGGACGCTA	GCCAAACAGC	TCGTTTCATTG	600
TCATCAGTTG	ACGCTGCCGT	TGTAAACAAT	ACCTTCGTTA	CAGAAGCAAA	ATTGGACTAC	660
AAGAAAGCAC	TTTTTCAAAGA	ACAAGCTGAT	AAAAACTCAA	AACAATGGTA	CAACATCATT	720
GTTGCAAAAA	AAGATTGGGA	AACATCACCT	AAGGCTGATG	CTATCAAGAT	AGTAATCGCA	780
GCTTAA						786

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

ACCTTGTC	AA	ATGGTTGGTG	TAGTATGAGC	GACAGTCGCG	GAAAGTCAAC	CTTGGCTCAA	60
TTGATTCCAC	GTCTCTTTGA	TCCACAGAAC	GGGGCCATTA	AAATCGGTGG	CACGGATATT		120
CGAGACGTGA	GTGAAGGGAA	CCTGCGTCAA	ACAGTTTCAT	CGTTCTCCAA	ACGTTCCATT		180
CTTTTTAGTG	TGACGNTTGC	AGATAACTTG	AGACAGGGGA	AGGGAAATGC	TACTCTATTT		240
GAAATGGAGC	GCGCAGCCAA	TATTGCCCCAG	GCTAGTGAAT	TCATTCAATCG	TATGGAGAAA		300
AACTTTGAAA	GTCCAGTTGA	AGAACGGGGA	ACCAATTTCT	CTGGTGGACA	AAAACAAAGG		360
ATGTCGATTG	CGCGTGGGAT	TGTCAGCAAT	CCACGTATTC	TGATTTTTTGA	CGATTCGACC		420
TCAGCCTTGG	ATGCCAAATC	AGAGCGCTTG	GTGCAAGAAG	CTTTGAATAA	GGACTTGAAG		480
GGGACGACAA	CCATTATTAT	TGCTCAAAAA	ATTAGCTCGG	TTGTCCATGC	AGACAAGATC		540
TTGGTTCTAA	ATCAAGGACG	ATTGATTGGT	CAAGGCACGC	ATGCAGACTT	GGTTGCCAAC		600
AATGCCGTTT	ACCGTGAAAT	CTATGAAACA	CAGAAATGA				639

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

ATATCGTCAA	AGCAGACGCT	GCTAAACGTT	TTCCTTGACA	AACTTGCTGG	CGTTTCTGAT	60
CCTGAACAAA	AACGTAAAAT	CATCGGTAAC	GAGTCTGTCT	ATGTATTCGA	TGACGAAGCC	120
GGCAAGCTCA	AAGATGTGAA	ATTCCCTTGCT	CAAGGTACTT	TATATACAGA	TGTTGTCGAG	180
TCTGGTACGG	ATACAGCTCA	GACTATCAAG	TCACACCACA	ACGTGGGTGG	TCTTCCAGAA	240
GATATGCAGT	TTGAATTGAT	TGAACCACTC	AATACTCTTT	ACAAGGATGA	AGTTCGTGCT	300
CTTGGTACAG	AGCTTGGTAT	GCCAGACCAT	ATCGTATGGC	GCCAACCATT	CCCAGGACCA	360
GGACTTGCTA	TCCGTGTCAT	GGGTGAAATC	ACTGAAGAGA	AACTTGAAAC	CGTTCGTGAA	420
TCAGACGCTA	TTCTTCGTGA	AGAAATCGCT	AAAGCTGGAC	TTGACCGCGA	TATTTGGCAA	480
TACTTCACTG	TTAACACAGG	CGTTCGTTCA	GTCTGGTGTTA	TGGGTGACGG	TCGTACGTAT	540
GACTACACGA	TTGCAATCCG	TGCTATCACT	TCTATCGATG	GTATGACTGC	TGATTTTGCC	600
AAAATTCCAT	GGGAAGTACT	TCAAAAAATC	TCAGTACGTA	TCGTAAATGA	AGTGGATCAT	660
GTAAACCGTA	TCGTCTACGA	TATTACAAGT	AAACCACCTG	CAACAGTTGA	GTGGGAGTAA	720

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

AATGCGTCAA	AGGCTATTTT	TTTCATTCTT	TTTCTTCTAA	TACTCTTCGA	AAATCTCTTC	60
AAACCACGTC	AGCGTCGCCT	TACCGTGCGT	ATGTTACCGA	CTTCGTCAGT	TTTATCTGCA	120
ACTTCAAAGC	TGTACTTTGA	GCAGCCTACG	ACTAGCTTCC	TAGTTTGCTC	TTTGATTTTC	180
ATTGACTATA	AAATGGTTTT	AATTCTTTTT	TTCAAACTCG	GCACTACTTC	TGCCTCAAAC	240
CAAGGATTTT	TGGCCATCCA	GATTTGA				267

(2) INFORMATION FOR SEQ ID NO:941:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

CTCCCTCCAA	AGTTTGCCGC	CCTTGCCCAA	ATCATTTCAA	GCCCTGTCCT	CGGTGGTGCC	60
ATGCTGGTGA	TGTTTGTTTT	TGTATCGATT	CAAGGGATGC	AAATCCTCGC	CCGTGTTGAC	120
TTTGCTAACA	ATGAACACAA	CTTCCTTATC	GCAGCTGTTT	CAATCGCTGC	AGGTGTCGGA	180
CTCAATAACA	GTAATCTCTT	TGTCAGCATG	CCGACAGCCT	TCCAAATGTT	CTTCTCAAAC	240
GGAATCGTCG	TAGCCAGCCT	ACTCGCTATT	GTCCTCAATG	CCGTATTAAA	TCATAAAAAAG	300
AAATAA						306

(2) INFORMATION FOR SEQ ID NO:942:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

TGGCCTCCAA	AGCTGGATTG	CCCTTTTCCC	CTCCAAAGGG	CTCAAAACCT	GTCACCTAATA	60
CTTTCATTTT	TAATCCTTCA	AAACCAATTC	AATGAGACTT	TTTTCTTAAA	AACAAGTATA	120
ACATATTTCC	CTTATTCTGG	ATTAAAAAGG	ATTAGCGAGA	TTAGAATCGA	CCTTCAAGTG	180
TATTTAAAGA	GTAAATAACT	AATCAAGGCC	AAAATAGCTG	ATCCACCTTG	TTTCAAAATA	240
ATTTTTTTAT	CCGCTGTAA	AGAGCCGTAA				270

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

AAATATCCAA	AAAGTAGCGA	GTTTGAAGAT	ATCACAGATG	ACATTTTCAA	ATTTACAACC	60
AAC TTCACAG	AAGAAACGCT	GGAAGCTGGG	GAAGCTTGGG	TCAATGATAA	TGTCCCTGGT	120
GT TAAGGCCA	TGACA ACTGG	CTTTGAATCT	ATTGATATTG	TTCTGGACTA	TGTCGATAAG	180
GGAGTGGCCA	TTGTTGAATT	AGTTAAAAAA	CTTGGTATCA	CAATGGATCA	GGTCATGGCT	240
TTTGGAGACA	ATCTTAATGA	CTTACATATG	ATGCAGGTTG	TGGGACATCC	TGTAGCTCCT	300
GAAAATGCAC	GACCTGAAAT	TTTAGAATTA	GCAAAGACTG	TGATTGGTCA	CCATAAGGAC	360
CAGTCGGTTA	TAGCTTGTAT	GGAGGGCTTA	TAA			393

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

CCACCACCAA	AAGCAGGGGG	AAAATCGAAA	TCAACCAATA	GTAGGCTACT	GCGACACTGG	60
TCAACTCACT	ATCTGATGCT	TGATAATAAT	GCAAAAAAGC	TTTTAATAAA	GGCTTGTCTA	120
TCAGCTCTTT	CCACCACTTT	TTCATGTCAT	ACTCCTTCAT	TTATAATCTT	ATACTCAATG	180

AAAATCAAAG AGCAAAC TAG AAAGCTAGCC GCAAGCTGCT CAAAACACTG TTTTGAGGTT	240
GTAGATAAGA CTGACGAAGT CAGTCACATA CATACGGTAA GGCGACGCTG A	291

(2) INFORMATION FOR SEQ ID NO:945:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...468
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

CATTTTACAA AAGAGGAGAA AATAAAAATG AAAC TTCATG AATTGAAACC TGCAGAAGGT	60
TCTCGTAAAG TACGTAACCG CGTTGGTCGT GGTACTTCAT CAGGTAACGG TAAACATCT	120
GGTCGTGGTC AAAAAGGTCA AAAAGCTCGT AGCGGTGGCG GAGTTCGCCT TGGTTTTGAA	180
GGTGGACAAA CTCCATTGTT CCGTCGTCTT CCAAAACGTG GATTCACTAA CATCAACGCT	240
AAAGAATACG CAATTGTGAA CCTTGACCAA TTGAACGCTT TTGAAGATGG TGCTGAAGTA	300
ACTCCAGTTG TTCTTATCGA AGCAGGAATT GTTAAAGCTG AAAAGTCAGG TATTAAAATT	360
CTTGGAACG GTGAGTTGAC TAAGAAATTG ACTGTGAAAG CAGCTAAATT CTCTAAATCA	420
GCTGAAGAAG CTATCACTGC TAAAGGTGGT TCAGTAGAAG TCATCTAA	468

(2) INFORMATION FOR SEQ ID NO:946:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 873 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

CCAAACACAA	AAACTAGAAG	AATTAAACAA	ATAATGAAAT	TAGCTCAATT	ATTTTCAAAT	60
TTTGAAGAAG	AGTTGATAAG	ACAAGGAGAG	GAAGCGGAAA	GCCTCTCTTT	TGTCCTATCGT	120
AGTCTGAAAA	ATCTATCTTT	TACAGACTTT	ATTTTTGCCC	TCCAGCAGGA	GGTGACAACA	180
GAGGAAGAAA	AACAATTTGT	AGAAGATATT	TACCAGCAAC	TAGCAGCTCA	CAAGCCAGCT	240
CAGTACATCA	TTGGACAGGC	AGATTTTTAT	GGAATGCATT	TAAAGGTGGA	TGAACGGGTT	300
TTGATTCCTC	GTCCAGAAAC	AGAGGAGTTA	GTGGAGCTTA	TTCTAACTGA	AAATCTTGAG	360
ACGAATCTCT	CAGTTCCTGA	TATTGGAACA	GGTAGTGGAG	CTATTGCTCT	CGCTCTAGCA	420
AAAAATAGAC	CAGATTGGTC	AGTGACAGCA	GCAGATGTTT	CTCAAGAGGC	CTTAGAGCTT	480
GCATCAGAGA	ATGCTAGCGA	TCAAAATCTT	AATATATTTT	TTAAAAATC	TGATTGTTTT	540
GCAGAAATTT	CTGAAAAATA	TGATATAATT	GTATCCAATC	CACCCATATAT	CTCTCGTGAA	600
GATGAGTCAG	AGGTAGGCTT	GAATGTTTTG	CATTCGGAGC	CTCATCTAGC	TCTCTTTGCA	660
GACGAGGATG	GCCTAGCTAT	TTACTGTAGA	ATTGCGGAAG	ATGCAAAAGA	CTATCTCAAG	720
GATGGTGGTA	AGATTTACCT	TGAAATTGGA	TACAAGCAAG	GTCAAAGTGT	TCCCGAAGTT	780
TTTAGAAAAC	ATCTTCCTGA	AAAAAAAGTT	CGAACACTCA	AAGACCAATT	TGGTCAAGAT	840
AGGATGGTCG	TGGTTGATGA	TGGACAGGAT	TAG			873

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

TGCATAACAA	AAAGCTCTAC	TTTACCTAGT	AGAGCCCAAA	GTCTATGTCA	AAAAAACTCT	60
ATTAACATGC	CAGAAAAAGA	GCATAAAAGA	GCACACAAAA	AGAGACAAAA	ACAAGATCTA	120
CTAAATAAAG	GTTCTTTTAT	TGATAGACTT	AGTTGTTCAT	GTCTCCCTTA	CCTCCGAGTA	180
TTAGTATCTT	TATACTATAC	CTTTAAGGAA	ATTTTGTCAA	CAGAAAACTG	GAAATTCTAT	240
GCTCTAAAAT	CCAAAAACAG	GTCCATAAAA	ACTTAG			276

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

AATGTAACAA	ATTCATTTAC	AACAAATCGA	AATCTAAATG	AAATGGAATT	TTCTATGAAA	60
TCAGTCAAAG	GACTACTCTT	TATCATAGCT	AGTTTTATCT	TGACTCTTTT	GACTTGGATG	120
AACACTTCTC	CCCAATTCAT	GATTCCAGGA	CTAGCTTTAA	CAAGCCTATC	TCTGACTTTT	180
ATCCTAGCCA	CTCGTCTCCC	ACTACTAGAA	AGCTGGTTTC	ACGGTTTGGA	GAAGGTCTAC	240
ACCGTCCACA	AATTCACAGC	CTTCTCTCC	ATCATCCTAC	TAATCTTTCA	TAACTTTAGT	300
ATGGGCGGTT	TGTGGGGCTC	TCGCTTAGCT	GCTCAGTTTG	GTAATCTTGC	CATCTATATC	360
TTTGCCAGCA	TCATCCTTGT	CGCCTATTTA	GGCAAATACA	TCCAATACGA	AGCTTGGCGA	420
TGGATTCACC	GCCTGGTTTA	CCTAGCCTAT	ATTTTAGGAC	TCTTTCACAT	CTACATGATA	480
ATGGGCAATC	GTCTCCTTAC	ATTTAATCTT	CTAAGTTTTC	TTGTTGGTAG	CTATGCCCTT	540
TTAGGCTTAC	TAGCTGGTTT	TTATATCATT	TTTCTATATC	AAAAGATTTT	CTTCCCCTAT	600
CTAGGGAAAA	TTACCCATCT	CAAACGCTTA	AATCACGATA	CTAGAGAAAT	TCAAATCCAT	660
CTTAGCAGAC	CTTTCAACTA	TCAATCAGGA	CAATTTGCCT	TTCTAAAGAT	TTTCCAAGAA	720
GGCTTTGAAA	GTGCTCCACA	TCCCTTTTCT	ATCTCAGGAG	GTCATGGTCA	AACTCTTTAC	780
TTTACTGTTA	AAAATTCAGG	CGACCATACC	AAGAATATCT	ATGATAATCT	TCAAGCCGGC	840
AGCAAAGTAA	CCCTAGACAG	AGCTTACGGA	CACATGATCA	TAGAAGAAGG	ACGAGAAAAT	900
CAGGTTTGGA	TTGCTGGAGG	TATTGGGATC	ACCCCCTTCA	TCTCTTACAT	CCGTGAACAT	960
CCTATTTTAG	ATAAACGGGT	TCACTTCTAC	TATAGCTTCC	GTGGAGAAGA	AAATGCAGTC	1020
TACCTTGATT	TACTCCGTGA	CTATGCTCAG	AAAAATCCTA	ATTTTGAAC	CCATCTAATC	1080
GACAGTACAA	AAGACGGCTA	TCTTAATTTT	GAACAAAAAG	AAGTGCCCGA	ACATGCAACC	1140
GTCTATATGT	GTGGTCCTAT	TTCTATGATG	AAGGCACTTG	CCAAACAGAT	TAAGAAACAA	1200
AATCCAAAAA	CGGAGCTTAT	TTACGAAGGA	TTCAAGTTCA	AATAA		1245

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1467 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

GAATTGACAA	ACGATCTTTA	TCGTCATATT	CTTTCCTTGC	CCAAGCATAG	CAGAGACCGT	60
CTGACAACCT	CTAGTTTGGT	CACTCGCTTG	ACTTCGGATA	CCTACCAGAT	TCAGACTGGT	120
ATCAATCAAT	TCCTGCGTCT	CTTTTTGCGA	GCGCCCATTA	TCGTTTTTTGG	TGCCATTTTT	180
ATGGCTTATC	GAATCTCAGC	TGAGTTGACT	TTCTGGTTCT	TAGTCATGGT	TGCCATTTTTG	240
ACCATTGTCA	TTGTAGGGTT	ATCTCGATTG	GTCAATCCTC	TCTACAGTAG	TCTCAGAAAAG	300
AAAACGGACC	AACTGGTTCA	GGAAACGCGC	CAGCAATTGC	AAGGGATGCG	GGTTATTCGT	360
GCTTTTGGTC	AAGAAAAACG	AGAGTTACAG	ATTTTTCAAA	CCCTTAACCA	AGTTTATGCT	420
AGATTACAAG	AAAAGACAGG	TTTCTGGTCT	AGTTTATTAA	CACCTCTGAC	CTATCTGATT	480
GTCAATGGAA	CTCTTCTCGT	TATTATCTGG	CAAGGCTATA	TTTCAATTCA	AGGAGGAGTG	540
CTCAGTCAAG	GTGCTCTCAT	TGCTCTTATC	AATTACCTCT	TACAGATTTT	GGTGGAATTG	600
GTCAAGCTAG	CCATGTTGAT	CAATTCCCTC	AACCAGTCCT	ATATCTCAGT	CAAGCGAATC	660
GAGGAAGTCT	TTGTTGAGGC	TCCAGAGGAT	ATCCATTGAG	AGTTAGAACA	AAAGCAAGCT	720
ACCAGAGATA	AGGTTTTTACA	AGTCCAAGAA	TTGACTTTTA	CCTATCCTGA	TGCGGCCCCAG	780
CCTTCTCTGA	GATACATTTT	CTTTGATATG	ACTCAAGGAC	AAATTCTAGG	TATCATCGGG	840
GGAACCTGGT	CTGGTAAATC	AAGCTTGGTG	CAACTCTTAC	TTGGACTTTA	TCCAGTAGAC	900
AAGGGGAACA	TTGACCTTTA	TCAAAATGGA	CGTAGTCCTC	TTAATTTGGA	GCAGTGGCGG	960
TCTTGGATTG	CCTATGTACC	TCAAAAGGTC	GAACCTCTTA	AAGGAACCAT	TCGTTCCAAC	1020
TTGACTCTAG	GTTTCAATCA	AGAAGTATCT	GACCAGGAAC	TCTGGCAGGC	CTTGGAGATT	1080
GCGCAAGCTA	AGGATTTTGT	CAGTGAAAAG	GAAGGACTCT	TGGATGCTCT	AGTTGAGGCA	1140
GGGGGGCGAA	ATTTCTCAGG	TGGACAAAAA	CAAAGATTGT	CTATCGCCCC	AGCAGTCTTG	1200
CGCCAAGCTC	CGTTTCTCAT	CCTAGATGAT	GCAACCTCGG	CACTGGATAC	CATTACAGAG	1260
TCCAAGCTCT	TGAAAGCTAT	TAGAGAAAAA	TTTCCAAACA	CGAGCTTAAT	TTTGATCTCT	1320
CAACGAACCT	CAACTTTTACA	GATGGCGGAC	CAGATTCTCC	TCTTGGAATA	AGGTGAGTTG	1380
CTAGCTGTTG	GCAAGCACGA	TGACTTGATG	AAATCCAGCC	AAGTCTATTG	TGAAATCAAT	1440
GCATCCCAAC	ATGGAAAGGA	GGACTAG				1467

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

GATATGACAA	AAGAATTTCA	TCATGTAACG	GTCTTACTCC	ACGAAACGAT	TGATATGCTT	60
GACGTAAAAC	CTGACGGTAT	CTACGTTGAT	GCGACTTTGG	GTGGAGCAGG	CCATAGCGAG	120
TATTTATTAA	GTAAATTAAG	TGAAAAAGGC	CATCTCTATG	CCTTTGACCA	GGATCAGAAT	180
GCCATTGACA	ATGCGCAAAA	ACGCTTGGCA	CCTTACATTG	AGAAGGGAGT	GGTGACCTTT	240
ATCAAGGATA	ACTTCCGTCA	TTTACAGGCA	CGTTTGCGCG	AAGCTGGTGT	TCAGGAAATT	300
GATGGAATTT	GTTATGACTT	GGGAGTGTCT	AGTCCTCAAT	TGGACCAGCG	TGAGCGTGGT	360
TTTTCTTATA	AAAAGGATGC	GCCACTGGAC	ATGCGGATGA	ATCAGGATGC	TAGTCTGACA	420

GCCTATGAAG	TGGTTAATCA	TTATGACTAT	CATGATTTGG	TTCGTATTTT	CTTCAAATAC	480
GGTGAGGATA	AATTCTCTAA	ACAGATTGCG	CGTAAGATTG	AGCAAGCGCG	TGAAGTGAAG	540
CCGATTGAGA	CAACGACTGA	GTTAGCAGAG	ATTATCAAGT	TGGTCAAACC	TGCCAAGGAA	600
CTCAAGAAGA	AGGGTCATCC	TGCTAAGCAG	ATTTTCCAGG	CTATTCTGAAT	TGAAGTCAAT	660
GATGAACCTGG	GGGCGGCAGA	TGAGTCCATC	CAGCAGGCTA	TGGATATGTT	GGCTCTGGAT	720
GGTAGAATTT	CAGTGATTAC	CTTTCATTCC	TTAGAAGACC	GCTTGACCAA	GCAATTGTTC	780
AAGGAAGCTT	CAACAGTTGA	AGTTCCAAAA	GGCTTGCCCT	TCATCCCAGA	TGATCTCAAG	840
CCCAAGATGG	AATTGGTGTC	CCGTAAGCCA	ATCTTGCCAA	GTGCGGAAGA	GTTAGAAGCC	900
AATAACCGCT	CGCACTCAGC	CAAGTTGCGC	GTGGTCAGAA	AAATTCACAA	GTAA	954

(2) INFORMATION FOR SEQ ID NO:951:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...570
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

TCCGTGACAA	ATTCTCTTAA	AAATGATAAG	ATAGGAGAAA	TATTTGACTA	TCAAATTTTC	60
AAGGAGGGAA	TCGTGTCGTA	TTTTGAACAG	TTTATGCAAG	CCAATCAGGC	TTATGTTGCC	120
CTACATGGGC	AGTTAAATCT	GCCACTTAAA	CCTAAAACCA	GAGTAGCCAT	TGTGACCTGT	180
ATGGACTCAC	GTTTGACACG	TGCGCAAGCT	CTAGGTTTGG	CACTTGGGGA	TGCTCATATT	240
TTGCGGAATG	CAGGTGGTCG	AGTGAAGTAA	GACATGATTC	GTTTCGCTAGT	TATTTCCCAG	300
CAACAAAATG	GGACAAGAGA	GATTGTGGTA	TTGCACCATA	CAGACTGTGG	TGCTCAGACC	360
TTTGAAAATG	AACCTTTTCA	GGAGTATTTA	AAAGAGGAAT	TAGGTGTAGA	TGTGTCAGAC	420
CAGGATTTCT	TGCCCTTCCA	AGATATAGAA	GAGAGTGTA	GCGAGGATAT	GCAACTGCTT	480
ATCGAGTCTC	CCCTAATACC	AGACGATGTC	ATTATCTCTG	GTGCCATTTA	CAATGTTGAT	540
ACAGGAAGTA	TGACAGTCGT	AGAATTATAA				570

(2) INFORMATION FOR SEQ ID NO:952:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

AAAGCGACAA	AACAACTCAT	TAGAAAGATT	CATATGGAAC	AATTACATTT	TATCACAAAA	60
TTACTAGACA	TTAAAGACCC	TAATATCCAG	ATTTTAGACA	TCATCAATAA	GGATACACAC	120
AAGGAAATCA	TCGCCAAACT	GGACTACGAC	GCCCCATCTT	GCCCTGAGTG	CGGAAACCAA	180
TTGAAGAAAT	ATGACTTTCA	AAAACCTTCT	AAAATTCCTT	ATCTTGAAAC	GA CTGGTATG	240
CCTACTAGAA	TTCTCCTTAG	AAAGCGTCGT	TTCAAGTGCT	ATCACTGTTC	AAAAATGATG	300
GTCGCTGAAA	CTTCTATCGT	CAAGAATAAT	CACCAAATCC	CTCGTATCAT	CAACCAAAAG	360
ATTGCTCAAA	AGTTAATTGA	AAAGATTTCCT	ATGACTGATA	TTGCCCATCA	GCTTTCCATC	420
TCAACTTCAA	CTGTTATTCG	TAAGCTCAAT	GATTTTCACT	TTAAACATGA	TTTTTCTTGT	480
CTTCCTGAGA	TTATGTCCCTG	GGACGTTGAA	ACAGTCCGGG	GAGTGACTGT	TTCAATCGGG	540
AGATGGAGAT	GA					552

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

AAAGCGACAA	AACAACTCAT	TAGAAAGAAT	CATATGGAAC	AATTACATTT	TATCACAAAA	60
TTACTAGACA	TTAAAGACCC	TAATGTCCAG	ATTTTAAACA	TCATCAATAA	GGATACACAC	120
AAGGAAATCA	TCGCCAAACT	GGACTACGAC	GCCCCATCTT	GCCCTGAGTG	CGGAAACCAA	180
TTGAAGAAAT	ATGACTTTCA	AAAACCTTCT	AAAATTCCTT	ATCTTGAAAC	GA CTGGTATA	240
CCTACTAGAA	TTCTCCTTAG	AAAGCGTCGA	TTCAAGTGCT	ATCACTGTTC	AAAAATGATG	300
GTCGCTGAAA	CTTCTGATGA	CGTACAGTCA	TATTTATTCT	CTTTTTATTA	TATCACAGTT	360
TTAAATCTAG	CTTTACTAGA	TTCACCGCTA	CTATCTATTT	ATTTCGAAAA	AAGACGAAAA	420
AACCTGAGAA	TCATCTCAGG	CTTGGTCATT	AAATTTTTTT	CTCAATATCG	AAAAGTGGAG	480
AAAGTGGTCG	TTTTTCATGA	ATACGTACGA	TAG			513

(2) INFORMATION FOR SEQ ID NO:954:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1263
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

AAAGCGACAA	AACAAC	TCAT	TAGAAAGATT	CATATGGGAC	AATTACATTT	TATCACAAAA	60
CTACTCGATA	TCAAAGACAC	AAATATCCAA	ATTATAGATG	TCGTCAATAG	GGATTCACAC		120
AAAGAAATCA	TCGCCAAACT	GGACTACGAC	GCCCCATCTT	GCCCTGGGTG	CGGAAACCAA		180
TTGAAGAAAT	ATGACTTTCA	AAAACCGTCT	AAGATTCCTT	ACCTTGAGAC	AACTGGTATG		240
CCTACTAGAA	TCCTCCTTAG	AAAGCGTCGC	TTTAAGTGCT	ATCAGTGCTC	AAAAATAGCG		300
GTCGCTGAGA	CTTCCCTCGT	CAAGAAAAAT	CACCAAATCC	CTCGTATCAT	CAACCAAAAG		360
ATTGCTCAAA	AGTTGATTGA	AAAGATTTCT	ATGACTGATA	TTGCCCATCA	GCTTTCCATC		420
TCAACTTCAA	CTGTTATTCG	TAAGCTCAAT	GATTTTCACT	TTAAACATGA	TTTTTCTTGT		480
CTTCCTGAGA	TTATGTCTTG	GGATGAGTAT	GCTTTTACAA	AGGGAAAGAT	GAGCTTCATT		540
GCGCAAGATT	TTAACAATCT	CAATATCATC	ACTGTTCTTG	AGGGTAGAAC	ACAAGCTATC		600
ATTCGAAATC	ACTTTCTTCG	CTACGATAGA	GTTGTCCGAT	GTCGCGTCAA	AATTATTACT		660
ATGGATATGT	TTAGCCCTTA	CTATGGCTTG	GCTAAACAGC	TTCGCTTTCA	CATTGTACAA		720
CATCTTAGCT	GTGCTATGAG	TCGTGTGCGT	GTTCAAATCA	TGAATCAGTT	TCATCGAAAA		780
TCCCATGAAT	ACAAGGCTAT	CAAGCGCTAC	TGGAAGCTCA	TACAACAGGA	TAGCCGTAAA		840
CTGAGTGATA	AGCGATTTTA	TCGTCCCTACT	TTTCGTATAC	ATTTAACCAA	TAAAGAGATT		900
TTAGACAAGC	TTTTTGAGCTA	TTCAACAAGAC	TTGAAACATC	ACTATCAGCT	CTATCAACTC		960
TTGCTGTTTC	ACTTTCAGAA	TAAGGAACCG	GAGAAATTTT	TCGGACTCAT	TGAGGACAAT		1020
CTTAAGCAGG	TTCATCCTAT	TTTTCAGACT	GTCTTTAAAA	CCTTCCTCAA	AGATAAAGAA		1080
AAGATTGTCA	ACGCCCTTCA	ACTACACTAT	TCTAATGTCA	AACTGGAAGC	GACCAATAAT		1140
CTCATCAAAC	TTATCAAGCG	CAATGCCTTT	GGTTTTCGAA	ACTTTGAAAA	CTTCAAAAAA		1200
CGGATTTTCA	TCGCTCTGAA	TATCAAAAAA	GAAAGGACAA	AATTTGTCCT	TTCTCGAGCT		1260
TAG							1263

(2) INFORMATION FOR SEQ ID NO:955:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

AAAGCGACAA	AACAACTCAT	TAGAAAGAAT	CATATGGAAC	AATTACATTT	TATCACAAAA	60
TTACTAGACA	TTAAAGACCC	TAATATCCAG	ATTTTAGACA	TCATCAATAA	GGATACACAC	120
AAGGAAATCA	TCGCCAAACT	GGACTATGAA	GCTCCATCTT	GTCCTGAGTG	CGGAAGTCAA	180
ATGAAGAAAT	ATTACTTTCA	AAAACCTTCT	AAAATTCCCT	ATCTTGAAAC	AACTGGTATG	240
CCTACTAGAA	TTCTCCTTAG	AAAGCGTCGT	TTCAAGTGCT	ATCATTTGTT	TAAAATTATG	300
GTTGCTGAAA	CTTCTATCGT	CAAGAAGAAT	CATCAAATCC	CTCGTATCAT	CAACCAAAAG	360
ATTGCTCAAA	AGTTAATTGA	AAAGATTTCT	ATGACTGATA	TTGCCCATCA	GCTTTCCATC	420
TCAACTTCAA	CTGTCATTCG	AAAGCTCAAT	GACTTCCACT	TTGAGTGTA	TTTTAGAAAT	480
CTGCCTAAGA	TTATGTCTTG	GGACGTTGAA	ACAGTCCGGG	GAGTGACTGT	TTCAATCGGG	540
AGATGGAGAT	GA					552

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

AAAGCGACAA	AACAACTCAT	TAGAAAGAAT	CATATGGAAC	AATTACATTT	TATCACAAAA	60
TTACTAGACA	TTAAAGAACC	TCACATCCCC	ACTTTTTTACA	TCCTCCCTCC	AGGAGGGAGA	120
CCCCGGAGGA	ATCCCCCCCC	CGGGGGACGA	AAAACCCCCC	TGTTCTCTCGT	TGTGGAGTTT	180
CTTTAA						186

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 552 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...552
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

AAAGCGACAA AACAACTCAT TAGAAAGAAT CATATGGAAC AATTACATTT TATCACAAAA	60
TTACTAGACA TTAAAGACCC TAATATCCAG ATTTTAGACA TCATCAATAA GGATACACAC	120
AAGGAAATCA TCGCCAAACT GGACTACGAC GCCCCATCTT GCCCTGAGTG CGGAAACCAA	180
TTGAAGAAAT ATGACTTTCA AAAACCGTCT AAGATCCCTT ACCTCGAAAC AACTGGTATG	240
CCTTCTAGAA TTCTCCTTAG AAAACGCCGT TTCAAGTGCT ATCACTGTTC AAAAATGATG	300
GTCGCTGAAA CTTCTATCGT CAAGAAGAAT CATCAAATTC CTCGTATTAT CAACCAAAAA	360
ATTGCGCAAA AGTTGATTGA GAAGATTCTT ATGACCGATA TTGCTCATCA GCTGGCCATT	420
TCAACTTCAA CTGTCATTCT CAAGCTCAAT GATTCTCACT TTGAGCATGA TTTTTCGCGT	480
CTTCCTGAGA TTATGTCTTG GGACGTTGAA ACAGTCCGGG GAGTGACTGT TTCAATCGGG	540
AGATGGAGAT GA	552

(2) INFORMATION FOR SEQ ID NO:958:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...552
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

AAAGCGACAA AACAACTCAT TAGAAAGAAT CATATGGAAC AATTACATTT TATCACAAAA	60
TTACTAGACA TTAAAGACCC TAATATCCAG ATTTTAGACA TCATCAATAA GGATACACAC	120
AAGGAAATCA TCGCCAAACT GGACTATGAA GCTCCATCTT GTCCTGAGTG CGGAAGTCAA	180
ATGAAGAAAT ATGACTTTCA AAAACCTTCT AAAATTCTCT ATCTTGAAAC GATTGGTATG	240
CCTTCTAGAA TTCTCCTTAG AAAACGCCGT TTCAAGTGCT ATCACTGTTC AAAAATGATG	300
GTTGCTGAGA CTCCCCTGGT AAAGAAAAAT CACCAAATCC CTCGTATCAT CAACCAAAAA	360
ATTGCTCAAA AGTTAATTGA AAAGATTCTT ATGACTGATA TTGCCCATCA GCTTTCATC	420

TCAACTTCAA	CTGTCATTCG	CAAGCTCAAT	GATTCTCACT	TTGAGCATGA	TTTTTCGCGT	480
CTTCCTGAGA	TTATGTCTTG	GGACGTTGAA	ACAGTCCGGG	GAGTGACTGT	TTCAATCGGG	540
AGATGGAGAT	GA					552

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

AAAGCGACAA	AACAACATCAT	TAGAAAGAAT	CATATGGAAC	AATTACATTT	TATCACAAAA	60
TTACTAGACA	TTAAAGACCC	TAATATCCAG	ATTTTAGACA	TCATCAATAA	AGATACACAC	120
AAGGAAATCA	TCGCCAAACT	GGACTACGAC	GCCCCATCTT	GCCCTGAGTG	CGGAAGTCAA	180
ATGAAGAAAT	ATGACTTTCA	AAAACCTTCT	AAAATTCCCT	ATCTTGAAAC	GACTGGTATG	240
CCTACTAGAA	TTCTCCTTAG	AAAGCGTCGA	TTCAAGTGCT	ATCAGTGCTC	AAAAATAGCG	300
GTCGCTGAGA	CTTCCCTCGT	CAAGAAAAAT	CACCAAATCC	CTCGTATCAT	CAACCAAAAG	360
ATTGCTCAAA	AGTTGATTGA	AAAGATTTCT	ATGACTGATA	TTGCCCATCA	GCTTTCCATC	420
TCAACTTCAA	CTGTTATTCT	TAAGCTCAAT	GATTTTCACT	TTAAACATGA	TTTTTCTTGT	480
CTTCCTGAGA	TTATGTCTTG	GGATGAGTAT	GCTTTTACAA	AGGGAAGAT	GAGCTTCATT	540
GCGCAAGATT	TTAACAATCT	CAATATCATC	ACTGTTCTTG	AGGGAAGAAC	ACAAGCTATC	600
ATTCGAAATC	ACTTTCTTAA	ATATGATAGA	GCCGTCCGAT	GTCGCGTCAA	AATTATTACT	660
ATGGATATGT	TTAGCCCTTA	CTATGACTTA	GCTAGACAAC	TTTTCCCGTG	TGCTAAAATC	720
GTGTTGGATC	GCTTTCACAT	TGTACAACAT	CTTAGCCGTG	CTATGAGTCG	TGTGCGTGTT	780
CAAATCATGA	ATCAATTGGA	TCGAAAGTCT	CATGAATACA	AGGCTATCAA	GCGCTACTGG	840
AAACTCATTC	AACAGGATAG	CCGTAAACTG	AGTGATAAGC	GATTTTATCG	TCCTACTTTT	900
CGTATACATT	TAACCAATAA	AGAGATTTTA	AACAAGCTTT	TGAGTTATTC	GGAAGACTTG	960
AAACACCACT	ATCAGCTCTA	TCAGCTCTTG	CTTTTTCCTT	TCCAGAATAA	GGAACCAGAG	1020
AAATTTTTCG	GGCTTATTGA	GGACAATCTA	AAGCAGGTTC	ATCCTCTTTT	TCAGACTGTC	1080
TTTAAACCT	TCCTCAAAGA	TAAAGAAAAG	ATTGTCAACG	CCCTTCAACT	ACACTATTCT	1140
AATGCCAAAC	TGGAAGCGAC	CAATAATCTC	ATCAAACCTA	TCAAGCGCAA	TGCCTTTGGT	1200
TTTCGAAACT	TTGAAAACCT	CAAAAAACGG	ATTTTTATCG	CTTTGAATAT	CAAAAAAGAA	1260
AGGACAAAAT	TTGTCTTTTC	TCGAGCTTAG				1290

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...768
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

CCAAATGCAA	ACGGAGGATT	TGAAATAATG	ACACAAGCAA	TCCTTGAAAT	TAAACACCTC	60
AAAAAATCCT	ATGGACAAAA	CGAAGTGCTA	AAAGACATTT	CACTCACTGT	CCACAAGGGA	120
GAGGTCATCT	CTATCATCGG	AAGCTCTGGA	AGCGGAAAAAT	CGACCTTCCT	ACGCTCCATT	180
AACCTACTTG	AAACACCAAC	TGATGGACAA	ATCCTTTATC	ATGGACAAAA	CGTCCTCGAA	240
AAAGGCTATG	ACCTCACGCA	ATACCGTGAA	AAGTTGGGGA	TGGTTTTCCT	ATCCTTTAAC	300
CTCTTTGAAA	ATCTCAATGT	TCTTGAAAAC	ACAATCGTCG	CTCAGACAAC	TGTCCTAAAA	360
CGCGAACGCA	CAGAAGCTGA	AAAGATTGCC	AAAGAAAAAC	TGGAAAAGGT	CGGCATGGGA	420
GAACGCTACT	GGCAAGCCAA	ACCAAAAACAA	CTCTCAGGTG	GTCAAAAACA	ACGTGTGGCC	480
ATCGCTCGTG	CCCTCTCCAT	GAATCCGGAC	GCTATTCTCT	TTGATGAACC	AACATCAGCT	540
CTCGATCCAG	AAATGGTTGG	AGAAGTCCTC	AAAAATCATGC	AGGACCTGGC	TCAGGAAGGC	600
TTGACCATGA	TTGTCGTAAC	CCATGAAATG	GAATTTGCCC	GTGATGTCTC	TCACCGTGTT	660
ATCTTTATGG	ATAAGGGCGT	GATCGCTGAA	GAAGGTAAAC	CAGAAGACCT	CTTCACCAAT	720
CCTAAAGAAG	ACCGAACAAA	AGAGTTCCTT	CAACGCTATC	TCAAATAA		768

(2) INFORMATION FOR SEQ ID NO:961:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

GGTATGGCAA	AAGAACCGTG	GCAAGAAGAT	ATTTATGATC	AAGAAGAATC	AAGAGCAGGG	60
CGTCGGCATC	GAAACCACGG	AGGGGCTGAT	AGGATGGCTA	ATCGTATTTT	GACGATCCTA	120
GCTAGTATTT	TCTTTGTAAT	TGTGGTGGTG	ATGGTCATCG	TTCTCATCTA	TCTATCATCG	180
GGGGGGAGTA	ATCGCACAGC	AGCCTTAAAA	GACTTTCATG	ATTCTGATGC	AAGTGTAGTA	240

CAAATCTCAT	CTTCAAGCAG	TTCTCAGCCT	GAGCAGAGTT	CAGAGCCAGA	ATCTACTTCT	300
AGTAGTTCAG	AAGAAGCTGC	TAATCCTGAA	GGAACGATTA	AAGTTCTCGC	AGGAGAAGGG	360
GAAGCAGCTA	TTGCCGCTCG	TGCAGGAATC	TCCATTGCTC	AGTTAGAGGC	CTTGAATCCT	420
GGGCACATGG	CTACAGGATC	TTGGTTTGCT	AATCCAGGTG	ATGTTATAAA	AATAAAATAG	480

(2) INFORMATION FOR SEQ ID NO:962:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...486
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

ATAATGGCAA	AAAAAGTTAA	AATCAAAAAA	ACATTGGTGG	AACAAATCCT	ATCTAAAGCA	60
GCTATCCCTC	ATCAGGGGAT	TCAAATCAAT	GCCCTAGAAG	GAGAGCTTCC	TCAAGGTTAT	120
GAACGAGATC	AGATTTTCAA	AACCTTGGCG	CTTTTGGGAG	ACAAGACCGG	ACCGATTATC	180
GGAATTGTCC	CTATCACTCA	GCACTTGTCT	GAAAAGAAAC	TAGCTAAAAT	TTCTGGCAAT	240
AAAAAAGTGA	GCATGATTCC	ACAAAAGGAC	TTAGAAAAAA	CAACTGGTTA	CATTTCATGGA	300
GCCAATAATC	CTGTCGGAAT	TCGTCAGAAA	CACAATTATC	CCATTTTTTAT	CGATAAAATT	360
GCTCTAGATT	TGGATCGAAT	GATTGTCTCT	GCAGGCGAAG	TCGGACACAG	CATTATCGTC	420
GCGCCACAAG	ACTTGGCTAG	CTTTGTAAAG	GCAGACTTTG	TAGATATTTT	GGAGGACATC	480
AAGTAA						486

(2) INFORMATION FOR SEQ ID NO:963:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...1419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

AAGATGGCAA	ATAAAGCAGT	AAATGACTTT	ATACTAGCTA	TGAATTACGA	TAAAAAGAAA	60
CTCTTGACCC	ATCAGGGAGA	AAGTATTGAA	AATCGTTTCA	TCAAAGAGGG	TAATCAGCTA	120
CCCGATGAGT	TTGTTGTTAT	CGAAAAGAAAG	AAGCGGAGCT	TGTCGACAAA	TACAAGTGAT	180
ATTTCTGTAA	CAGCTACCAA	CGACAGTCGC	CTCTATCCTG	GAGCACTTCT	CGTAGTGGAT	240
GAGACCTTGT	TAGAGAATAA	TCCCACTCTT	CTTGCGGTCG	ATCGTGCTCC	GATGACTTAT	300
AGTATTGATT	TGCCTGGTTT	GGCAAGTAGC	GATAGCTTTC	TCCAAGTGGA	AGACCCCAGC	360
AATTCAAGTG	TTCGCGGAGC	GGTAAACGAT	TTGTTGGCTA	AGTGGCATCA	AGATTATGGT	420
CAGGTCAATA	ATGTCCCAGC	TAGAATGCAG	TATGAAAAAA	TCACGGCTCA	CAGCATGGAA	480
CAACTCAAGG	TCAAGTTTGG	TTCTGACTTT	GAAAAGACAG	GGAATTCCTCT	TGATATTGAT	540
TTTAACTCTG	TCCATTCAGG	CGAAAAGCAG	ATTTCAGATTG	TTAATTTTAA	ACAGATTTAT	600
TATACAGTCA	GCGTAGACGC	TGTTAAAAAT	CCAGGAGATG	TGTTTCAAGA	TACTGTAACG	660
GTAGAGGATT	TAAAAACAGAG	AGGAATTTCT	GCAGAGCGTC	CTTTGGTCTA	TATTTGAGT	720
GTTGCTTATG	GGCGCCAAAGT	CTATCTCAAG	TTGGAAACCA	CGAGTAAGAG	TGATGAAGTA	780
GAGGCTGCTT	TTGAAGCTTT	GATAAAAGGA	GTCAAGGTAG	CTCCTCAGAC	AGAGTGGAAA	840
CAGATTTTGG	ACAATACAGA	AGTGAAGGCG	GTTATTTTAG	GGGGCGACCC	AAGTTCGGGT	900
GCCCGAGTTG	TAACAGGCAA	GGTGGATATG	GTAGAGGACT	TGATTCAAGA	AGGCAGTCGC	960
TTTACAGCAG	ATCATCCAGG	CTTGCCGATT	TCCTATACAA	CTTCTTTTTT	ACGTGACAAT	1020
GTAGTTGCGA	CCTTTCAAAA	TAGTACAGAC	TATGTTGAGA	CTAAGGTTAC	AGCTTACAGA	1080
AACGGAGATT	TACTGCTGGA	TCATAGTGGT	GCCTATGTTG	CCCAATATTA	TATTACTTGG	1140
AATGAATTAT	TACTGATCA	TCAAGGTAAAG	GAAGTCTTGA	CTCCTAAGGC	TTGGGACAGA	1200
AATGGGCAGG	ATTTAACGGC	TCACTTTACC	ACTAGTATTC	CTTTAAAAGG	GAATGTTTCGT	1260
AATCTCTCTG	TCAAAAATTAG	AGAGTGTTACC	GGGCTTGCCCT	GGGAATGGTG	GCGTACGGTT	1320
TATGAAAAAA	CCGATTTGCC	ACTAGTGCGT	AAGCGGACGA	TTTCTATTTG	GGGAACAAC	1380
CTCTATCCTC	AGGTAGAAGA	TAAGGTAGAA	AATGACTAG			1419

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2076 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

ATCGTTCCCC	TTGTAAGAAA	TTACAGGGGG	AATTTTGT	TTT	ACAAGGAGTC	TACTATGAAG	60
AAACTATTCA	TATTATTATC	AACTTTTTTT	CTCAGCTTCT	TCCTTGCTTG	GATTATTGTC		120
TTACGTGCGC	CACAATATTT	ATATGCAAGC	TATGATTCCG	TTTCTTTACT	TCGTGTCAAA		180
AAAGATACTC	AGGAACCGAC	GCGTGAGGTA	TTTGAACAGG	AATTGGAGAA	TTTTGCAAAC		240
TCAGAACAGA	GTTTAATAGC	TAGAAGAATT	GTAGAGCCGA	GTAAGGATGG	GACGACTCAC		300

TTTACTTATG	CAACTTATGG	TCAGGGAACT	TTACCAAAAG	AATTCCAAGA	AGCTAGCCAA	360
GAAAGTCGTG	AACGTAGTGA	TCCGCTAAAT	AGTTATCTCC	TTTTGTCAGG	CTCCTTGACG	420
AAAGAAAAGC	TTGCCGATAA	ATTAGGAGAT	TTGGGTTATA	AAGCAAGTGC	TGACCGAAAG	480
ATACCGCCCT	ATTTTCTTGC	TTTTCGAATA	TTACTAAATC	CCCTTATTTT	AATTAGTTTA	540
GCAATATTTG	GCTTATCTTT	CTTTGCTTTA	GTGATTATCA	CTCGGATTAA	GGAAATGAGA	600
GCAGCAGGTA	TAAAACTCTT	TTCTGGTCAG	ACTCTCTTAT	CCATCATGGG	GCATTCTTTA	660
TCTACTGATA	TCAAATGGCT	CCTTCTATCA	GCCCTCCTTT	CCTTCCTAGG	TGGGGGAGTC	720
GTTCTTTTTA	GTCAAGGTTT	GTTTTATCCT	ATCTTGTTAG	CCACCTATGG	TTTTGGGATT	780
AGTTTCTATC	TGTTGTTTTT	ATTGGCGATT	TCAATTTTAC	TAATGCTTCT	TTATCTAATG	840
AGTTTGAGTT	ACAAAGCATT	AGTTCCCGTT	ATTAAGGGGA	GATTACCCCT	TAAACGCCTG	900
ATGATTTTAA	CCCTATTGTG	TCAGTTGGTT	GCTGTCCTTA	CAGTAGGCTA	CGCTGTTAAG	960
ACAGGTTTGA	TGTCTTACCA	ACGATTGAAA	GAACTTGAAA	TTTCAAAACA	AGCATGGCAG	1020
GATAGAGCAG	ACTATTATCA	AATTTCTTTT	GGCTTAGGTG	ATAGAGGAAA	AGATACAGAA	1080
AATCAGAGCA	AGTGGTATGC	CTTTGCCAAG	GAAGCAATCG	AAGAAGAACA	AGCTCTTTAT	1140
GTAAAGGATA	ATCTGCTCCA	TTTTGCCAAT	CCACAAGGAA	AAAATGAACA	GGGAGAGACA	1200
CTGGATACCT	ATAGTCCAGA	TGCTAATACG	CTCTATGTTA	GTCCCAGTTA	TTTGGACAAG	1260
GAAAAGGTCG	TGGTAGATGC	TGAGACCAAA	CAGAAGTTAG	CCCATCTCCA	AAAAGGTGAG	1320
TTTATCCTCT	TGCTCCCAAG	ACATTTGCGC	TCTCGAGAAG	CAGAACTTAA	GAAAGTTTTT	1380
GAAGAAAAGAT	TGAGTTATTA	TGGAAAATCT	GGTGAGGAGG	CAAGTGCTCC	TTTGGATTAT	1440
GAGATGAAAAG	CGCACGTTAG	TTATCTTTCA	ATGGGAGAAA	AGCGGTTTGT	TTATAATAAC	1500
GGTGAGAATC	CCGTATCTAC	TCAGTATTTG	ACTGATCCGA	TTTTAGTTGT	ATTCACGCCG	1560
ACTTCTACAG	GTGATAGTTT	TATATCCTTA	TCTAGTTGGT	CTATCAATGC	TGGAAAACAA	1620
CTCTTTATCA	AAGGATATGA	GAGTGGGCTA	GAACTCTTGA	AGAAAAGCTGG	AATTTATGAG	1680
CAAGTATCCT	ATCTTAAAGA	AGGAAGAAGT	GTTTATCTAA	CTCGTTATAA	TGAAGTTCAA	1740
ACTGAAACAG	CAACTTTAAT	CTTAGGAGCT	ATTGTGGGGA	TAGCTAGTTC	CTTGTTACTA	1800
TTTTATTCTG	TCAATCTTCT	ATATTTTCGAG	CAATTCGCC	GAGATATCTT	GATTAAACGA	1860
ATTTACAGGT	TACGATTTTT	TGAAACACAT	GCTCAGTATA	TGGTTAGCCA	ATTTGCCAGT	1920
TTTGATTTTG	GTGCTAGTCT	CTTTATTTTA	AGCAGTCGAG	ACTTGGTGAT	TGGCTTGCTC	1980
ACTTTATTAG	TCTTCTAGC	TAGTGCAGTT	CTGACGCTTT	ACCGTCAAGC	GCAGAAAGAA	2040
TCTCGTGTTT	CTATGACAAT	TATGAAAGGA	AAATAG			2076

(2) INFORMATION FOR SEQ ID NO:965:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1521
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

CCTCTTCAAA	ATGACCCAAA	TGCAAACCAA	TTTTGGTTTC	AATATGCTCG	CTATCCAAAA	60
TGGTATACCG	AAAAATTTGT	CTCTTCGTCA	GATTTTGGAT	GCTTATATCG	AGCACCAAAA	120

AGAATGGTTG	TTCGTCGTAC	ACGTTTTGAT	AAGGAAAAAG	CGGAAGCGCG	CGCTCATATC	180
TTAGAAGGTC	TCTTGATTGC	GCTAGACCAT	ATCGACGAAG	TGATTTCGTAT	CATCCGTGCT	240
AGTGAAACGG	ATGCGGAAGC	TCAAGCTGAG	TTGATGAGCA	AGTTTAAAGCT	TTCTGAACGT	300
CAAAGTCAAG	CTATCCTTGA	TATGCGTCTT	CGTCGTTTGA	CAGGTTTGGG	ACGCGATAAG	360
ATTCAATCTG	AGTATGATGA	CCTCTTGGCT	CTGATTGCGG	ATTTAGCAGA	TATTCCTTGCT	420
AAGCCTGAAC	GTGTTTCTCA	AATTATCAAA	GACGAATTGG	ATGAAGTTAA	ACGTAAATTT	480
TCTGATAAAC	GCCGTACAGA	GTTGATGGTT	GGACAGATCT	TGAGTCTCGA	GGATGAGGAC	540
TTGATTGAAG	AATCGGATGT	CTTGATTACC	CTTTCTAACA	GAGGCTACAT	TAAGCGTTTG	600
GATCAGGACG	AGTTCACTGC	TCAAAAAACGT	GGGGGTCGTG	GTGTCCAAGG	AACGGGAGTG	660
AAAGATGATG	ACTTTGTTTC	TGAGTTAGTG	TCAACTAGCA	CACATGATCA	TCTGCTCTTC	720
TTCACAAACA	AGGGACGTGT	CTATCGTCTT	AAAGGTTATG	AAATTCCTGA	GTATGGTCGG	780
ACTGCCAAAG	GGCTACCACT	AGTCAATCTC	TTGAAATTGG	ATGAAGACGA	AAGTATTTCAG	840
ACGGTTATCA	ATGTTGAGTC	TGATCGCAGT	GATGATGCTT	ATCTCTTCTT	TACAACCCGT	900
CACGGTATTG	TGAAGAGAAC	TAGTGTTAAG	GAGTTTGCCA	ATATTCGTCA	AAATGGTCTC	960
AAAGCGCTGA	ATTTAAAGGA	TGAAGATGAG	TTAATCAATG	TCTTGTTGGC	AGAAGGAGAT	1020
ATGGATATTA	TCATTGGTAC	CAAGTTTGGT	TATGCAGTTC	GCTTTAATCA	ATCAGCCGTT	1080
CGTGGTATGA	GCCGTATCGC	CACTGGTGTG	AAAGGTGTTA	ACCTTCGTGA	AGGAGACACA	1140
GTTGTTGGTG	CCAGCTTGAT	TACTGATCAA	GATGAGGTTT	TTATTATCAC	AGAAAAAGGA	1200
TATGGTAAGC	GTACAGTCGC	TACTGAATAC	CCAACAAAAG	GTCGTGGTGG	TAAGGGAATG	1260
CAGACAGCTA	AAATTACCGA	AAAAAATGGC	TTGCTGGCCG	GTCTTATGAC	TGTTCAAGGG	1320
GATGAGGATT	TGATGATTAT	CACTGATACA	GGTGTCATGA	TTCGAACCAA	TCTTGCCAAT	1380
ATTTACAAA	CAGGACGTGC	AACTATGGGA	GTTAAAGTAA	TGCGCCTGGA	TCAAGATGCT	1440
CAGATAGTGA	CTTTCACAAC	GTTGCGGTG	GCAGAAAAAG	AAGAAGTTGG	GACAGAAAAC	1500
GAAACAGAAG	GTGAAGCATA	A				1521

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

AAACTTCAAA	AAACGGATTT	TCATCGCTCT	GAACATCAAA	AAAGAAAGGA	CAAAATTTGT	60
CCTTCTCGA	GCTTAGCTTT	TCTCAACCC	ACTACAGTTG	ACAAAGAGCC	CTTTTTATTA	120
TTCAAGAACT	TGATTAGCTC	AATGCATCCA	AGGCGTCATC	CATTGAAAGA	ACTTCGTGGA	180
AGACACGTTG	TGTCAAATTCA	GTTTTTTGTT	CTGGAGTGA			219

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

AAACTTCAAA	AAACGGATTT	TTATCGCTCT	GAACATCAAA	AAAGAAAGGA	CGAAATTTGT	60
CCTTTCTCAA	GCTTAGCTGA	CTTCAACCCA	CTACAGTTGA	CAAAGAGCCA	AAAAATTCTC	120
TTTTCATACT	CATTTAAAAT	CAAAAAGGGA	ATTTATCGTT	TTACGGACAT	GTATATTACA	180
GATTTCATATA	GGTCGTGTAT	AGACAGGATA	TCATCGCTTG	GAAGTTTTC	TTTTTGA	237

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

CAGTATCAAA	ACACAGTTGC	TAGAATCAAG	ACTGGCACCC	AGATTAGAGG	AGGAATTCTC	60
ATGACAGATA	CAGACCCTAT	CAAAAGAGCT	CAGACTTTGA	TTACTGACTT	AAACAAAGCC	120
TATCAAGCAT	GCAAACAGGC	AACCGCTGAC	GACGTCCGCT	TTCAGGAGCA	ATTAAACTCT	180
ATTCTTGGTT	TTCTAGCCAA	GGCTGAAACA	GTGGATAATC	GATTCTTGAT	TGAATTGGAA	240
AAATTTTACC	AGACTTCCAG	TCTTCTCATG	GGACTCAGCG	CTCTTGATCC	AGATGCTCCA	300
ACTCGCGCCG	CTTGGCGGGC	CTATGACCGC	TTCCACTTTG	ACCAAGTCAA	GACCAAGTTA	360
ATACTCAATG	AGAATCAAAG	AGCAAAC TAG				390

(2) INFORMATION FOR SEQ ID NO:969:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GTTAGTCAAA AAGAAGGAAT TCAAGCAAAA CAAATTGTTA TTAAGATTAC AGATCAAGGT	60
TATGTAACTT CTCATGGCGA TCATTATCGC TACTATAATG GTAAAGTTCC TTTTGATGCG	120
CTCTTTAGTG AAGAGCTATT AATGAAAGCC CCCAACTATC AGCCGAAAGA TCAAGATATC	180
GTCAGTTAG	189

(2) INFORMATION FOR SEQ ID NO:970:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GTTATCCAAA ATCACTTTTC CCCCAATGGT TTTGGTAATA TTTTTCAACT CAATCATAAG	60
ATGCCCCCTT TCAATAACTC TACTAGACTT CTTTCTCCA TCCTAGAAGC TAAGCCTAGC	120
ACAAATAGTA TATCCAGACA TGTAACACCT GCAAACAGTA GAAGTGGTAA GAACGCATGG	180
GCAAAGAAAA TCAAGACTAG AAGAGGGAAA CTATAG	216

(2) INFORMATION FOR SEQ ID NO:971:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1407
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

TTAAACAAA	ATCTAGAAAG	GGAATCTATG	TTACACAACG	CATTTGCCCTA	TGTTACAAGG	60
AAGTTTTTCA	AATCGATTGT	CATCTTCCTG	ATTATTCTCC	TCATGGCGAG	CTTGAGTTTG	120
GTCGGCTTGT	CAATCAAGGG	AGCTACTGCC	AAGGCTTCTC	AGGAGACCTT	TAAAAATATC	180
ACCAATAGCT	TCTCCATGCA	AATCAATCGT	CGCGTCAACC	AAGGAACGCC	TCGCGGTGCT	240
GGGAATATCA	AGGGTGAAGA	CATCAAAAAA	ATCACCGAAA	ACAAGGCCAT	TGAGTCTTAT	300
GTCAAACGTA	TCAACGCTAT	CGGAGATTTG	ACTGGATATG	ACCTGATTGA	AACGCCAGAA	360
ACCAAGAAGA	ATCTCACTGC	TGATCGTGCC	AAACGTTTTG	GAAGTAGCTT	GATGATTACA	420
GGTGTCAATG	ACTCCTCTAA	AGAAGACAAG	TTTGTCTCTG	GTTCTTATAA	ACTAGTCGAA	480
GGAGAGCACT	TAACCAACGA	CGACAAGGAT	AAAATCCTCT	TGCACAAGGA	CTTGGCAGCC	540
AAACACGGCT	GGAAAGTAGG	GGACAAGGTT	AAACTGGACT	CTAATATCTA	CGATGCAGAT	600
AATGAAAAAG	GAGCCAAGGA	AACAGTTGAA	GTGACAATCA	AGGGACTCTT	TGATGGTCAT	660
AATAAGTCAG	CAGTAACCTA	CTCACAAGAA	CTTTACGAAA	ACACAGCTAT	TACAGACATT	720
CACACTGCTG	CAAAACTTTA	TGGATACACA	GAAGACACAG	CCATTTATGG	GGACGCAACC	780
TTCTTTGTAA	CAGCAGACAA	GAACCTTGGAT	GATGTTATGA	AAGAGTTGAA	TGGCATCAGT	840
GGTATCAACT	GGAAGAGCTA	CACACTCGTC	AAGAGCTCCT	CTAACTACCC	AGCTCTTGAG	900
CAATCTATAT	CTGGTATGTA	CAAGATGGCC	AACCTCCTCT	TCTGGGGTAG	TTTGAGCTTC	960
TCAGTTCTCC	TCCTTGCCCT	CTTGCTCAGC	CTTTGGATCA	ACGCCCCTCG	CAAGGAAGTG	1020
GGAATTCTCC	TCTCTATCGG	CCTCAAGCAG	GCAAGTATCT	TGGGTCAATT	CATCACCGAA	1080
TCTATCTTGA	TTGCTATCCC	TGCTCTAGTT	TCTGCTTACT	TCCTAGCTAA	TTCACTGCC	1140
CTTGCAATTG	GAAACCTTGA	CCTTGCCAAAT	GTGACTTCAG	GTGTTGCCAA	ACAGGCTAGT	1200
AAGGCGGCTC	AAGCCTCTAA	CCTTGGTGGT	GGTGCAGAA	TAGATGGCTT	TAGCAAGACC	1260
TTGTGAGGCC	TAGACATTTC	TATTCAGACA	TCAGACTTTA	TCATCATTTT	TGTCCTTGCC	1320
TTGGTTCTAG	TGGTTCTCGT	TATGGCGCTT	GCTTCAAGCA	ATCTCCTTAG	AAAACAACCA	1380
AAAGAGCTCT	TGCTGGATGG	TGAATAA				1407

(2) INFORMATION FOR SEQ ID NO:972:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

AAAAAACAAA	AAGGAGAAAT	ACTCATGGCA	GTAATTTCAA	TGAAACAAC	TCTTGAGGCT	60
GGTGTA	CACTTTGGT	CACCAAACT	CGTCGCTG	GAATCCTA	AGATGGCTAA	120
GTACATCTTT						
ACTGAACGTA	ACGGAATCCA	CGTTATCGAC	TTGCAACAAA	CTGTAAAATA	CGCTGACCAA	180
GCATACGACT	TCATGCGTGA	TGCAGCAGCT	AACGATGCAG	TTGTATTGTT	CGTTGGTACT	240
AAGAAACAAG	CAGCTGATGC	AGTTGCTGAA	GAAGCAGTAC	GTTTCAGGTCA	ATACTTCATC	300
AACCAACCGTT	GGTTGGGTGG	AACTCTTACA	AACTGGGGAA	CAATCCAAAA	ACGTATCGCT	360
CGTTTGAAAAG	AAATTAAACG	TATGGAAGAA	GATGGAAC	TTTCGAAGT	TCCTAAGAAA	420
GAAGTTGCAC	TTCTTAACAA	ACAACGTGCG	CGTCTTGAAA	AATTCCTTGGG	CGGTATCGAA	480
GATATGCCTC	GTATCCCA	GATGTGAT	GTAGTTGACC	CACATAAAGA	GCAAATCGCT	540
GTCAAAGAAG	CTAAAAAATT	GGGAATCCCA	GTTGTAGCGA	TGGTTGACAC	CAATACTGAT	600
CCAGATGATA	TCGATGTAAT	CATCCCAGCT	AACGATGACG	CTATCCGTGC	TGTTAAATTG	660
ATCACAGCTA	AATTGGCTGA	CGCTATTATC	GAAGGACGTC	AAGGTGAGGA	TGCAGTAGCA	720
GTTGAAGCAG	AATTTGCAGC	TTCAGAAACT	CAAGCAGATT	CAATTGAAGA	AATCGTTGAA	780
GTTGTAGAAG	GTGACAACGC	TTAA				804

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

TTAAGACAAA	AGGATAAGAG	AAAGGAGACT	AAGATGTCCT	GGACATTTGA	CAACAAAAAA	60
CCCATCTATT	TACAGATTAT	GGAGAAAATC	AAGCTTCAGA	TTGTTTCCCA	TACACTGGAA	120
CCCAATCAAC	AACTTCCAAC	CGTGAGGGAG	CTAGCTAGCG	AGGCTGGTGT	CAATCCCAAT	180
ACCATCCAAA	GAGCCTTATC	AGACCCTTGAA	CGAGAAGGAT	TTGTCTACAG	CAAGCGAACA	240
ACTGGACGAT	TTGTGACTAA	GGATAAGGAG	CTAATCGCTC	AGTCACGCAA	ACAATTATCA	300
GAAGAAGAA	TGGAACACTT	CGTTTCCTCC	ATGACCCATT	TTGGCTATGA	AAAAGAAGAA	360
CTACCAGGCG	TAGTCAGTGA	TTATATTAAA	GGAGTTTAA			399

(2) INFORMATION FOR SEQ ID NO:974:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

AAAAGACAAA AATGGCAGAA GAATTTATTT ATTAGGAGGA CTACAATGGA TAATAAAAAA	60
TTAAAAGTAA AAGATTTAGT AAGCATCGGT GTTTTTGGCG TAATTTATTT TGCCTTCATG	120
TTTGGAGTTG GTATGATGGG CTTGATTCCA ATATTGTTCT TAATATACCC GACAGTATTA	180
GCCATAGTTG CAGGAACTGT TGTATGTGTA TTTATGGCTA AGGTTCAAAA GCCATGGGCA	240
CTATTTATAT TTGGTATGAT ATCACCATT GTGATGTTTG CAGCTGGTCA TACCTACGTA	300
GTTGTGGTTT TATCACTTAT AGTAATGATA ATAGCAGAAT TAATTAGAAA GATTGGTAAT	360
TATAATTCAT TTAAATACAA TATGCTTTCT TATGCAATCT TCAGCACATG GATATGTAGC	420
TCTTTAATGC AAATGCTTTT AGCAAAAGAA AAATATATGG AGTGGTCTTT GATGACTATG	480
GGAAAAGATT ATGTTGATGT ATTAGAAAAG TTAATAACTT ATCCTCACAT GGCTTTAGTA	540
GCCTTAGGTG CTTTCTTAGG AGGAATTCTT GGAGCATATA TAGGCAAGGC TCTATTGAAA	600
AAACACTTTG AAAAAGCAGG CATCGTATAA	630

(2) INFORMATION FOR SEQ ID NO:975:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

CTAATGCAAA	ATTTAATTAT	AGGTATTCAA	AAAAGAAAAA	ATAGAATAAC	ACTATTTTCC	60
TCACTATTTT	TATTAATAAT	AATCAGTCTA	TCATTTTTTC	TTTTACTTAT	CGGAAATGAA	120
AGTTATTCTT	TTTCAACTTT	GATTAAAGTC	TTAAATAGTG	AAACTGTTCC	TGGAGCTAGT	180
TTTTCGATTA	TGGAAATTAG	ATTACCAAAA	TTATTAGCAG	GAATTATAGC	TGGCTGGTCT	240
TTTGGATTGG	CAGGATTTAT	CTTTCAAAC	ATGTTAAGAA	ATCCTCTTGC	AAGTCCTGAT	300
ATAATCGGTG	TCACAAGTTC	TTCATCTATT	GCAGCGGTCT	TTTGCATATT	GGTATTAAAA	360
ACAAAAGTGT	TAACTACTGG	AATTATTTCA	ATAACTTGTG	GACTAACATC	ATCTTTAATA	420
TTATTTTTTAC	TAGCTAAAAA	AGATGGTTTT	TCAGCAGCAA	GACTGATAAT	ATTAGGTATT	480
GGTTTTCAAG	CTGTCACAAG	AGCAGGCACC	TCATTTTTTAT	TGTTGAAAGT	AGCAAGATAT	540
GAATTACAAG	AAGTTATGAG	ATGGCTCAGT	GGCTCTTTTAT	CTTTTACAAA	GTTAGATGAC	600
ATACCTCTTG	TTCTAATNAG	TAAGTATTAT	TGCTACTATA	TTAGTTTTTAT	TTTTTTAA	657

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GAAATGCAAA	AAACAGCTTT	TATTTGGGAT	TTAGACGGGA	CTTTATTGGA	CTCTTACGAA	60
GCGATTTTAT	CAGGGATTGA	GGAGACTTTT	GCTCAGTTTT	CTATTCCTTA	TGATAAGGAG	120
AAGGTGAGAG	AGTTTATCTT	CAAGTATTCG	GTGCAAGATT	TGCTTGTGCG	GGTGGCAGAA	180
GATAGAAATC	TGGATGTTGA	GGTGCTAAAT	CAGGTGCGTG	CCCAGAGTCT	GGCTGAGAAG	240
AATGCTCAGG	TAGTTTTGAT	GCCAGGTGCG	CGTGAGGTGC	TAGCTTGGGC	AGACGAATCA	300
GGAATTCAGC	AGTTTATATA	TACTCATAAG	GGGAACAACG	CTTTTACCAT	TCTCAAGGAC	360
TTGGGGGTGG	AATCCTATTT	TACAGAGATT	TTAACCAGTC	AGAGTGGCTT	TGTGCGGAAG	420
CCAAGTCCAG	AAGCGGCTAC	CTATCTGCTA	GATAAGTATC	AGTTGAATTC	TGATAATACT	480
TATTATATAG	GGGATCGGAC	TCTGGATGTG	GAATTTGCCC	AGAATAGTGG	GATTCAAAGC	540
ATCAACTTTT	TAGAGTCTAC	TTATGAAGGG	AATCACAGGA	TTCAAGCGTT	AGCAGATATT	600
TCCCGTATTT	TTGAGACTAA	GTGA				624

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

GTTTATAAAA	AAGAAAAGGA	GTATTTGATT	ATGTTACAAA	AAATTTATGA	GCAGATGACT	60
AATTTCTATG	ATAGTATTGA	AGAAGAGTAT	GGTCCTACAT	TTGGTGATAA	TTTTGACTGG	120
GAACATGTTT	ATTTTAAATT	TTTAATTTAT	TATTTAGTGA	GATATGGCAT	TGGTTGTCGT	180
AAGGATTTTA	TCGTTTACCA	TTATCGTGTT	GCTTATCGTT	TGTATCTTGA	AAAATTGGTA	240
ATGAATCGGG	GTTTTATTTC	TTGTTGA				267

(2) INFORMATION FOR SEQ ID NO:978:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...699
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

TGTTATAAAA	ATAAAATAGG	AGCCGATATG	AAAACAATTC	AAATTGCTAT	TGATGGTCCT	60
GCTTCCAGCG	GTAAGAGTAC	GGTCGCAAAG	ATTATTGCTA	AGGATTTTGG	ATTCACCTAC	120
CTTGATACAG	GAGCTATGTA	TCGTGCAGCG	ACCTATATGG	CTCTTAAGAA	CCAATTAGGA	180
GTTGAAGAAG	TCGAAGCCCT	TCTAGCCTTG	TTGGACCAGC	ATCCAATCAG	CTTTGGACGT	240
TCAGAAACTG	GAGACCAGCT	TGTTTTTGTA	GGAGATGTGG	ATATTACCCA	TCCTATCCGT	300
GAAAATGAAG	TGACCAATCA	TGTTTCTGCT	ATTGCAGCAA	TTCCCTCAAGT	GCGTGAGAAA	360
CTGGTTTCTC	TCCAACAAGA	AATTGCCAG	CAAGGCGGGA	TTGTCATGGA	TGGTCGCGAT	420
ATTGGAACTG	TTGTATTGCC	ACAAGCAGAA	TTGAAAATTT	TCCTAGTAGC	TTCTGTTGAT	480
GAGAGAGCAG	AGCGTCGTTA	CAAGGAAAAT	ATTGCCAAGG	GAATTGAAAC	AGACCTTGAA	540
ACCCATAAAA	AGGAAATTGC	TGCGCGTGAC	TACAAGGATA	GTCATCGTGA	GACTTCTCCT	600
CTCAAACAAG	CAGAGGATGC	TGTCTACCTT	GATACAAC TG	GTTTGAACAT	TCAAGAAGTA	660
GTTGAAAAAA	TCAAAGCAGA	AGCTGAAAAA	AGAATGTAA			699

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

AATAATAAAA	AAGGAGAACT	TATCATGAAA	AAAAATGAAAG	TTTGGTCTAC	TGTACTTGCA	60
ACGGGAGTTG	CTCTTACTAC	ACTTGCTGCT	TGCTCTGGAG	GTTCAAATTC	TACGACTGCT	120
TCTTCATCTG	AAGAAAAAGC	TGATAAAAGT	CAAGAATTAG	TTATCTATTC	GAAGTCAGTC	180
TCAAATGGTC	GTGGTGATTG	GTAACTGCT	AAAGCAAAAG	AAAGCTGGTT	TTAA	234

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

ATCAATAAAA	AGAGAGGGGA	AGAAATGCTA	GAGATTCAAG	ATTTACTGTA	TCAACTCCGC	60
TTGTCTGAGC	AAGCGAGTAC	GCAATTGTTT	GAAAAAAGGC	TTGGGATTAG	TTTGACACGG	120
TATCAGATTT	TACTGTTTTT	GCTGGAGCAT	TCTCCTTGTA	ACCAAATGGC	GGTTCAGGAG	180
CGTTTGAAAA	TTGATCAGGC	TGCTTTGACA	CGGCATTTCA	AAATTTTGGA	AACGGAAGGT	240
TTGGTGGAGC	GTCATCGTAA	TCCTGAAAAT	CAGCGGGAAG	TGTTGGTAGA	GGCTGCGAAG	300
TATGCCAAGG	AGCAGTTAGT	GGTGAATCCC	CCTCTGCAAC	ATATCAGGGT	TAAGGAAGAG	360

ATAGAAAGTA TCTTAACAGA GTTTGAGAGA ACAGAACTCA GCCGTTTATT AAATAAATTG	420
GTTTTGGGTA TTGAAAATAT AGAAATTTAA	450

(2) INFORMATION FOR SEQ ID NO:981:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

CCTCGTAAAA AGGAGAAGAG GATGCAAATT CCAAGTAGAT TTACCATTGC GACTCATATG	60
CTGATAATCA TTGCCCTCGA GGGGAAGGAA AGCAAGGTGA CCAGTGATTT TCTGGCTGCT	120
AGTGTCTGGG TCAATCCTGT CATTATCAGA AAGATCTTGT CCCAGTTGAA GAAGGCAGAG	180
CTGATTTTCAG TAGCGCGTGG AACGGGCGGA ACAGAGATTG TCAAGGACCT TAAGGATATT	240
AGTCTTTTAG ATGTTTATCA AGGCGGGTCG AATGTCTTGG TAAGACAGGT CAACTCTTCA	300
GTTTCCATGA CAATCCGAAT CCAAATTGCC CTGTAG	336

(2) INFORMATION FOR SEQ ID NO:982:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

AGAGGTAAAA ACATGATTGA AGCAAGTAAA TTTAAAGCTG GTATGACCTT TGAAACAGCT	60
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GACGGCAAAT	TGATTCGCGT	TTTGGAAGCT	AGTCACCACA	AACCAGGTAA	AGGAAACACG	120
ATCATGCGTA	TGAAATTGCG	TGATGTCCGT	ACTGGTTCTA	CATTTGACAC	AAGCTACCGT	180
CCAGAGGAAA	AATTTGAACA	AGCTATTATC	GAGACTGTCC	CAGCTCAATA	CTTGTACAAA	240
ATGGATGACA	CAGCATACTT	CATGAATACA	GAAACTTACG	ACCAGTACGA	AATCCCTGTA	300
GTCAATGTTG	AAAACGAATT	GCTTTACATC	CTTGAAAAC	CTGATGTGAA	AATCCAATTTC	360
TACGGAAC	TG	TG	TG	TG	TG	420
ACTCAACCAT	CTATCAAAGG	TGCTACTGTT	ACAGGTTCTG	GTAAACCAGC	AACGATGGAA	480
ACTGGACTTG	TCGTAAACGT	TCCAGACTTC	ATCGAAGCAG	GACAAAAACT	CGTTATCAAC	540
ACTGCAGAAAG	GAACCTACGT	TTCTCGTGCC	TAA			573

(2) INFORMATION FOR SEQ ID NO:983:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 906 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

TTGGTCAAAA	AATTAAAGAG	ATTGGGGATA	GAAAAAGGAA	TTAGTCGTCC	AGATTTTTTGT	60
GGAGATGAGC	AAGAACTGAC	AGTTCGTCAA	CTGTCGCGAA	TTGAAAGTGG	AGCTTCGCAA	120
CCGAGTTTGC	CCAAGTTAGA	CTATATTGCT	CGCCGGCTAG	GAGTTCCAGT	TTATAGCCTT	180
ATGCCCGATT	TTTCAGCTCT	TCCTTCTGCT	TATTTAGAAAT	TGAAATACCA	GATTTTACGT	240
GAACCAATCT	ATGATAAAGA	AGAGGAGTAT	GATAAGAAAG	AAGCGTGTTT	GGAAGAGATA	300
GAGGATTTAT	TTTATGAGCA	ACTTCCTAAT	GAGGAGAAAG	TATGGTTTGA	AGCTACTAGA	360
GCAACGATAG	ATGTTATTTCG	AAGCGGACAA	CCAGAATACG	GGGAAACCGT	ACTGGACGAT	420
TATTTTAAAA	CAATTTATGA	TAAGGAATTG	TTTTTGATAA	ATGAATTAGA	AGTTATCAAC	480
TTATATTTTG	CTATAGTGCT	TACAAAAGATA	AAACAAGGTC	AAAATCAGAT	TGAAGAAATT	540
AACAGAAATC	ATTTCGTTTTT	AGTTCGTTTG	ACAAATCATG	TAGAATTAAT	TGCACCAGAA	600
TATCTGTTTG	CTTTAAGTAA	CACTTTGTTT	TCGGGTCTAG	CCTGTTTGGA	TAATTTGTCTG	660
TCTTATGATT	CACTAGGAGC	TTATATCTTT	AGCCTTAATC	ATATAATGGA	AAAAACACAA	720
GATTTCCAGA	AGAAACCAAT	TATATTAATG	TTGGAGTGGA	AATTATCTCT	AATAATAAAC	780
AATGATTATG	TTTCTGCCGA	ACAGTTCTAT	CAGAAATCGA	AGCTATTTGC	TGATATAATA	840
GAAAAATCTT	ATTTAGTTAC	TATGTTAGAA	AAACAATGGC	AAGAAGATTT	AAAAAAATAT	900
TTATAA						906

(2) INFORMATION FOR SEQ ID NO:984:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

TTTTCCAAAA	AGAATACAAT	AAATTTTCAA	GTATCTCAAA	GAGGGAGGCA	TAAGATGTCA	60
GATGCATTTA	CAGATGTAGC	CAAGATGAAA	AAAATCAAAG	AAGAAATCAA	GGCACATGAG	120
GGACAAAGTCG	TAGAAATGAC	TTTGGAGAAT	GGTCGTAAAGC	GCCAAAAAAA	TAGATTGGGT	180
AAGCTAATTG	AAGTTTATCC	ATCCCTATTT	ATTGTGGAGT	TTGGGGATGT	GGAAGGAGAT	240
AAACAAGTTA	ATGTTTACGT	TGAATCCTTT	ACTTACTCAG	ATATTCTTAC	AGAAAAGAAT	300
TTGATTCATT	ATCTTGACTA	A				321

(2) INFORMATION FOR SEQ ID NO:985:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

ACAAACAAAA	AAACTTCAGA	CACTATAAAC	CTTGCTGGTA	AGGGAAGGGC	TCTTTATACC	60
AGTATTTATT	TCTTATTAGA	AGAAACGAAT	CCTTCACATT	TTCACCGATT	GACAGCAGAT	120
GAAATCTGGT	ATTTTCATGC	AGGATCCCCA	CTTACTGTTC	ACATGATTAC	AGCAGATGGT	180
CACTACGAAG	CAGTCACTTT	AGGCCTGGAC	ATATCCAAAG	GGCAACAACT	TCACTACTGT	240
GTTCCTAAGG	GCACTATTTG	GGGATCAACA	GTTGATAAGG	ATTATGCTCT	GGTTTCTTGT	300
CTTGTTGCTC	CTGGTTTTGA	ATGTTGA				327

(2) INFORMATION FOR SEQ ID NO:986:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

ATTATAAAAA	AATTTGAATT	TGATATGATG	GAGAAAGTAG	CTTCTCTTGG	AGTTCCGATG	60
TGTAAACCAA	TTAGCATTGA	ACTCTGCGAT	GACGAAGTAC	ATTCTTTACA	CGAATGGATA	120
GACGGAAGAG	ATGCAATAGA	TAGCATTTTA	ACTTATTCAG	AAAACCAACA	ATACACATAT	180
GGTGTAGAAG	CAGGAAAGAT	ACTTAGAAAG	ATTCATACAA	TTCTTGCTAC	AGAAGTTTGT	240
GAAGATTGGG	AAATCTTTTT	TAATCTAAAA	ATTGATGATA	AAATCTCCAA	CGAAATGATA	300
TGGTAA						306

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

AATATAAAAA	ATTTGGAGCT	TTATCAAATC	TCAATGCTTG	TTTCAACTGT	TTTTCAAAAT	60
CCTAAGACAT	ATTTTTTTAA	TGTCAATACG	ACATTAGAAT	TATTATTTTA	TTTGGAAAAT	120
ATCGGTCTTG	CAAGAGAAGA	GATGGACAGG	CGTTTGAAGG	ATATACTTGA	GATATTCCCG	180
ATAAAAAATC	TTTTAAACAG	AAATATATTT	AATCTATCCG	GCGGTGAAAA	ACAAATTCTT	240
TGCATTGCAG	CTTCTTATAT	AGCAGGTACA	AAGATTATAG	TTATGGATGA	GCCTTCATCG	300
AATTTAGATA	TTAAAAGCAT	AAGTGTTTTG	GCAAAGATGC	TAAAGATATT	AAAAGAGAAA	360
GGCATAAGCA	TAATTGTTGC	AGAGCATAGA	ATTTATTATT	TGATGGACAT	AGTTGACCGT	420
GTATTTTTAA	TAGATAAAGG	AAAGCTTAAA	AAAACCTTATA	CTAGAAGTGA	ATTTTAAAG	480

CTAGATAAAA	ATGAATTAAA	TGCTTTAAGT	TTAAGAGATA	AAGAATTAAG	TAAATTAAAA	540
GTTCCCTATT	TAAAAGAAGG	TGGAGAGTAT	CAGATAAAAA	ATCTTAGCTA	CAAATTTACT	600
GATGATGAGT	GTTTAAGCTT	AAAAGATATT	TCATTCAAGC	TTGGGAAAAT	TTATGGCATA	660
ATAGGATCCA	ACGGACGAGG	AAAATCAACG	CTTTTAAGAT	GTTTAATAGG	TCTTGAGAAA	720
AAATCAAAAG	AAGAAATTTA	TTTTAAGGGA	GAGAAGCTAT	CTAAAAAAGA	AAGACTCAAA	780
AACTCTTCAC	TTGTTATGCA	AGATGTAAAT	CATCAATTAT	TCACAGATGA	AGTATTCAAC	840
GAGCTTAGAT	TAGGAGTAAA	GAATTTTGAT	GAAGAAAAGG	CGAAAATCAT	TTTAAAAGAT	900
TTATGCCTGG	ACGAATTTAT	TGAAAGGCAT	CCGATGAGTT	TATCAGGAGG	GCGAAAGCAA	960
AGGCTTGCAA	TAGCATCTGT	TATGTGCAAG	AATTCTCCAT	TTGTCTTTTT	TGACGAACCT	1020
TCAAGTGGTA	TGGATTATTC	CAATATGATA	AAAATATCTG	AACTGATTAA	TAAGTATAAA	1080
ACCATGGATA	AAATAATTTT	TATTGTTTCC	CATGATATAG	AATTTTTAAA	TGAAGTGGCA	1140
GATGAAATTT	TTGAATTGTA	A				1161

(2) INFORMATION FOR SEQ ID NO:988:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

AATTCAAAAA	ACGCATCATA	TCAGGTGTAC	ATGAACTACA	CCCCAAAAGT	TAGACAGAAA	60
AAATCTAACT	TTTGGGGTGT	TTTTATTATG	AAATTAAGTT	ATGATGATAA	AGTTCAGATC	120
TATGAACTTA	GAAAACAAGG	ATATAGCTTA	GAGAAGCTTT	CAAATAAATT	TGGGATAAAC	180
AATTCTAATA	TTAGGTACAT	GATTAAATTG	ATTGATCGTT	ACGGAATAGA	GTTTCGTCAA	240
AAAGGGAAAA	ATCGTTACTA	TTCTCCTGAT	TTAAAACAAG	AAATGATTAA	TAAAGTCTGA	300

(2) INFORMATION FOR SEQ ID NO:989:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

```
AAATCAAAAA AGGGGGAAGT TGTGTCATC CTAGGGGCAT CTGGTTGTGG GAAAAGTACC      60
CTCCTTCGTT GCCTCAACGG CTTAGAAAGT ATTCAAGGTG GAGATATTCT TCTGGATGGT      120
CAGTCTATCG TTGAAAATAA AAAAGATTTT CACCTAGTTC GCCAAAAGAT TGGCATGGTC      180
TTTCAAAGTT ATGAACTCTT TCCCCATCTG GATGTCTTAC AAAACCTCAT CCTAGGCCCT      240
ATCAAAGCTC AAGGAAGGGA CAAGAAAGAA GTAACGGAAG AAGCTTTGCA ATTACTAGAG      300
CGTGTGCGTT TGCTGGATAA ACAACATAGC TTTGCCCGTC AATTATCTGG TGGACAGAAG      360
CAACGTGTTG CAATTGTCCG TGCCCTCCTA ATGCATCCAG AAATCATCCT TTTTGACGAG      420
GTGACTGCTT CGCTGGATCC AGAAATGGTG CGTGAGGTGC TGGAACTTAT CAATGATTTG      480
ACCCAAGAAG GCCGTACCAT GATTTTAGTA ACCCACGAAA TGCAGTTTGC CCAAGCCATT      540
ACTGACCGGA TTATCTTCCT CGACCAAGGG AAAATCGCTG AAGAAGGAAC AGCTCAAGCC      600
TTCTTTACCA ATCCGCAAAC CAAACGAGCC CAGGAATTTT TAAACGTCTT TGACTTTAGC      660
CAATTCGGCT CATATCTATA A                                     681
```

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

```
AAAGCAAAAA ATAATCTACT GTGGCAGTAT GGTCTAGGGA TGACGATTTT GTTTGTGGTT      60
ATCAGTGCTT CCTTTCTGTA TATGGTTTCT CTTAGCATGA AACCTATCA AACAGCTAAA      120
AGTGAAGGAG AAAAATTAGC TCAGCAGTAT GCAGGATTAG AGCAGGCCGA TCAGGTTGAT      180
TTATACAATG GCTTGGAATC TTATTACAGC GTTCTTGCTC GTAATAAACA GCAAGAAGCA      240
CTTGCTGTTT TGATTGGAAG AGATGATCAT AAGATTACG TTTATCAGCT AAATCAGGGT      300
GTTTACAAG AAAAAGCAGA AACGGTTTCT AAGGAAAAGG GAGCTGGCGA AATTGACAAG      360
ATTATCTTTG GTCGTTATCA AGATAAGCCA ATCTGGGAAG TCAAGTCAGG ATCTGATTTT      420
TATCTAGTAG ATTTTGAAAC AGGAGCATTG GTCAACAAGG AGGGCCTATG A                                     471
```

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

ACAAGAAAAA AGGAGGAAAAG TTCAATGACA AATTTTGACA TTCTTGACAA TCAATTTTTA	60
TCCTTATCTG AAAATGAATT ATCAGATATT GATGGCGGTC TCGCTCCCTT GGTTATCTTT	120
GGAGTAGCAG TATCTTGGA GGCTATTGCA GGTGGAACAG CACTTATAGG TTCTGGTTTG	180
GCAGCTGGTT ATTTTTTAGG AGGAGATTAA	210

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

AGGAGAAAAA ACATGGCTCA ACAACGTCGT GGCGGATTCA AACGCCGTAA AAAAGTTGAT	60
TACATCGCAG CAAACAAAAT TGAATATGTT GATTACAAAG ATACTGAGCT TC'TTAGCCGT	120
TTCTGTTTTCAG AACGTGGGAA AATCCTTTCCT CGTCGTGTAA CAGGAACTTC AGCTAAAAAC	180
CAACGTAAAG TAACAACAGC TATCAAACGC GCTCGCGTAA TGGCTTTGAT GCCTTTCGTA	240
AACGAAGATT AA	252

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GATGGAAAAA	AGGAGATTAC	AGGAGACAAG	ATGAACTACT	TTAATGTTGG	GAAAATCGTT	60
AATACGCAGG	GATTACAGGG	TGAGATGCGA	GTCTTGTCTG	TGACGGATTT	TGCAGAAGAA	120
CGGTTTAAAA	AAGGAGCTGA	GCTGGCTTTG	TTTGATGAAA	AAGATCAGTT	TGTCCAAACA	180
GTGACCATCG	CTAGCCACCG	TAAACAGAAG	AACTTTGACA	TTATTAAATT	CAAAGATATG	240
TACCATATCA	ATACTATCGA	AAAGTACAAG	GGATACAGTC	TCAAGGTCGC	TGAGGAAGAT	300
TTGAATGACC	TAGACGATGG	TGAATTTTAC	TATCACGAGA	TTATCGGTTT	GGAAGTCTAT	360
GAGGGTGATA	GCTTG GTTGG	AACCATCAAG	GAAATCCTGC	AACCAGGTGC	TAATGATGTC	420
TGGGTGGTCA	AACGAAAAGG	CAAACGTGAT	TTGCTTTTAC	CTTATATCCC	ACCAGTGGTT	480
CTCAATGTTG	ATATTCCAAA	TAAACGGGTC	GATGTGGAAA	TCTTAGAAGG	GTTAGACGAT	540
GAAGATTGA						549

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1038 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

ATCATGAAAA	AATCAGATGT	TCTTGATTTA	ATAAAGTATC	ATTATGAGGG	CAGAGAGACA	60
GAATTTAGAA	ATCAATCCAT	AGCAATTGCT	CGGAAC TTCA	ATAAACATGG	TGATACACAA	120
ATAGCACAAT	ATATTATGGG	GTTAATGTCT	CAAAGTGATA	GATTCATGCC	ACAAATAGAA	180

AATCCTAGTG	AGTATTTGAC	TCCTGCTAAA	CTAGATATTG	GTCCTCTCCC	ATTGCCTCTT	240
TCAATTATGA	ATGATTTAAA	AGGAATAATA	AACGCTGTCA	ATCATCATAT	TGGAATAAAAT	300
AAATTTTTAT	TTGTGGGATC	TACAGGTACT	GGAAAACTG	AAAGTGTAAG	GCAGGTGGCT	360
AGACTTATTG	GCAAGGAATT	ACTTGTAGTA	GATTTTCAGT	ACTTAGTAGA	TAGTAAGCTA	420
GGGCAAACAG	TCAAAAACCT	AGCAACTCTT	TTTAATGAAA	TCAATAATCT	TCCTTTCAAG	480
CAAAATTATA	TCATCCTATT	TGATGAAATT	GATTCCATAG	TGTTGGATAG	GGTTAATCAG	540
AATGATTTAA	GAGAAATGGG	ACGAGTGACT	TCTGCCTTTT	TAAAGGAGTT	GGATAGGCTG	600
TCACCAGAAA	TTGTATTAAT	TGCAACAACA	AATCTTTTTG	AAAATCTTGA	TAAAGCAGTT	660
ACGAGAAGAT	TCGATGCCAT	AATTGACTTT	GACCGTTATA	CTGATGAAGA	TAAAGTAGAA	720
GTAGCTACTA	TTATTTTAAA	TGAGTTATTA	AAGCAATTTA	AGAATGTAGC	TAGAGATTTA	780
AAATTATTTA	AAAAAATTAT	CAATAGTGCC	AATGTAATAC	CGAATCCTGG	TGATTTGAGA	840
AACTCAATAA	GAACGTCATT	GGCATTTAGT	GATCCATCAG	ATCCGCATGA	TTACCAAAAA	900
CGCCTGCTAA	GAAGTTTGCA	TAATGGTAGA	AATTTATCTA	TTTCTAAATT	ATCGAAGCTA	960
GGTTTTACTG	TTAGAGAAAT	TGAGATTTTG	ACAGGTGTTT	CTAAGAGTAG	TGTATCACGA	1020
GAGTTAAGCG	AGGATTAA					1038

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

AAAATGAAAA	ATGAAATGTT	AGCTTTGATT	CTTGCTGGTG	GGCAAGGAAC	TCGTCTCGGT	60
AAACTCACTC	AAAGCATCGC	AAAACCAGCT	GTGCAATTTG	GGGGGCGCTA	CCGTATCATT	120
GACTTTGCCC	TATCAAACCTG	TGCCAACTCA	GGGATTTCATA	ATGTTGGGGT	CGTTACACAG	180
TATCAACCAC	TTGCTCTCAA	CAACCATATT	GGGAATGGTT	CAAGCTGGGG	ACTAGACGGT	240
ATTAATTCAG	GTGTCTCTAT	TCTTCAACCT	TATTCTGCAA	GTGAAGGAAA	TCGTTGGTTT	300
GAGGGGACTA	GTCACGCTAT	TTACCAAAAAT	ATCGACTATA	TCGACAGTGT	CAATCCTGAG	360
TATGTCTTGA	TTTTGTCTGG	GGACCACATC	TACAAAATGG	ACTATGATGA	TATGCTCCAG	420
TCTCATAAGG	ATAATAATGC	CAGCTTGACA	GTAGCAGTTT	TAGACGTCCC	TCTTAAAGAA	480
GCAAGCCGTT	TTGGTATCAT	GAACACAGAT	GCTAACAATC	GTATTGTTGA	ATTTGAAGAA	540
AAACCAGCTC	AACCTAAATC	TACAAAAGCT	TCTATGGGAA	TCTACATTTT	TGATTGGCAA	600
CGCCTTCGTA	ATATGTTAGT	CGCTGCTGAA	AAGAGCAAGG	TTGGCATGTC	AGACTTTGGT	660
AAAAATGTCA	TTCCAAATTA	CCTTGAGTCA	GGTGAAAGTG	TTTATGCCTA	CGAATTTAGT	720
GGTTATTGGA	AAGATGTTGG	TACTATTGAG	TCACTTTGGG	AAGCGAACAT	GGAGTATATT	780
TCTCCAGAAA	ATGCCTTGGA	TAGTCGTAAC	CGTCAATGGA	AGATTTACTC	AAGAACTTG	840
ATTTCAACCAC	CAAACCTCCT	CGGGGCAAAAT	GCTCATGTGG	AAGACTCATT	AGTTGTAGAC	900
GGATGTTTCG	TTGATGGAAC	TGTTAAACAT	TCTATCCTTT	CAACAGGCGC	GCAAGTTCGC	960
GAAGGAGCGG	AAGTCCTTGA	TTCAAGTTATC	ATGAGTGAG	CTATCATTGG	TCAAGGAGCT	1020
AAGATTAAAC	GTGCCATTAT	TGAGTGA				1047

(2) INFORMATION FOR SEQ ID NO:996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...720
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

AGAATGAAAA	AATATTTTAT	TGGCGGTTTG	GGAAGCAATG	CCTATCATAG	CAAGGATTTT	60
CTTCAAGAAC	TAGATTCGCA	GGTCTATTTT	CTAAATCCAT	ATGAAAAGCA	TCTTCGAGAT	120
GAAACAGAAT	TGAAATCATG	GTTTAAAAAT	GAGATTGTAG	AGGAAGAATT	TATCTGTCTG	180
ATAGGTCATT	CTCTGGAGG	AGATTTAGCT	CGTTATCTCG	CATCGGAATT	TGAAGAAGTA	240
AAGAACTGA	TTCTTTTGA	TGGTGGCTAT	CTAGATTTAG	ATAAGATTTT	ACCTTTGGAT	300
ACAGAGTTAG	AGGAACTAA	AAATTATATC	AAATCTCAAA	TTGTTTTGGA	CTTAGATGTT	360
CTTACTTCTA	AAGAAAAATC	TGAAGCAAAG	CATTGGTCAG	AAAATATGGA	GAAAGCTGTA	420
AGACAGTCCT	ATCACTGGAA	TGTTGAGTAT	AATAGATATG	AGTTGGCTAT	AAATTATGAA	480
AATATAGAAG	CGATACTCCG	CCTACGGAGA	AAAATACAAG	CTTTTAAGAG	AGAAGTGGGA	540
GATACCTTGT	TTATTAGTCC	TCGCTATCCT	AATGAAGCTA	CATGGAGAGA	GGAAGCCCTA	600
AAAGAATTGC	CAGACTATTT	TGATACTATT	TTTTTAGAAA	ACTTTGGCCA	TGAGCTTTAT	660
ACTCAAGCAC	CTAAAGAAAT	CGCTAGTCTA	ATGAATGAGT	GGCTCGCTTA	TTTTCTATGA	720

(2) INFORMATION FOR SEQ ID NO:997:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

AGGATGAAAA	AACAAGCCTA	TGTCATTATT	GCTCTCACCT	CCTTCCTATT	TGTCCTTTTTT	60
TTCTCCACA	GCTTGCTGGA	AATACTTGAT	TTTGACTGGT	CTATCTTTTTT	GCACGATGTC	120
GAAAAAACAG	AAAAATTTGT	CTTTTTTATTG	TTGGTTTTTCA	GCATGTCCAT	AACCTGTCTC	180
TTAGCCCTGT	TTTGCCGAGG	GATCGAAGAG	CTTTCTCTAA	GAAAAATGCA	GGCTAATCTC	240
AAGCGTTTAT	TGGCAGGGCA	AGAAGTGGTT	CAGGTTGCAG	ATCCAGATTT	GGATGCCAGT	300
TTCAAGTCCT	TATCAGGTAA	ACTTAACCTT	TTGACAGAAG	CTCTTCAAAA	AGCTGAAAAT	360
CATAGCCTTG	CTCAGGAAGA	GGAAATCATC	GAGAAAGAAC	GGAAGCGAAT	TGCTCGGGAT	420
TTGCACGATA	CAGTCAGTCA	GGAGTTGTTT	GCGGCCCA	TGATTTTATC	GGGTATCAGT	480
CAGCAGGCTT	TGAAATTGGA	TAGAGAAAAG	ATGCAGATCC	AGTTGCAGAG	TGTCACAGCT	540
ATTTTAGAAA	CTGCCAGAA	GGATTTGCGG	GTTTTGCTCT	TGCATTTGCG	ACCAGTTGAA	600
CTGGAGCAGA	AGAGCTTGAT	AGAAGGGATT	CAGATTCTCT	TAAAAGAGCT	TGAGGACAAG	660
AGTGATCTTA	GGGTTAGTCT	CAAGCAGAAT	ATGACGAAAT	TGCCTAAGAA	AATCGAGGAG	720
CATATCTTCC	GTATCCTGCA	AGAGTTGATT	AGCAATACGC	TCCGCCATGC	CCAGGCATCT	780
TGCCTAGATG	TCTACCTCTA	TCAGACAGAT	GTTGAATTGC	AACTGAAGGT	GGTGGACAAT	840
GGGATTGGTT	TCCGGTTAGG	GAGCTTAGAC	GACTTGAGTT	ATGGACTGCG	AAATATCAAG	900
GAGAGGGTTG	AAGATATGGC	TGGAACAGTT	CAACTCTTGA	CAGCTCCCAA	GCAAGGGCTG	960
GCAGTTGATA	TCCGTATTCC	CCTGTTAGAT	AAGGAATGA			999

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

AAACAGAAAA	AGGAGTGGGG	AGGCGATGTG	CTTCACTCAC	TCCTTTTTTCC	ATTTTGCTAC	60
TCTTCGAAAA	TCTCTTCAAA	CCACGTCAGC	GTCGCCTTGC	CGTATGTATG	GTTACTGACT	120
TCGTCACTTT	CATCTACAAC	CTCAAAACAG	TGTTTTGAGC	AACCTGCGGC	TAGTTTCCTA	180
GTTTTCTCTT	TGATTTTTAT	TGAGTATTAG				210

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...3363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

AGTGAGAAAA	AAATGGGAAA	TTTTAGCTTT	CTTTTAAAAA	ATGACGAATA	TGAATCTTTT	60
TCAAAACCTT	GCATTGAAGC	TGAGAATATG	ATTGCTACAT	CAACTGTGGC	TACTGCCTTT	120
ATGGCGCGTC	GTGCTTTAGA	GCAGGCTGTC	CATTGGATAT	ATAGTCACGA	TTCATATTTA	180
GAAGCTCCCT	ATCGTGCTAC	TCTATCTTCT	TTAGTATGGG	ATGATGATTT	TAGGGATATC	240
GTAGATTCTG	AACTCCACAA	GCAGATAGTT	CTGTTGATTC	GGTGGGGAAA	CCATGCTGCT	300
CATGGTGGTG	AAATTAAGGA	ACGAGAAGCG	ATTTTAGCTT	TGCATCATTT	GTATCAGTTT	360
GTTAATTTTA	TCGATTATTG	TTACAGCAAT	GAGTTTGTGG	AGCGTTATTT	TGATGAGAAG	420
TGCTTACCAC	TTTCAGCAAA	CATCAAATAC	CGAGAAACTC	CACAATCTAT	GATAAAGTTA	480
CAAGACAGTT	TACCAGAACT	GCCTGATTTT	CATGAACAGA	TGGCTGCTCA	GTCCGTAGAA	540
GTTCAAGAGA	CTTATACTGA	AAAACGTGAG	ACTGCAGCGC	AACGGCAAGA	TGTGCCTTTC	600
CATATTGATC	AATTATCTGA	GGCAGAGACA	AGAAAGCTCT	TTATTGATAT	CGATCTCCGT	660
TTAGCAGGAT	GGATATTTGA	AGAAAACGTG	CGTGTGAGA	TAGCCGTTGA	TGGTCTCAAG	720
CACGGTTCAG	GAATTGGTTA	CTGTGACTAT	GTACTTTATG	GTAAAAATGG	GAAAATTTTA	780
GCGATTGTAG	AGGCTAAAAA	AGCCTCTGTC	AATCCAGAAG	TAGGGGAAGT	ACAGGTCAAA	840
GAATATGCTG	AAGCTCTTGA	GAAACATATC	GGCTATCAGC	CAATTTGCTT	TATTACAAAT	900
GGCTTGAAGC	ACTATATACT	TGATGGTCCG	AACCGCCGCC	AGATTGCAGG	CTTTTACTCT	960
CAAGAAGAAAT	TGCAATTAGT	GATGGATAGA	CGTCATCTTC	AAAAACCAC	TGAGGATATT	1020
TCTAGTAAAA	TTAGGGACGA	TATTTCCGGG	CGTCACTACC	AAAAACACGC	CATTGCAAGC	1080
GTTTGTAAG	CTTCTCTAA	TCATCGTAGA	CAGGCACTTT	TGGTTATGGC	AACTGGGGCT	1140
GGGAAAACTC	GTACAGCAGT	TTCTCTAGTT	GATATCTTAT	CACGTCATAA	CTGGGTAAAA	1200
AACGTTCTCT	TCTTAGCCGA	TAGAACTTCC	TTGGTTAAGC	AAGCCTATGA	TTCGTTTAGA	1260
AAATTACTCC	CAGATCTTTC	CGTTTGTAAC	TTCTTAGAAG	ATAAAGAAGG	AGCTCAATCA	1320
AGTCGCATGG	TCTTTTCAAC	TTATCCGACC	ATGATTGGAG	CGATTAGTGG	TCAAGAAGAA	1380
GTAATCAAC	GCCCTTTCAC	TGTTGGGCAT	TTTGACCTTA	TCATAATTGA	CGAATCTCAC	1440
CGTTCTATTT	ATCAGAAATA	CAAGTCCATT	TTTGATTATT	TTGATGCAAG	AATTGTAGGC	1500
TTAACAGCTA	CTCCGCGTCA	AGATTTAGAT	AAAAACACCT	ATGGATTCTT	TAATTTGGAG	1560
AATGGGGTTC	CAACATATGC	ATATGATTTG	GAAGAGGCTG	TTAAAGACGG	ATATTTAGTA	1620
GCCTATCAT	CTATCGAAAC	CAAACTGAAA	CTACCTACGG	ATGGTCTACA	TTATGATGAT	1680
TTGTCCGAAG	AAGAAAAGGA	ACATTTTGAT	AGCAAATTTG	AAGACGATAG	CTGTGAAAAA	1740
GATATTGATG	GGAGTGTATT	TAATTCCTTT	GTTTTCAATA	AAAGTACAGT	AGAAATTGTT	1800
TTAAATGAAC	TCATGACAAG	AGGAATTCAG	ACAGCCTCGG	GTGATGAAAT	TGGTAAAACT	1860
ATTATTTTGT	CTAAAAATCA	TGATCATGCG	GAATATATCA	GAGGTATTTT	TAACAACCGC	1920
TATCTGAAA	AAGGGAGCGA	CTATGCTCAG	GTGATTGATT	ATAGTATTAA	GCATTATCAG	1980
ACCTTGATTG	ATGATTTTAA	AATTAAGGAG	AAGTATCCTC	AAATTGCGAT	TTCTGTGCGAT	2040
ATGTTAGATA	CAGGTATTGA	TGTACCAGAG	GTTGTTAATT	TAGTCTTCTT	CAAGAAAGTA	2100
CGCTCTAAAA	CTAAGTTTTG	GCAGATGATT	GGTCGAGGAA	CCCGTCTATG	TAAAGATTTA	2160
TTTGACCTG	AGCAGGATAA	GGAAAACCTC	TTGGTATTTG	ATTATGGGGA	TAATTTTGAT	2220
TATTTTCGTG	CAGATCCAAG	AGATGGAGAG	GGTCGTCACA	TTGTTTCGTT	GACTCAGCGT	2280
TTATTTAATA	TCAAAGTGGA	CTTGATTCTGA	GAACCTCAGG	GACTCCAATA	CCAAGAAGAT	2340
CAGTTTGCGA	GAGCATACCG	TCAGCAGCTT	GTCTCGGAAC	TTCAAGGTCG	TATAGAGAGC	2400
TTAAATGAGT	TGGACTTCAG	GGTTCGTATG	GTTTLAGATA	CAGTTTATAG	CTATAGGAAA	2460

TTGGAAAGTT	GGCAGAATCT	AACTGCTGTT	ACAAGTGAAA	CCATTCAAAA	AAATCTCTCT	2520
CCGCTTTTAT	TTGATGAAGA	TAAAGAAGAT	GAGATGGCGA	GGAGATTGGA	TTTGTGGTTG	2580
CTTCATATTC	AGTTGGGGCA	ACTGACAGCT	AAATCTTCCA	CTGTTTCATAT	TTCCCAAGTG	2640
ATGAAGACGG	CTAGAGCTCT	TTCTGCTATT	GGCAATATCC	CGCAGGTTTT	TGAGCAGGCT	2700
GAAATTATCA	GGAAAGTACA	GGAGCCTGAA	TTTTGGAAAG	AAGTTAACTT	GTCTGATTTG	2760
GAAAAAATTC	GTCTTGCTAT	TCGAGATTTA	TTACAGTTTT	TGGATAAAAC	AGACCGTAAA	2820
CCCTACTATG	TTAACTTTGA	AGATCGTATA	CTCTCCACTG	TTCACGAGAC	CACAGCATT	2880
TTGCAGGTCA	ACGATCTTCG	GTCTTACAAT	GAAAAAGTTG	AGCATTATTT	GAAAACTCAT	2940
CTGGATGAGG	AGTCCATTTT	TAAGCTATAC	CATAATAAAA	AGTTGACATC	TGATGATATG	3000
CTTGCACTTG	AAAAATTGCT	CTGGGAAAAA	TTAGGTAGTA	AAGCAGACTA	CCAAAGTCAT	3060
TATGAAAATA	AGGCAATTCC	GAGATTGGTT	CGTGAGATTA	TTGGCTTAGA	TAGAGAGTCT	3120
GCCAATCGTA	TTTTTTCTAA	ATTTTTGTCT	GATGAGAATC	TTAATGCCAG	GCAGATTTCA	3180
TTTGTAATA	TGATTGTAGA	CTACATTGTA	GAAAATGGTT	TTTTAGAGAC	GAAAGTGTTA	3240
ACGCAAGAGC	CGTTTAAATC	TTATGGTTCT	GTTCAACTAC	TCTTCCAACA	CCAACTACCA	3300
GTACTTCGTA	ATATTGTTCA	AATCATTGAA	CTTATCAATA	ATCGAGCTGG	AGAAGCGGCT	3360
TAA						3363

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GGAGAGAAAA	AGATGAAGAA	AAAATTTGCC	CTATCGTTTG	TGGCGCTTGC	AAGTGTAGCA	60
CTTCTTGAG	CCTGTGGAGA	AGTGAAGTCT	GGAGCAGTCA	ACACTGCTGG	TAAGTCAGTA	120
GAGGAAAAGA	CAATTAAAA	CGGGTTTAAC	TTTGAAGAGA	CAGGTTCTTT	ANCTGCATAC	180
GGAACAGCTG	AACAAAAAGG	TGCCCAATTG	GCTGTTGATG	AAATCAATGC	CGCAGGTGGT	240
ATCGATGGAA	AACAAATCGA	AGTANTCGAT	AAAGATAATA	AGTCTGAAAC	AGCTGAGGCT	300
GCTTCAGTTA	CAACTAACCT	TGTAACCCAA	TCTAAAGTAT	CAGCAGTCGT	AGGACCTGCG	360
ACATCTGGTG	CGACTGCAGC	TGCGGTAGCG	AACGCTACAA	AAGCAGGTGT	TCCATTGATC	420
TCACCAAGTG	CGACTCAAGA	TGGATTGACT	AAAGGTCAAG	ATTACCTCTT	TATTGGAAGT	480
TTCCAAGATA	GCTTCCAAGG	AAAAATTATC	TCAAACATATG	TTTCTGAAAA	ATTAAATGCT	540
AAGAAAGTTG	TTCTTTACAC	TGACAATGCC	AGTGACTATG	CTAAAGGGAT	TGCCAAATCT	600
TTCCGCGAGT	CATACAAGGG	TGAAATCGTT	GCAGATGAAA	CTTTCGTAGC	AGGTGACACA	660
GACTTCCAAG	CAGCCCTTAC	AAAAATGAAA	GGGAAAGACT	TTGATGCTAT	CGTTGTTCTT	720
GGTTACTATA	ATGAGGCTGG	TAAGATTGTA	AACCAAGCGC	GTGGTATGGG	AATTGACAAA	780
CCAATCGTTG	GTGGTGATGG	ATTCAACGGT	GAGGAGTTTG	TACAACAAGC	AACTGCTGAA	840
AAAGCATCAA	ACATCTACTT	TATCTCAGGC	TTCTCAACTA	CTGTAGAAGT	TTTCACTAAA	900
GCTAAAGCCT	TCCTTGACGC	TTACCGTGCT	AAGTACAATG	AAGAGCCTTC	AACATTTGCA	960

GCCTTGGCTT ATGATTTCAGT TCACCTTGTA GCAAACGCAG CAAAAGGTGC TAAAAATTCA	1020
GGTGAAATCA AGAATAACCT TGCTAAAACA AAAGATTTTG AAGGTGTAAC TGGTCAAACA	1080
AGCTTCGATG CAGACCACAA CACAGTCAAA ACTGCTTACA TGATGACCAT GAACAATGGT	1140
AAAGTTGAAG CAGCAGAAAGT TGTAAACCA TAA	1173

(2) INFORMATION FOR SEQ ID NO:1001:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

GAGGAGAAAA ACAAAATGGT TATGACTGAC CCAATCGCAG ACTTCCTAAC TCGTATTCGT	60
AATGCTAACC AAGCTAAACA CGAAGTACTT GAAGTACCTG CATCAAACAT CAAAAAAGGG	120
ATTGCTGAAA TCCTTAAACG CGAAGGTTTT GTAAAAACG TTGAAATCAT CGAAGATGAC	180
AAACAAGGCG TCATCCGTGT ATTTCTTAAA TACGGACCAA ATGGTGAAAA AGTTATCACT	240
AACTTGAAAC GTGTTTCTAA ACCAGGACTT CGTGTCTACA AAAAACGTGA AGACCTTCCA	300
AAAGTTCTTA ACGGACTTGG AATTGCCATC CTTTCAACTT CTGAAGGTTT GCTTACTGAT	360
AAAGAAGCAC GCCAAAAGAA TGTGTTGGT GAGGTTATCG CTTACGTTTG GTAA	414

(2) INFORMATION FOR SEQ ID NO:1002:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 894 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GAAAGGAAAA	AGATGAGCAA	CATTTCAACT	GATTTGCAAG	ATGTAGAAAA	AATCATCGTA	60
TTGGACTATG	GTAGCCAGTA	CAACCAGCTG	ATTTACAGCC	GTATCCGTGA	GATTGGTGTT	120
TTTTCAGAAC	TAAAAAGCCA	TAAAAATTCA	GCTGCTGAAG	TTCGTGAAGT	CAATCCTGTA	180
GGAATTATTC	TATCAGGTGG	TCCAAATTCT	GTATATGAAG	ATGGTTCATT	TGATATTGAC	240
CCAGAAATCT	TCGAACTCGG	AATTCCAATT	TTGGGAATCT	GTTATGGTAT	GCAGTTATTG	300
ACCCATAAAC	TTGGAGGAAA	AGTTGTTCCT	GCAGGTGATG	CTGGAAATCG	TGAATACGGT	360
CAATCAACCC	TAACTCACAC	ACCATCAGCG	CTTTTTGAAT	CAACACCTGA	TGAACAGACT	420
GTTTTGATGA	GCCATGGTGA	TGCGGTACT	GAGATTCCTG	CTGACTTTGT	TCGTACAGGT	480
ACATCAGCTG	ACTGCCATA	CGCAGCCATC	GAAAACCCAG	ATAAACACAT	TTACGGTATC	540
CAATTCCACC	CAGAAGTTCG	TCATTCTGTA	TACGGAAATG	ATATCCTTCG	TAACTTTGCC	600
CTTAACATTT	GTAAGGCTAA	AGGTGACTGG	TCAATGGATA	ATTTCATTTGA	CATGCAGATC	660
AAAAAAATTC	GTGAAACCGT	CGGTGATAAA	CGTGTCCCTC	TTGGTCTATC	AGGTGGTGTT	720
GACTCATCTG	TCGTGGGGT	TCTTCTCCAA	AAAGCGATTG	GCGATCAATT	GATCTGTATC	780
TTCGTAAACC	ACGGTCTTCT	TCGTAAAGGC	GAAGCTGATC	AAGTTATGGA	CATGCTCGGT	840
GGTAATTTGG	GTTTGAATAT	CGTCAAAGCA	GACGCTGCTA	AACGTTTTTC	TTGA	894

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GAATTTGAAA	AGATGATTGA	CCAACTATCT	AAGTATTACA	GTTGTAGGAT	ACTAACTGAA	60
AAGGATATTC	CAAGTATTTT	ATCTTTATAT	GAAAGTAATC	CTCTGTATTT	TCAGCATTGT	120
CCACCAGAGC	CAAAATTTTG	AACTGTAAAA	GAGGACATGC	TTTGTCTACC	TGAAGGTAAA	180
GCTAAGGCTG	ATAAGTTTTT	TGTTGGATTT	TGGAATGGCT	CTGACCTTGT	GGCTGTTATG	240
GATTTTGTCT	ATGCATATCC	TGATGAGGAG	ACTGTTTTTA	TTGGTTTGTT	TATGGTTGAT	300
CAAGCCTATC	AGAGGAAAGG	GATTGGTAGT	CATATTGTGA	CAGAAGCACT	AGCTTATTTT	360
GCTAAGAACT	TTCGAAAGGC	ACGTTTGGCT	TATGTTAAGG	GAAATCCGCA	ATCTCAGCAT	420
TTTTGGGAAA	AGCAGGGCTT	TAAATCAATT	GGATGCGAGG	TTAAGCAAGA	ACTCTATACG	480
GTTGTTATCG	TTGAACAGAG	CCTAGATGAT	TAG			513

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

AAGCTTGAAA	ATTTCTATAA	AAATCGGTAT	TATATTTTCG	AAAGAAATAA	AAATATTTTC	60
GAAAGAAAGG	TGCTTACGAT	GGTAAATACA	GAAGTAGCAA	GAACAACAAT	CAAGACAGAA	120
TATTTTGGCA	GCCTTACTGA	AAGGATGAAC	AAATATCGAG	AAGATGTTTT	AAATAAAAAA	180
CCTTATATTG	ATGCTGAGAG	AGCAGTTCTA	GCAACACGCG	CCTATGAACG	ATACAAGGAA	240
CAACCTAATG	TCCTAAAACG	TGCATATATG	CTGAAAGAAA	TTTGTGAAAA	TATGACTATC	300
TATATTGAAG	AAGAATCTAT	GATTGCGGGA	AATCAAGCTT	CTTCCAATAA	AGATGCTCCT	360
ATTTTTCGGG	AATATACGCT	AGAATTTGTT	CTCAATGAGT	TGGATCTTTT	TGAAAAGCGT	420
GATGGAGATG	TTTTCTATAT	TACAGAAGAA	ACAAAAAGAAC	AACTTAGAAG	TATTGCTCCG	480
TTTTGGGAAA	ATAATAATTT	ACGTGCTAGA	GCTGGTGCCT	TATTACCTGA	AGAAGTGTCT	540
GTTTATATGG	AAACAGGATT	CTTCGGTATG	GAAGGTAAGA	TGAATTCTGG	AGATGCTCAC	600
TTAGCAGTTA	ACTATCAGAA	ACTTTTGCAA	TTTGGTTTAA	GAGGTTTTGA	AGAGCGGGCT	660
CGTAAAGCGA	AAGTAGCTCT	AGATTTAACA	GATCCAGCAA	GTATTGATAA	ATATCATTTT	720
TACGACTCTA	TATTTATTGT	AATCGATGCT	ATTAAAGTAT	ATGCAAAGCG	CTTTGTTGCT	780
CTTGCTAAAA	GTTTAGCCGA	AAATGCAAAT	CCTAAACGTA	AGAAAGAATT	ACTTGAGATT	840
GCAGATATTT	GCTCTAGAGT	CCCATATGAA	CCGGCAACTA	CTTTTGCAGA	AGCTATTCAA	900
TCAGTTTGGT	TTATTCAATG	TATTTTACAA	ATTGAATCTA	ATGGCCACTC	TCTTTCATAT	960
GGCCGTTTTG	ATCAATATAT	GTATCCATAT	ATGAAGGCTG	ATTTAGAAAAG	TGGTAAAGAA	1020
ACAGAAGATA	GCATTGTTGA	ACGTCTGACA	AATCTTTGGA	TTAAGACAAT	TACAATCAAT	1080
AAGGTTTCGA	GTCAATCACA	TACATTTTCT	TCAGCAGGAA	GTCTCTCTATA	TCAAAATGTT	1140
ACAATTGGTG	GACAGACTCG	AGATAAGAAAG	GATGCTGTTA	ACCCATTATC	TTATTTGGTA	1200
TTAAAATCAG	TTGCACAAAC	CCATCTACCG	CAACCTAATC	TAAGTGTACG	TTACCATGCA	1260
GGTTTAGATG	CTCGTTTCAT	GAATGAGTGT	ATTGAAGTGA	TGAAACTTGG	TTTTGGTATG	1320
CCTGCATTTA	ATAATGATGA	GATTATTATT	CCTTCTTTTA	TTGCAAAAGG	AGTATTGGAA	1380
GATGATGCTT	ATGATTACAG	TGCCATTGGA	TGTGTTGAAA	CGGCAGTTCC	AGGGAAATGG	1440
GGCTATCGTT	GCACAGGTAT	GAGTTATATG	AACTTCCCTA	AGGTTCCTACT	TATCACGATG	1500
AATGATGGAA	TTGATCCGGC	TTCGGGTAAA	CGGTTTGCAC	CAAGCTTTGG	TCATTTTAAG	1560
GATATGAAGA	ACTTTTCTGA	ATTAGAAAAT	GCTTGGGATA	AAACACTAAG	ATATTTGACA	1620
CGAATGAGTG	TTATTGTTGA	AAATTCTATT	GATTTATCAT	TGGAACGAGA	AGTTCCTGAT	1680
ATTCTATGTT	CAGCATTGAC	TGATGATTGT	ATTGGTCGTG	GAAAAACACCT	TAAAGAAGGT	1740
GGAGCAGTAT	ATGATTATAT	ATCAGGATTG	CAAGTTGGAA	TTGCAAATTT	GTCCGATTCA	1800
TTAGCTGCAA	TTAAAAAATT	GGTGTTTGAG	GAAGAACGTA	TAAGCCCAAG	TCAGCTTTGG	1860
CATGCACTGG	AAACAGATTA	TGCCGGAGAA	GAAGGTAAGG	TCATTCAAGA	AATGTTGATT	1920
CATGATGCAC	CTAAGTATGG	TAATGATGAT	GATTATGCTG	ACAAATTGGT	TACTGCTGCT	1980
TATGACATTT	ATGTTGATGA	AATTGCTAAA	TATCCTAATA	CACGTTATGG	AAGAGGGCCT	2040
ATTGGAGGAA	TTCGTTATTC	AGGAACATCT	TCTATATCAG	CCAACGTAGG	GCAGGGACGT	2100
GGAACATTAG	CAACTCCAGA	TGGACGCAAC	GCGGGTACAC	CGTTAGCAGA	GGGTTGTTCA	2160
CCATCACATA	ATATGGATCA	ACACGGCCCC	ACATCTGTTT	TAAAACTGT	TTCAAAATTA	2220
CCAACAGATG	AAATCGTAGG	TGGGGTTCTC	TTAAATCAGA	AAGTAAATCC	TCAAACGTTA	2280
GCCAAAGAAG	AAGATAAATT	AAAACTAATT	GCTTTGTTAC	GAACATTCTT	TAATCGTTTA	2340
CATGGGTACC	ATATTCAATA	CAATGTTGTT	TCCAGAGAGA	CGCTGATTGA	CGCTCAGAAA	2400

CATCCTGAAA AACACAGAGA CTTAATTGTT CGTGTTCAG GATACTCTGC ATTCTTCAAT	2460
GTTCTTTCTA AGGCAACCCA AGATGACATT ATAGGACGTA CTGAGCATAC TTTGTAA	2517

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

TTTCCTGAAA AAGAAGGCAG CAGAATAGAG GGCTTGTATA TGAAATCGGA ATTACGCAAG	60
CAAGTCTTGC ATGAAATGAA GGCTTTATCT CAAGAACAAA AACAGGCTAT AGACCAAGCT	120
TTAACCGAGC GAATTTTACA ACACCCCTTT TATCAAGAAG CCAAGGTCAT CGCAACCTAC	180
CTCTCTTTTT CTCATGAGTT TCAAACGCGG GAACTGATTG AGCAGGCGCT GAAGGACGGC	240
AAGAAGGTTT TAATACCCAA AACTTATCCC AAGGGGCGCA TGGACTTTGT AGTCTATGAT	300
CCGCAGCAGT TGGTAAAAAC TGCCTTTGCC TTACTGGAGC CACAGGGAGA TTTGGAAGTG	360
GTGGATGTAT CTCAGATTGA TTTGATTTCAT GTTCCTGGCC TGGCTTTTAC GACGGATGGA	420
TATCGGATTG GATATGGTGG AGGTTATTAT GACCGCTATC TGGAACATTT TTCTGGTCAT	480
ACTTTGAGTA CGGTTTCATCC TTGTCAAAT CAGGACTTTA TACCTGAAAA CCATGATATT	540
CCTGTTTCAGG AGGTATTAAT TGATGAAGGA AATCTTTGA	579

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

CAATATGAAA	ACTGTTGTTT	TCTTGTATAT	CCTATGATAG	GGACTTTCGC	CGCTGCTCTT	60
GTAGCTGTAC	TAGCAAGTTT	CATCGTCCCT	ATTGAAATTA	CCCTAAATAG	TGCCAATACT	120
GAAATTGCAC	CACCAGATGG	GATTGGGCAG	GTCCTCAGCA	ACCTCTTGCT	CAAACGGTTT	180
GACAGCCCAG	TCAACGCCCT	GCTTACTGCT	AACTATATTG	GAATCTTATC	TTGGGCAGTC	240
ATTTTGTATA	TCGCTATGAG	AGAAGCCAGG	AAAAATAGTA	AAGAATTGGC	TAAAAACTAT	300
CGCTGA						306

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

AAAAATGAAA	AGATTGGACC	GTTTGGTGCA	GTCTTTTCT	CTTCCCGAAA	TGCCTGTGAA	60
ATATGGTATA	ATAGAAGAAT	GGCAAACAAG	AATACAAGTA	CAACAAGACG	GAGACCGTCT	120
AAAGCAGAAC	TGGAAAGAAA	AGAAGCGATT	CAACGAATGT	TGATTTTCGTT	AGGAATTGCG	180
ATTTTATTGA	TTTTTCGCAGC	CTTCAAATTA	GGGGCTGCAG	GTATAACCCCT	TTATAAATTTA	240
ATTCGCTTGC	TAGTGGGTAG	CCTAGCTTAT	CTGGCGATAT	TCGGCCTATT	AATCTATCTC	300
TTCTTTTCA	AGTGGATACG	AAAACAGGAA	GGACTCTTAT	CTGGCTTTT	CACCATATTT	360
GCTGGCTTAC	TCTTGATTTT	TGAGGCCTAC	TTGGTTTGGA	AATATGGTTT	GGACAAGTCC	420
GTTCTAAAAG	GGACCATGGC	TCAGGTTGTG	ACAGATCTGA	CTGGTTTTTCG	AACGACTAGC	480
TTTGCTGGAG	GGGGCTTGAT	CGGGGTCGCT	CTTTATATTC	CAACAGCCTT	TCTCTTTTCA	540
AATATCGGAA	CTTACTTTAT	TGGTTCTATC	TTGATTTTAG	TGGGTTCTCT	CCTAGTCAGC	600
CCTTGGTCTG	TTTACGATAT	TGCTGAATTT	TTCAGTAGAG	GCTTTGCCAA	ATGGTGGGAA	660
GGGCACGAGC	GTGAAAAAGA	GGAACGCTTT	GTCAACAAG	AAGAAAAAGC	TCGCCAAAAG	720
GCTGAGAAAG	AGGCTAGATT	AGAACAAGAA	GAGACTGAAA	AAGCCTTACT	CGATTTGCCT	780
CCTGCTGATA	TGGAAACGGG	TGAAATTCTG	ACAGAGGAAG	CTGTTCAAAA	TCTTCCACCT	840
ATTCCAGAAG	AAAAGTGGGT	GGAACCAGAA	ATCATCCTGC	CTCAAGCTGA	ACTTAAATTC	900
CCTGAACAGG	AAGATGACTC	AGATGACCAA	GATGTTCAAG	TCGATTTTTC	AGCCAAAGAA	960
GCCCTTGAAT	ACAAACTTCC	AAGCTTACAA	CTCTTTCAC	CAGATAAACC	AAAAGATCAG	1020
TCTAAAGAGA	AGAAAATTGT	CAGAGAAAAT	ATCAAAATCT	TAGAAGCAAC	CTTTGCTAGC	1080
TTTGGTATTA	AGGTAACAGT	TGAACGGGCC	GAAATTGGGC	CATCAGTGAC	CAAGTATGAA	1140
GTCAAGCCGG	CTGTTGGTGT	AAGGGTCAAC	CGCATTTCCA	ATCTATCAGA	TGACCTCGCT	1200
CTAGCCTTGG	CTGCCAAAGA	TGTCCGGATT	GAAGCACCAA	TCCCTGGGAA	ATCCCTAATC	1260
GGAATTGAAG	TGCCCAACTC	CGATATTGCA	ACTGTATCTT	TCCGAGAACT	ATGGGAACAA	1320
TCGCAAACGA	AAGCAGAAAA	TTTCTTGGA	ATTCTTTTAG	GGAAGGCTGT	TAATGGAACC	1380
GCAAGAGCTT	TTGACCTTTC	TAAAATGCC	CACTTGCTAG	TTGCAGGTC	AACGGGTTC	1440

GGGAAGTCAG	TAGCAGTTAA	CGGCATTATT	GCTAGCATTC	TCATGAAGGC	GAGACCAGAT	1500
CAAGTTAAAT	TTATGATGGT	CGATCCCAAG	ATGGTTGAGT	TATCTGTTTA	CAATGATATT	1560
CCCCACCTCT	TGATTCCAGT	CGTGACCAAT	CCACGCAAAG	CCAGCAAGGC	TCTGCAAAAG	1620
GTTGTGGATG	AAATGGAAAA	CCGTTATGAA	CTCTTTGCCA	AGGTGGGAGT	TCGGAAATATT	1680
GCAGGTTTTA	ATGCCAAGGT	AGAAGAGTTC	AATTCCCAGT	CTGAGTACAA	GCAAAATTCCG	1740
CTACCAATTC	TTGTCTGTAT	TGTGGATGAG	TTGGCTGACC	TCATGATGGT	GGCCAGCAAG	1800
GAAGTGGAAG	ATGCTATCAT	CCGTCTTGGG	CAGAAGGCGC	GTGCTGCAGG	TATCCACATG	1860
ATTCTTGCAA	CTCAGCGTCC	ATCTGTTGAT	GTCATCTCTG	GTTTGATTAA	GGCCAATGTT	1920
CCATCTCGTG	TAGCATTTGC	GGTTTCATCA	GGAACAGACT	CCCGTACGAT	TTTGGATGAA	1980
AATGGAGCAG	AAAAACTTCT	TGGTCGAGGA	GACATGCTCT	TTAAACCGAT	TAATGAAAAT	2040
CATCCAGTTC	GTCTCCAAGG	CTCCTTTATC	TCCGATGACG	ATGTTGAGCG	CATTGTGAAC	2100
TTCATCAAGA	CTCAGGCAGA	TGCAGACTAC	GATGAGAGTT	TTGATCCAGG	TGAGGTTTCT	2160
GAAAATGAAG	GAGAAATTTT	GGATGGAGAT	GCTGGTGGTG	ATCCGCTTTT	TGAAGAAGCT	2220
AAGTCTTTGG	TTATCGAAAT	ACAGAAAGCA	GTTGGAATCC	ATGATTTCAGC	GTCGTTTGTC	2280
AGTTGGATTT	AA					2292

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

ACTAGTGAAG	ATCAAGCTTT	GATTGGTTGG	AAAAGTATGG	AATCAATTTT	TGTAAACTT	60
GCCCAGTATC	CGTCTATAGA	AACGGAGCGT	TTATTGCTTA	GACCTGTAAC	TTTGGATGAT	120
GCGGAAGCAA	TGTTTGACTA	TGCCTCGGAC	AAGGGTAATA	CACGTTACAC	TTTTCCAACC	180
AATCAAAGTT	TGGAAGAAAC	CAAGAATAAC	ATTGCTCAGT	TCTATTTGGC	TAATCCCTTG	240
GGACGTTGGG	GAATAGAACT	AAAAAGCAAT	GGTCAGTTTA	TTGGAACCAT	TGACTTGCAC	300
AAGATTGATT	CTGTTCTTAA	GAAGGCAGCT	ATTGGCTACA	TTATCAATAA	AAAGTATTGG	360
AATCAAGGAT	TAACGACAGA	AGCCAATCGT	GCTGTGATTG	AGCTAGCTTT	TGAGAAGATA	420
GGGATGAATA	AGTTGACTGC	CCTTCACGAT	AAGGACAATC	CTGCGTCAGG	AAAGGTCATG	480
GAGAAATCAG	GCATGCGTTT	TTCCCATGCA	GAACCATATG	CTTGTATGGA	CCAGCATGAA	540
AAAGGCCGAA	TCGTGACAAG	AGTTCATTAT	GTCTTGACCA	AGGAAGACTA	TTTTGCAAAAT	600
AAATAA						606

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

ATGAACGAAA	AAGAATTACT	AGAACTAGTC	GTGAAAGCGG	CTGATGAGAA	ACGTGCGGAG	60
GATATCCTCG	CACTTGATGT	ACAAGATTTG	ACTAGTGTGA	CGGACTACTT	TGTCATCACT	120
AGCTCAATGA	ATAGCCGTCA	GTTGGACGCT	ATCGCAGCTA	ATATCCGTGA	AAAAGTAGCT	180
CAAGCAGGCT	TTAAAGGTAG	CCATGTCGAA	GGCGATGCAG	CTGGAGGCTG	GGTCTTACTG	240
GACCTCGGTG	CTGTTGTCGT	GCATATCTTT	TCAGAAGAAA	TGCGTGCCCA	TTATAATCTA	300
GAGAAGCTAT	GGCATGAGGC	GAATTCAGTA	GATATTTTCT	AAGCTCTTGC	TTAG	354

(2) INFORMATION FOR SEQ ID NO:1010:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 792 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...792
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

ATGGACGAAA	AAAAACGAAT	GCAAATTATT	GCTGAAAATA	TTACACACTT	TAGAAAGCAA	60
CGTGGCATCA	CCCAAAAAGA	TTTGGCTAAA	GAAGTTGGAA	TTACAGCAAG	TACTATGACA	120
GACTATATGA	AGTTAAGAAG	CGCTCCTTCT	TTTGGTGTTA	TCCAAAAACT	GGCTGATTAT	180
TTTCGTGTTA	AAAAATCAGA	TATAGATACT	ACTTTTAAAG	AAGAAATCCAC	CAACTCACTG	240
CCAGACGCTC	CAGATTCGCT	CACACAGCAG	ATAATGGATA	AGGTAGTGCA	ATTAACCCCA	300
CCCAATCAAA	AAATCGTGCT	ACGGACCTCT	GAAGAGCTTC	TGGAGAGCCA	AAACGAAGAA	360
GAAACGAAGA	TAAACGAAGT	ATCGGAAGTT	ATCAGCTTGT	ACCAAGTTGA	GGTTGTATCT	420
GAGACGGCAG	CAGCTTCTGG	ATTTAACAT	GGATTTGGGT	ACGACGATAC	AGACAGAGAG	480
ACTATAGAGG	TTGACGAGCG	ACCACCACGC	CACGATATTG	CGACCAAGGT	CAGTGGAGAC	540
TCCATGCAAC	CCGACTACCA	AGACGGAGAC	ATTCTCTATT	TAGTAGACAA	AGGACTGACT	600

ACCTACAACG GAGATTTAGC AATTATCGCA TATGGAGACC GTTCTTACTT CAAGAAGATA	660
TATACCGAAA ACGGACGCTT ACGCCTAGTG TCACTCAATG ACAAGTACGA AGACATCATC	720
CTAGACTTCC CACCAGCCGA AGACACACAC ATCAAGATTT ATGCAGTAGT CGGGGTGTAT	780
AGAGGGGAAT AA	792

(2) INFORMATION FOR SEQ ID NO:1011:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

AATTTAGAAA ATAGGTACAA GCAAATGATG TTAAAACCCT CTATTGATAC CTTGCTCGAC	60
AAGGTTCCCTT CAAAATATTC ACTCGTAATC TTGGAAGCAA AACGTGCCCA CGAATTGGAA	120
GCAGGTGCCC CAGCAACTCA AGGTTTCAAG TCTGAAAAAT CAACTCTTCG CGCTTTAGAA	180
GAAATCGAAT CAGGAAACGT TACAATTAC CCAGATCCAG AAGGAAAACG TGAAGCAGTG	240
CGTCGCCGTA TCGAAGAAGA AAAACGCCGC AAAGAAGAAG AAGAAAAGAA AATCAAAGAG	300
CAAATTGCTA AAGAAAAAGA AGATGGTGAA AAAATTAA	339

(2) INFORMATION FOR SEQ ID NO:1012:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

AGCTTAGAAA	AGGGGAATAA	TATGATATTT	AAGGCATTCA	AGACAAAAAA	GCAGAGAAAA	60
AGACAAGTTG	AACTACTTTT	GACAGTTTTT	TTCGACAGTT	TTCTGATTGA	TTTATTTCTT	120
CACTTATTTG	GGATTGTCCC	CTTTAAGCTG	GATAAGATTC	TGATTGTGAG	CTTGATTATA	180
TTTCCCATTA	TTTCTACAAG	TATTTATGCT	TATGAAAAGC	TATTTGAAAA	AGTGTTTCGAT	240
AAGGATTGA						249

(2) INFORMATION FOR SEQ ID NO:1013:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1413
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

AAAGAAGAAA	AAATGACAGC	AATTGATTTT	ACAGCAGAAG	TAGAAAAACG	CAAAGAAGAC	60
CTCTTGGCTG	ACTTGTTTAG	CCTTTTGGAA	ATCAATTCAG	AACGTGATGA	CAGCAAGGCT	120
GATGCCCAGC	ATCCATTTGG	GCCTGGTCCA	GTAAAAGCCT	TGGAGAAATT	CCTTGAAATC	180
GCAGACCCGC	ATGGCTACCC	AACTAAGAAAT	GTTGATAACT	ATGCAGGACA	TTTTGAGTTT	240
GGTGATGGAG	AAGAAGTTCT	CGGAATCTTT	GCCCATATGG	ATGTGGTGCC	TGCTGGTAGC	300
GGTTGGGACA	CAGACCCTTA	CACACCAACT	ATCAAAGATG	GTCGCCTTTA	TGCGCGCGGG	360
GCTTCGGACG	ATAAGGGTCC	TACAACAGCT	TGTTACTATG	GTTTGAAAAAT	CATCAAAGAA	420
TTGGGTCTTC	CAACTTCTAA	GAAAGTTCGC	TTCATCGTTG	GAACAGACGA	AGAATCAGGC	480
TGGGCAGACA	TGGACTACTA	CTTTGAGCAC	GTAGGACTTG	CCAAACCAGA	TTTCGGTTTC	540
TCACCAGATG	CTGAATTTCC	AATCATCAAT	GGTGAAAAAG	GAAATATCAC	GGAATACCTC	600
CACTTTGCAG	GAGAAAATAC	AGGTGTTGCC	CGTCTTCACA	GCTTTACAGG	TGGTTTACGT	660
GAAAAATATG	TACCAGAATC	AGCAACAGCA	GTCGTTTCAG	GTGACTTGGC	TGACTTGCAA	720
GCTAAACTAG	ATGCCTTTGT	TGCAGAACAC	AAACTTAGAG	GAGAACTCCA	AGAAGAAGCT	780
GGCAAATACA	AGGTGACGAT	CATTGGTAAA	TCAGCCCACG	GTGCTATGCC	TGCTTCAGGT	840
GTCAATGGCG	CAACTTACCT	TGCCCTCTTC	CTCAGCCAGT	TTGGCTTTGC	TGGTCCAGCC	900
AAAGACTACC	TTGACATCGC	AGGTAAAAAT	CTCTTGAACG	ATCATGAGGG	TGAAAATCTT	960
AAGATTGCTC	ATGTGGATGA	AAAGATGGGT	GCTCTTTCTA	TGAATGCCGG	CGTCTTCCAC	1020
TTCGATGAAA	CAAGTGCTGA	TAATACCATT	GCCCTCAACA	TCCGCTATCC	AAAAGGAACA	1080
AGTCCAGAAC	AAATCAAGTC	AATCCTTGAA	AACTTGCCAG	TTGTTTCTGT	TAGCCTGTCT	1140
GAACACGGTC	ACACGCCTCA	CTATGTGCCA	ATGGAAGATC	CACTTGTGCA	AACCTTGTTG	1200
AATATCTATG	AAAAACAAAC	TGGCTTTAAA	GGTCATGAAC	AAGTCATCGG	TGGTGGAACC	1260
TTTGGTCGCT	TGCTAGAACG	CGGAGTTGCC	TACGGTGCTA	TGTTCCCAGA	CTCGATTGAT	1320
ACCATGCACC	AAGCCAATGA	ATTTATCGCC	TTGGATGATC	TTTTCCGAGC	AGCAGCAATT	1380
TATGCCGAAG	CTATTTACGA	ATTGATCAAA	TAA			1413

(2) INFORMATION FOR SEQ ID NO:1014:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

GAGGAAGAAA	ATATGTATAA	TAAAGTTATC	ATGATTGGGC	GTTTAACGTC	TACACCAGAA	60
TTGCACAAAA	CCAACAATGA	CAAGTCAGTA	GCGCGAGCAA	CTATCGCTGT	CAACCGTCGT	120
TACAAAGACC	AAAACGGTGA	ACGTGAAGCT	GATTTTGTCA	ATATGGTTCT	ATGGGGCAGA	180
CTAGCAGAAA	CTTTGGCAAC	GTACGCAACC	AAAGGTAGTC	TCATTTCCGT	TGATGGAGAA	240
TTGCGTACCC	GTCGCTTTGA	GAAAAATGGT	CAGATGAATT	ATGTAACCGA	AGTCCTTGTG	300
ACAGGATTCC	AACTCTTGGA	AAGTCGTGCC	CAACGTGCTA	TGCGTGAAAA	TAATGCAGGC	360
CAAGATTTGG	CAGATTTGGT	CTTGGAAGAG	GAAGAATTGC	CATTTTAA		408

(2) INFORMATION FOR SEQ ID NO:1015:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

CTTAGAGAAA	ATAGGAGGAC	TAATCGAATG	GAATTAAAAAG	ATTTTACAGA	AAAAGAACAG	60
GAAATGATTA	AGAAAAGGCT	TACAATGTCT	AATATTAGTG	ACAAAAGAAAC	TACTGAGAAG	120
ATTCTGGCGC	TAGTACCACA	AGACTTGATT	AAGCGAATCC	CGTTTTTTGT	CAGAAAACAT	180
GCTACAACAC	GTACGATTAA	ACGCATTTCA	ATTGAACACC	CTGAACTCTA	CGCTGTAGCT	240
CAAACAAGTG	GTGAGATTCC	AGAAAAAGAA	TGCGAAGAAT	TGCGTCAGAT	TATCACAACT	300

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

AAAAGAGAAA	ACAGGATGGT	TTTACCAAAT	TTTAAAGAAA	ATCTAGAAAA	ATATGCGAAA	60
TTGTTGGTTG	CGAACGGAAT	TAACGTGCAA	CCTGGTCACA	CTTTGGCTCT	CTCTATTGAT	120
GTGGAGCAAC	GTGAATTGGC	ACATCTAATC	GTGAAAGAAG	CTTATGCCTT	GGGTGCGCAT	180
GAGGTCATCG	TTCAGTGGAC	AGATGATGTG	ATTAACCGTG	AGAAATTCCT	CCATGCCCCG	240
ATGGAGCGTT	TGGACAATGT	GCCAGAATAC	AAGATTGCTG	AGATGAACTA	TCTCTTGGAG	300
AACAAGGCTA	GCCGTCTTGG	AGTTCGTTCA	TCTGATCCAG	GTGCCTTGAA	CGGAGTGGAC	360
GCTGACAAGC	TTTCAGCTTC	TGCTAAAGCT	ATGGGACTTG	CCATGAAGCC	AATGCGAATC	420
GCAACTCAAT	CTAACAAAGT	TAGCTGGACT	GTAGCAGCTG	CAGCAGGACT	TGAGTGGGCT	480
AAGAAAGTCT	TCCCAAATGC	TGCGAGCGAC	GAAGAAGCAG	TTGATTTCCCT	TTGGGACCAA	540
ATTTTCAAAA	CTTGCCGTGT	CTACGAAGCA	GATCCTGTTA	AGGCTTGGGA	GGAACATGCA	600
GCCATTCTCA	AGAGCAAGGC	CGATATGCTT	AATAAGGAGC	AATTTTCAGC	CCTTCACTAC	660
ACAGCGCCAG	GAACAGATTT	AACACTTGGT	TTGCCAAAGA	ACCACGTTTG	GGAATCAGCT	720
GGTGCTGTCA	ATGCACAGGG	CGAAGAAATC	TTGCCAAATA	TGCCGACAGA	AGAGGTCTTC	780
ACAGCGCCTG	ACTTCCGTCG	TGCAGATGGT	TATGTCACTT	CTACAAAACC	GCTTAGCTAC	840
AACGGAATA	TCATTGAAGG	CATTAAGGTG	ACCTTTAAGG	ATGGACAAAT	CGTAGATATC	900
ACTGCTGAGA	AGGGTGATCA	GGTTATGAAA	GACCTTGTCT	TTGAAAATGC	GGGTGCGCGT	960
GCCTTGGGTG	AATGTGCCTT	GGTACCAGAT	CCAAGTCCAA	TTTCTCAGTC	AGGCATTACC	1020
TTCTTTAACA	CCCTTTTCGA	TGAAAATGCG	TCAAACCACT	TGGCTATCGG	TGCAGCCTAT	1080
GCGACTAGCG	TTGTTGATGG	AGCGGAGATG	AGCGAAGAGG	AGCTTGAAGC	TGCAGGGGCTT	1140
AACCGTTCAG	ATGTTACCGT	AGACTTTATG	ATTGGTTCTA	ACCAAATGGA	TATCGATGGT	1200
ATTCGTGAGG	ATGGAACGCG	AGTACCTCTT	TTCCGTAATG	GGAATTGGGC	AAATTAA	1257

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

GATGGAGAAA	AGAAGTCTAG	TAGAGTTATT	GAAAGGGGGC	ATCTTATGAT	TGAGTTGAAA	60
AATATTACCA	AAACCATTGG	GGGAAAAGTG	ATTTTGGATA	ACTTATCTCT	CAGGATTGAT	120
CAGGGGGATT	TGGTAGCTAT	TGTTGGTAAG	AGTGGTAGTG	GGAAGTCGAC	CTTGTTAAAT	180
TTATTGGGTT	TGATAGATGG	TGATTATAGC	GGACGGTATG	AGATTTTTTG	TCAGACAAAT	240
CTAGCGGTTA	ATTCTGCTAA	GTGCGAAACA	ATAATCCGTG	AACATATCTC	TTATCTGTTT	300
CAAAATTTTG	CCCTGATTGA	TGATGAAACG	GTGAGTACA	ATCTCATGCT	GGCGCTGAAA	360
TATGTGAAAT	TGCCTAAGAA	AGACAAGCTC	AAAAAGGTGG	AAGAGATTTT	AGAGAGAGTA	420
GGTTTGTCAG	CTACTTTGCA	TCAAAGGGTC	TCCGAGTTGT	CTGGGGGCGA	ACAACAACGA	480
ATTGCAGTTG	CTAGAGCCAT	CTTAAACCC	AGCCAGCTGA	TTTTAGCCGA	TGAACCTACA	540
GGTTCGCTGG	ATCCTGAAAA	TAGAGATTTG	GTCTTGAAGT	TTCTCTTAGA	GATGAATCGA	600
GAAGGGAAAA	CAGTCATTAT	TGTGACCCAC	GATGCTTATG	TAGCCCAACA	ATGTCATCGT	660
GTCATTGAAT	TGGGCGAGGG	AAAATGA				687

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1839 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

CAAGGAGAAA	AACACATGTC	TAAAATTATC	GGTATTGACT	TAGGTACAAC	AAACTCAGCA	60
GTTGCAGTTC	TTGAAGGAAC	TGAAAGCAAA	ATCATCGCAA	ACCCAGAAGG	AAACCGCACA	120
ACTCCATCTG	TAGTCTCATT	CAAAAACGGA	GAAATCATCG	TTGGTGATGC	TGCAAAACGT	180
CAAGCAGTTA	CAAACCCAGA	TACAGTTATC	TCTATCAAAT	CTAAGATGGG	AACTTCTGAA	240
AAAGTTTCTG	CAAAATGGAAA	AGAATACACT	CCACAAGAAA	TCTCAGCTAT	GATCCTTCAA	300
TACTTGAAAAG	GCTACGCTGA	AGACTACCTT	GGTGAGAAAAG	TAACCAAAGC	TGTTATCACA	360
GTTCCGGCTT	ACTTCAACGA	CGCTCAACGT	CAAGCAACAA	AAGACGCTGG	TAAAATTGCT	420

GGTCTTGAAG	TAGAACGTAT	TGTTAACGAA	CCAACTGCAG	CAGCTCTTGC	TTATGGTTTG	480
GACAAGACTG	ACAAAGAAGA	AAAAATCTTG	GTATTTGACC	TTGGTGGTGG	TACATTTCGAC	540
GTCTCTATCC	TTGAATTGGG	TGACGGTGTC	TTTCGACGTAT	TGTCAACTGC	AGGGGACAAC	600
AAACTTGGTG	GTGACGACTT	TGACCAAAAA	ATCATTGACC	ACTTGGTAGC	AGAATTCAAG	660
AAAGAAAACG	GTATCGACTT	GTCTACTGAC	AAGATGGCAA	TGCAACGTTT	GAAAGATGCG	720
GCTGAAAAAG	CGAAGAAAGA	CCTTTCTGGT	GTAACTTCAA	CACAAATCAG	CTTGCCATTT	780
ATCACTGCAG	GTGAGGCTGG	ACCTCTTCAC	TTGGAAAATGA	CTTTAACTCG	TGCGAAAATTT	840
GATGATTTGA	CTCGTGACCT	TGTTGAACGT	ACAAAAGTTC	CAGTTCGTCA	AGCCCTTTTCA	900
GATGCAGGTT	TGAGCTTGTC	AGAAATCGAC	GAAGTTATCC	TTGTTGGTGG	TTCAACTCGT	960
ATCCCTGCCG	TTGTTGAAGC	TGTTAAAGCT	GAACTGGTA	AAGAACCAA	CAAATCAGTA	1020
AACCCGTGATG	AAGTAGTTGC	TATGGGTGCG	GCTATCCAAG	GTGGTGTGAT	TACTGGTGAT	1080
GTCAAGGATG	TTGTCCCTTCT	TGATGTAACG	CCATTGTCAC	TTGGTATCGA	AACAATGGGT	1140
GGAGTATTTA	CAAAACTTAT	CGATCGCAAC	ACTACAATCC	CAACATCTAA	ATCACAAGTC	1200
TTCTCAACAG	CAGCAGACAA	CCAACCAGCC	GTTGATATCC	ACGTTCTTCA	AGGTGAACGC	1260
CCAATGGCAG	CAGATAACAA	GACTCTTGGA	CGCTTCCAAT	TGACTGATAT	CCCAGCTGCA	1320
CCTCGTGGAA	TTCTCTCAAAT	CGAAGTAACA	TTTGACATCG	ACAAGAACGG	TATCGTGTCT	1380
GTTAAGGCCA	AAGACCTTGG	AACTCAAAAA	GAACAAACTA	TTGTCATCCA	ATCGAACTCA	1440
GGTTTGACTG	ACGAAGAAAT	CGACCGCATG	ATGAAAGATG	CAGAAGCAA	CGCTGAATCC	1500
GATAAGAAAC	GTAAAGAAGA	AGTAGACCTT	CGTAATGAAG	TGGACCAAGC	AATCTTTGCG	1560
ACTGAAAAGA	CAATCAAGGA	AACTGAAGGT	AAAGGCTTCG	ACGCAGAACG	TGACGCTGCC	1620
CAAGCTGCCC	TTGATGACCT	TAAGAAAAGCT	CAAGAAGACA	ACAACCTGGA	CGACATGAAA	1680
GCAAACTTG	AAGCATTGAA	CGAAAAAGCT	CAAGGACTTG	CTGTTAAACT	CTACGAACAA	1740
GCCGCAGCAG	CGCAACAAGC	TCAAGAAGGA	GCAGAAGGCG	CACAAGCAAC	AGGAAACGCA	1800
GGCGATGACG	TCGTAGACGG	AGAGTTTACG	GAAAAGTAA			1839

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

AAAGGAGAAA	AGTTCATGAA	CAAATTAATG	AAATTTATTT	CGGTTTTTTT	GACGTCAATT	60
GTGTTAATTG	TATCAGCGAT	TCCAAGTGTT	TCAGCTGTAT	ACGCTTCTGA	ACAAAGTATCA	120
CAAATTGAAA	CAAAATATGGA	ACTTCAACCT	GTCATTCTC	TAACAGAAGA	ACAAATCAAT	180
ACACTTGCAA	ACGAAATCCA	ATCTTTTCAT	CCAGACGTCT	CACAACAATG	GATCAAAGAA	240
GTAATTAACC	GACAATTACA	AGGCGATTAT	ACAATCCCAC	CTACATACTC	TCCATTTAGA	300
GCAGCTTGGC	AAGGTATTAC	AGTTAATCAA	ATGGGTGCTC	TATTAGATAC	TGCAATAGCT	360
TTAGCATTAG	GAGGAACTAC	TGCAGGCCTT	GCAAATCTAA	TTAAAGTAAA	AGGAAAACAT	420
GCAGCAAAAA	GTGCTATTCG	TTTCAAGCAAT	TCTAGATATC	TAGGTAGTTG	GTTTGTAAT	480
GATGTTGCTT	TAGAATTCGC	TATGAATTTA	TTATCACCGG	GGACTTATTT	AGCACAATTA	540

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

AGCTTGAAAA	AAAGAAATGG	AAACAAGCAA	GAAAATGAGG	TCAGCAGGAT	GAACCTACTA	60
TCAAGAAATCA	AAAACTATTT	TTCGGAAGAG	GTCAAAGAAA	CTAATCTCGA	CTGGAAAGAG	120
GTCGCTTTAG	ACCTCAATCA	ATCACTAATT	GAAACACAGG	AAAAACTTCA	AGAAGCGAAT	180
CAAGAAATCG	CAGACTTGAA	GAAAATCGTA	GCAATCTATA	AAGAAAAGGA	GAAAGAAAAA	240
CGATGGAATA	TATTACCTG	GTAA				264

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

GAAATGGAAA	AATTAAACGC	ATTAAGGAAA	CAAAAAATTA	GGGCAGTGAT	TTTACTGGAA	60
GCAGTAGTCG	CTCTAGCTAT	CTTTGCCAGC	ATTGCGACCC	TCCTTTTGGG	ACAAATTCAA	120
AAAAATAGGC	AAGAGGAAGC	AAAAATCTTG	CAAAAGGAAG	AAGTCTTGAG	GGTAGCTAAG	180

ATGGCCTTGC AGACGGGGCA AAATCAGGTA AGCATCAACG GAGTTGAGAT TCAGGTATTT	240
TCTAGTGAAA AAGGATTGGA GGTCTACCAT GGTTCAGAAC AGTTGTTGGC AATCAAAGAG	300
CCATAA	306

(2) INFORMATION FOR SEQ ID NO:1022:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: *misc_feature*
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

ATGAAGGAAA AAGAATTTTCG CCGAAATATG GCTGTTTTTC CTATCGGCAG TGTATGAAG	60
TTGACCGATC TATCGGCGCG TCAGATTCGT TATTATGAAG ATCAAGAGTT GATCAAGCCC	120
GATCGAAACG AAGGAAATCG TCGCATGTAT TCCTTGAATG ACATGGATCG TCTGCTTGAA	180
ATCAAAGATT ATATCTCTGA AGGTTATAAT ATCGCTGCCA TTAAGAAAAA ATATGCTGAA	240
CGTGAAGCGA AATCCAAGAA AGCGGTTAGT CAGACTGAAG TACGTCGTGC ACTTCACAAT	300
GAACTCCTCC AACAGGGGCG TTTTGCTTCA GTACAGTCAC CTTTTGGTCG CGGTTAG	357

(2) INFORMATION FOR SEQ ID NO:1023:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: *misc_feature*
 - (B) LOCATION 1...2229
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

AAGGAGGAAA	ACAAATTGAA	AATTTTTTAAG	GGAGAGTTTT	ATCGAATCTC	TGTATTAACA	60
GACAAAGCTAG	TAAGGTTAGA	ATACTCTCAA	ACTGGAAGTT	TTGAGGATAG	AACGACACAA	120
CTTATCTATA	ATAGAGATTT	TGGCCAAGTT	TCGTTAGATT	ATATCGAGAC	ATCAAACGTA	180
CTAGATATTA	TGACGGACTA	TTTTCATCTG	CACTTTAATA	AAGGAGAATT	TAACGCCGAA	240
AATTTATTTA	TAGAAATAAA	AGGAAATTTT	GCCGTATATG	GTAGTCGCTG	GTATTTTGGT	300
GAATCTATTG	AAACGTTAAA	AGGAACAGCT	CGGACTCTGG	ATAAGGCAGA	TGGAGCAATC	360
TCGTTAGAAG	ATGGAATTAT	TAGCCGAAAT	GGTATAGCCT	TATTGGATGA	TTCTCAAGGA	420
TTTATTTGGG	ATGAACAATC	TGGTTATATT	GAGAGAGAAA	ATCAAATTGA	CCTGTATTTT	480
TTTGCCATATG	GGCATGATTA	TAGAGGAGCA	ATCAGAGATT	TTTACCATTT	GACTGGTTCA	540
ACACCCTTGT	TGCCAAGATA	TGCTTTAGGC	AATTGGTGGA	GTAGATATTG	GCCTTATACG	600
TCGGATGAAT	ACTTGGATTT	AATAGACAGA	TTTGAAACAG	AGAAAATTCC	ATTATCTATC	660
GGTGTGTTAG	ATATGGATTG	GCATATAACT	GACATTCCAG	CTCGCTTTGG	AAGTGGCTGG	720
ACAGGATATA	GTTGGAATAG	AACTTAATA	CCAAATCCAG	AACAGTTATT	GCAACAACCTT	780
CATGATAGAA	AGCTAAAGCT	CTCCTTAAAT	GTCCATCCTG	CTGATGGGAT	ACGGGCTTAT	840
GAAGAAGCTT	ATCCTCAAAT	CGCAAAACGG	TTGGGGTTAA	ATGTAGAACT	AGAAGAACCT	900
GCTATTTTTG	ATTTTTTTAA	TCCCTCTTTT	AGGGAAGCCT	ACTTTAAAGA	TGTTTCATTAT	960
GAACTAGAAA	AGCAGGGAGT	AGATTTTTTG	TGGATTGACT	GGCAACAAGG	GACACAAGGT	1020
ATGCTAGATC	CACTTTGGCT	TTTAAACCAT	TATCACTATC	AGGATAGTTG	TAAAAATGCA	1080
GAAGGTGGTT	TGATTTTATC	AAGATATGCA	GGTCCTGGTA	GTCACCGCTA	CCCTGTTGGT	1140
TTTTCAGGGG	ACACTATTAT	TAGTTGGAAT	TCCTTAAGAT	TTCAACCCTA	TTTTACAGCG	1200
ACAGCATCTA	ATATCGGTTA	TAGTTGGTGG	AGTCATGATA	TCGGTGGACA	TATGTTGGGG	1260
GATTATGACG	AAGAGCTACA	AACTAGATGG	CTACAGTTTG	GTGTTTTTAG	TCCGATTACT	1320
CGATTACATA	GTTCTAGAAG	TCCTTTTAAAT	AGTAAAGAAC	CTTGTTCTTT	TTCAGAAACA	1380
ACATCTAAGA	TTATGAAGAA	ATACCTTCGT	TTGAGACATC	AGATGATTCC	CTATCTATAT	1440
ACCATGAATG	TAAAGACACA	TGAGGAAGGT	GCCCCATTAA	TCAGTCCAAT	CTATTATTTT	1500
TATCCAGAGA	ATGATGAGAG	CTATAATGTT	CCAAACCAAT	ACTTTTTTTG	AACAGAACTG	1560
ATGGTGGCTC	CCATTGTAGA	AAAGATGGAT	TTGACATTCC	AATCTGCAAA	AGTAGATGTA	1620
TGGTTCCCTG	AAGGTGAATG	GTATGACTTC	TTTTCAGAGA	AAAAATACAC	AGGTGGTGTG	1680
AAGTTAAGTG	TTTATAGGGA	CATCTCGACT	ACGCCTGTGT	TTGCAAAAAG	TGGTGCAATC	1740
ATTCCCTTGG	TTGGTTCTGA	GATAGGTATG	GGTGTTGATT	TACCTGAAGT	TGTAGATTGG	1800
TATGTATTCC	CAGGAAAACA	ACATTCTTTT	GAAATGCTTG	AAGATCAAAA	TGGTCAAAGA	1860
TATAAAACAA	GATTATCAAT	CGATTGGGAA	ATGGGAATGG	TAGAGTTAGC	ATTACAAGGA	1920
GATTCTAGTA	TCGTTCCAAG	CAATAGAAAA	CATAGAATTC	ATTTTAAAGG	AACGAATGTG	1980
TCTATAAATTG	AATTGCCAAA	TAAGAATGAT	ACAGCTAAAT	TTGAATGGAA	AGATAATAAA	2040
AGGACATCTT	TAAATGACGA	AGTTTTTTAGA	CTACTAAAAG	CAGCTTCTCT	TCCATATGAA	2100
TTAAAAGATA	GATTGTTAAA	TCAATTCATC	AATGCGAAAA	ACTCTCATGA	CTTAATGAAT	2160
ATCTTGCAATC	ATCAGGATAA	GGAATTGAGA	GGGCGTTTGT	TGGAAATGAT	ATTTACTAGC	2220
CAAAACTAA						2229

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

CTTTGGGAAA	ACTCTTATAA	GGAAATTGTT	GGTGAAATTG	ATGATGAAAC	GGACAAAGCA	60
GCAATAGATG	TTCATCAGAT	TGGCGAAGAT	ACCTACATTG	TTCAAAGAAC	TATGACCCTC	120
AATGATTTCA	ATAATTACTT	TGATGTTGAA	CTGGANAGTG	ATGACGTTGA	TACCATCGCT	180
GGTTATTATT	TGACAGGAGT	GGGAACTATT	CCAACGACTG	AGAAACTCAG	CTATGAATTG	240
GTTAGCCAAA	ACAAACAGTT	TATCTTAACC	AATGATAAAG	TATAG		285

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

AANCAACCCC	TATATAATAC	ATTTCTTGGA	GAAAAATTAA	CTGGGTTTGG	TTTTATCCCT	60
GACGGCCTGA	GTGTCAAGAG	GACACGAAAT	GTCTTTACAG	TGGACACCAA	TTTGAATCTC	120
CGAGTTTTTA	GGAGTGATTT	TCCGAATTAC	TGGTGCCTTA	TTGGAGCACT	ATCATCTATT	180
TGGTGGTGTG	AGGGAGATAT	CTCTTTTTTC	CTCCGCCCAA	TCGGGGTGAT	ATTTATTTTC	240
TTCCTACCC						249

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

ATGGTACGAA	ATAAAATAGG	TGATTTAACT	AACACGCTCT	TCGCTCAATT	AGAGACTCTG	60
GATGATAGGG	ATCTTACAGC	AGATGAATTA	AAAGTAGAAT	TACAGCGCTC	GAAACAAATG	120
GTCGCAATCT	CAGGTCAAAT	CTTACAAGCA	GGTCAATTGG	CGCTAGATGC	TGAAAAATTC	180
AAAGACAAGG	TAGGTGAAGT	CAATGCCCCG	ATCGCTTTGC	TGGAAGGATG	A	231

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

ATTATTAGAA	ATGAAGAAAG	AAAGGATACT	ATGGCTGAAG	AAAGAGTAGA	ACCAAAACCA	60
ATTGACCTTG	GTGAATATAA	ATTTGGTTTC	CATGACGATG	TAGAGCCTGT	CTTATCGACA	120
GGAAAAGGAC	TCAACGAAGG	TGTTATTCGT	GAATTATCTG	CTGCTAAGGG	TGAGCCTGAG	180
TGGATGTTGG	AGTTCCGTTT	GAAGTCTTAT	GAAACCTTCA	AAAAAATGCC	CATGCAAACCT	240
TGGGGAGCAG	ACTTGTCAGA	GATTGACTTT	GATGACTTAA	TCTACTACCA	AAAACCATCT	300
GACAAACCAG	CCCGTTCCTG	GGATGATGTA	CCTGAAAAGA	TTAAAGAAAC	CTTTGAACGT	360
ATCGGGATTTC	CAGAAGCTGA	ACGTGCTTAT	TTAGCAGGGG	CTTCTGCCCA	GTACGAGTCA	420
GAAGTGTTT	ACCACAACAT	GAAGGAAGAG	TTCCAAAAAT	TAGGTATTAT	CTTTACAGAT	480
ACAGATTCCG	CACTCAAGGA	ATACCCAGAC	TTATTTAAAC	AATACTTTGC	GAAGTTGGTA	540
CCGCCGACAG	ATAACAAGTT	GGCAGCCCTC	AACTCAGCAG	TATGGTCGGG	TGGAACCTTTT	600
ATCTACGTGC	CAAAAGGTGT	CAAGGTAGAT	ATTCCACTTC	AACTTATTT	CCGTATCAAT	660
AACGAAAATA	TAGGTCAGTT	CGAACGTACC	TTGATTATCG	TTGATGAGGG	AGCAAGCGTC	720
CACTACGTAG	AAGGATGTAC	AGCACCAACA	TATTCAAGCA	ATAGCTTACA	CGCTGCCATT	780
GTAGAAATTT	TTGCTTTGGA	CGGAGCTTAT	ATGCGTTATA	CAACTATCCA	AACTGGTCT	840
GATAACGTCT	ATAACTTGGT	AACAAAGCGT	GCTAAGGCTC	AAAAGGATGC	CACTGTTGAG	900
TGGATTGATG	GAAACTTGGG	TGCCAAAACG	ACTATGAAAT	ATCCATCTGT	TTACCTTGAT	960
GGAGAAGGAG	CGCGTGGTAC	CATGCTCTCT	ATCGCCTTTG	CTAATGCAGG	GCAACACCAA	1020
GACACGGGTG	CTAAGATGAT	TCACAATGCT	CCACATACCA	GCTCGTCTAT	TGTGTCTAAA	1080
TCCATCGCTA	AAGGTGGAGG	AAAGGTTGAC	TACCGTGGAC	AAGTCACCTT	TAACAAGAAC	1140
TCTAAGAAAT	CTGTTTCCCA	CATTGAATGT	GATACCATTA	TCATGGATGA	CTTGTCAGCA	1200
TCAGATACTA	TTCCATTTAA	TGAAATTCAC	AACTCGCAAG	TGGCTTTGGA	ACACGAAGCC	1260
AAAGTATCTA	AGATTTTACA	AGAGCAATTG	TATTATCTCA	TGAGCCGTGG	ATTGTCAGAA	1320
TCTGAGGCAA	CTGAAATGAT	TGTCATGGGA	TTTGTAGAAC	CCTTTACAAA	AGAACTTCCA	1380

ATGGAATACG CAGTTGAGCT GAACCGCTTG ATTAGCTATG AAATGGAGGG ATCAGTTGGA	1440
TAA	1443

(2) INFORMATION FOR SEQ ID NO:1028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 948 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

TTAATTAGAA	AGTATCGAAT	GGATATTCAA	TTTTTAGGAA	CGGGGGCTGG	TCAGCCCTCT	60
AAAGCCCGCA	ACGTTTCAAG	TCTCGCCCTG	AAACTTTTGG	ATGAGATTAA	CGAAGTTTGG	120
CTCTTTGACT	GTGGAGAAGG	TACGCAAAAT	CGCATTCTGG	AAACCACAAT	TCGACCACGT	180
AAGGTCAGCA	AAATCTTTAT	TACCCATCTG	CATGGAGACC	ACATTTTGG	TTTGCCAGGT	240
TTCTTTTCTA	GCCGTGCCTT	TCAGGCCAAT	GAAGAGCAGA	CAGATTTGGA	AATCTACGGA	300
CCTCAAGGAA	TCAAGTCATT	TGTCTTAACC	AGCCTTCGTG	TGTCAGGTTT	TCGTCTGCCC	360
TACCGCATTC	ATTTCCATGA	GTTTGACCAA	GATTCTCTAG	GTAAAATTCT	TGAAATCGAT	420
AAATTCACTG	TGTATGCAGA	GGAGCTGGAC	CACACTATTT	TCTGTGTTGG	CTATCGTGTC	480
ATGCAAAAGG	ATCTAGAAGG	GACGCTGGAT	GCTGAAAAAC	TCAAGGCTGC	TGGTGTTCGG	540
TTCGGCCCGC	TTTTTGGTAA	AATCAAAAAT	GGCCAGGATC	TTGTTTTGGA	AGACGGAAC	600
GAAATCAAGG	CAGCAGACTA	TATCTCAGCG	CCACGTCCAG	GTAAGATTAT	CACTATTTTA	660
GGAGACACTC	GAAAAACGGA	TGCCAGTGTG	CGTCTGGCTG	TCAATGCAGA	TGTCCTAGTT	720
CATGAGTCCA	CTTATGGCAA	GGGTGATGAA	AAAATTGCTC	GTAACCATGG	TCACTCAACT	780
AATATGCAAG	CTGCACAAGT	AGCGGTAGAA	GCAGGTGCCA	AACGCCTCCT	ACTCAACCAT	840
ATCAGTGCCC	GTTTCCTCTC	AAAAGATATT	AGCAAACCTA	AGAAAGACGC	TGCCACAATT	900
TTTGAAAAATG	TCCATGTGGT	CAAAGACTTG	GAAGAAGTGG	AAATCTAG		948

(2) INFORMATION FOR SEQ ID NO:1029:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

CCAAC TAGAA	ACACCGCGAG	AGGTCAAAGG	GTCTTGATG	AATTGCGAGA	TCGTTTGAAG	60
AGAAATCAGT	TTATACTCAA	TGATACCAAT	CCGGATATTG	TCATTTCCAT	TGGCGGGGAT	120
GGTATGCTCT	TGTCGGCCTT	TCATAAGTAC	GAAAATCAGC	TTGACAAGGT	CCGCTTTATC	180
GGTCTTCATA	CTGGACATTT	GGGCTTCTAT	ACAGATTATC	GTGATTTTGA	GTTGGACAAG	240
CTAGTGACTA	ATTTGCAGCT	AGATACTGGG	GCAAGGGTTT	CTTACCCTGT	TCTGAATGTG	300
AAGGTCTTTC	TTGAAAATGG	TGAAGTTAAG	ATTTTCAGAG	CACTCAACGA	AGCCAGCATC	360
CGCAGGTCTG	ATCGAACCAT	GGTGGCAGAT	ATTGTAATAA	ATGGTGTTC	CTTTGAACGT	420
TTTCGTGGAG	ACGGGCTAAC	AGTTTCGACA	CCGACTGGTA	GTACTGCCTA	TAACAAGTCT	480
CTTGCGCGTG	CTGTTTAC	CCCTACCATT	GAAGCTTTC	AATTAACGGA	AATTGCCAGC	540
CTTAATAATC	GTGTCTATCG	AACACTGGGC	TCTTCCATTA	TTGTGCCTAA	GAAGGATAAG	600
ATTGAACCTA	TTCCAACAAG	AAACGATTAT	CATACTATTT	CGGTTGACAA	TAGCGTTTAT	660
TCTTTCCGTA	ATATTGAGCG	TATTGAGTAT	CAAATCGACC	ATCATAAGAT	TCACTTTGTC	720
GCGACTCCTA	GCCATACCAG	TTTCTGGAAC	CGTGTTAAGG	ATGCCTTTAT	CGGTGAGGTG	780
GATGAATGA						789

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

TTTTATAGAA	AATTGGAGGA	ACCTGTTATG	ACAAACACAC	GTCGACTTTC	GACCATTGCA	60
ATTTTATCAG	CCATCTCATT	TGTGCTGATG	TACTTTGACT	TTCCGCTTTT	ACCAGCGGCA	120
TCTTTCCTCA	AGATCGAATT	TAGTATCTTG	CCAGTCCTTG	TGGGTCTGGT	GGTCATGGAT	180
TTGCCCTGCTG	CTCTAGGAGT	GCTCTTGCTT	CGCTCACTAT	TGAAATTGCT	TCTTAACAGC	240
CAAGGAGTGA	ATACTTACAT	TGGTTTGCCG	ATGAATATCG	TAGCTTTGGG	AGTTTTTGTC	300
ATCGTATTTG	CTTTGATTTG	GAAAAAGGAA	CGGACAACCC	TTCGTTTCCT	ACTAGGCTCT	360
CTAGCTGGAA	CTGTTGGTTT	AACCTTGGCC	ATGTTGGTTC	TCAACTATGT	TTATGCTGTT	420
CCTTTGTACG	CTAAGTTTGC	TAACTTTGAT	ATTGGAAAAA	TTTTGGGACT	TTCCAACCTAC	480
CTAATGACCA	TGGTATTACC	TTTTAACTTG	ATTGAGGGTG	TAATCTTTTC	CGTTTCATTG	540
TGGTTGTTGT	ACGTCCTTTT	GAAACCAACC	TTAAAACT	ATGAAAGATA	A	591

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

AGATATAGAA	AGAGGTTTGT	CATCGCAAAG	AAAAAAGCGA	CATTTGTATG	TCAAAATTGT	60
GGGTATAATT	CCCCTAAATA	TCTGGGACGT	TGCCCCAACT	GTGGGTCTTG	GTCTTCTTTT	120
GTGGAAGAGG	TTGAGGTTGC	CGAGGTCAAG	AATGCGCGTG	TGTCCTTGAC	AGGTGAGAAA	180
ACCAAGCCCA	TGAAACTAGC	TGAGGTGACT	TCCATCAATG	TCAATCGAAC	CAAGACGGAG	240
ATGGAGGAAT	TCAACCGTGT	GCTTGAGAGC	GGAGTGGTAC	CAGGAAGTCT	CGTCCTCATC	300
GGTGGGGATC	CTGGGATTGG	GAAATCAACT	CTTCTCCTAC	AAGTCTCAAC	CCAGTTGTCC	360
CAAGTGGGGA	CAGTTCTCTA	TGTCAGTGGG	GAGGAGTCTG	CCCAGCAGAT	TAAACTACGT	420
GCAGAGCGCT	TAGGTGATAT	TGATAGTGAG	TTTTATCTCT	ATGCAGAGAC	CAATATGCAG	480
AGTGTTTCGTG	CAGAAGTGGA	GCGTATCCAG	CCAGACTTTC	TCATTATTGA	TTCCATCCAG	540
ACCATCATGT	CTCCTGAGAT	TTCAGGGGTG	CAGGGGTCTG	TTTCTCAGGT	ACGTGAAGTG	600
ACCGCTGAAC	TCATGCAGTT	GGCCAAGACC	AATAACATTG	CCATCTTTAT	CGTAGGTCAT	660
GTGACCAAAG	AAGGAACCTT	GGCTGGGCCCT	CGTATGTTGG	AGCATATGGT	GGATACGGTG	720
CTTTACTTTG	AAGGGGAGCG	TCACCACACC	TTTCGTATTT	TGAGAGCGGT	CAAAAATCGT	780
TTTGGTTCCA	CTAATGAGAT	TGGGATTTTT	GAGATGCAGT	CGGGCGGCTT	GGTTGAGGTA	840
CTCAATCCGA	GTCAAGTTTT	CCTAGAAGAG	CGTTTGGATG	GGGCGACTGG	TTCTCCATC	900
GTTGTAACCA	TGGAAGGGAC	GCGTCCGATT	TTGGCGGAGG	TTCAGGCTTT	GGTAACACCG	960
ACCATGTTTG	GAAATGCCAA	GCGTACTACG	ACAGGACTTG	ATTTTAACCG	TGCTAGCTTG	1020
ATTATGGCTG	TTTTGGAAAA	ACGGGCAGGG	CTTCTCTTGC	AAAATCAGGA	TGCCTATCTC	1080
AAATCTGCTG	GTGGTGTTAA	ATTGGATGAA	CCTGCCATTG	ACTTGGCTGT	TGCAGTTGCT	1140
ATTGCTTCGA	GCTACAAAGA	CAAGCCAACCT	AATCCTCAGG	AATGTTTTGT	CGGAGAACTG	1200
GGCTTGACAG	GAGAGATTCG	GCGCGTGAAT	CGTATTGAGC	AACGCATCAA	CGAAGCTGCT	1260
AAACTGGGCT	TTACTAAGAT	TTATGTACCT	CAGAATTCCT	TGACAGGAAT	CACTCTGCCT	1320
AAGGAAATTC	AGGTCATTGG	CGTGACAACG	ATTCAGGAAG	TCTTGAAAAA	GGTCTTTGCA	1380
TAA						1383

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

TATAATAGAA	ATATTGACTT	CAAGAGTAAG	GAAGAGAAGA	TGAACGCATT	ATTAAATGGA	60
ATGAATGACC	GTCAGGCTGA	GGCGGTGCAA	ACGACAGAAG	GTCCCTTGCT	AATCATGGCA	120
GGGGCTGGTT	CTGGAAAGAC	TCGTGTTTTA	ACCCACCGTA	TCGCTTATTT	GATTGATGAA	180
AAGCTGGTCA	ATCCTTGGA	TATCTTGGCC	ATTACCTTTA	CCAACAAGGC	TGCGCGTGAG	240
ATGAAAGAGC	GTGCTTATAG	CCTCAATCCA	GCTACTCAGG	ACTGTCTGAT	TGCGACCTTC	300
CACCTCCATGT	GTGTGCGTAT	TTTGCGTCTCG	GATGCGGACC	ATATTGGCTA	CAATCGTAAT	360
TTTACAATTG	TGGATCCTGG	TGAACAGCGA	ACGCTCATGA	AACGTATTCT	CAAACAGTTG	420
AACCTGGATC	CTAAAAAATG	GAATGAACGA	ACTATTTTGG	GGACCATTTT	CAATGCTAAG	480
AATAATTTGA	TTGATGATGT	TGCTTATGCT	GCCCAAGCTG	GCGATATGTA	TACGCAAAT	540
GTGGTCCAGT	GTTATACAGC	CTATCAAAAA	GAACCTCGTC	AGTCTGAATC	CGTTGACTTT	600
GATGATTTGA	TTATGCTGAC	CTTGCGTCTC	TTTGATCAAA	ATCCTGATGT	TTTGACCTAC	660
TACCAGCAAA	AATTCCAATA	CATCCACGTT	GATGAGTACC	AAGATACCAA	CCACGCTCAG	720
TACCAATTGG	TCAAACCTTT	GGCTTCCCCT	TTTAAAAATA	TCTGTGTGGT	TGGGGATGCG	780
GACCAGTCTA	TCTACGGTTG	GCGTGGTGCT	GATATGCAGA	ATATCTTGGA	CTTTGAAAAG	840
GATTACCCCA	AAGCCAAGGT	TGTCTTGCTG	GAGGAAAATT	ACCGCTCAAC	CAAAACCATT	900
CTCCAAGCGG	CCAACGAGGT	TATTA AAAAAT	AATAAAAATC	GCCGTCCTAA	AAATCTCTGG	960
ACTCAAAACG	CTGATGGGGA	GCAAATCGTT	TACTATCGTG	CCGATGATGA	GCTGGATGAG	1020
GCTGTATTTG	TAGCCAGAAC	CATCGATGAA	CTTAGTTCGCA	GTCAAAACTT	CTTTCATAAG	1080
GATTTTGCAG	TTCTCTATCG	GACTAATGCC	CAGTCCCGTA	CAATTGAGGA	AGCCCTGCTC	1140
AAGTCTAACA	TTCTTTATAC	CATGGTTGGC	GGAACCAAAT	TCTACAGCCG	TAAGGAAATT	1200
CGCGATATTA	TTGCTTATCT	CAACCTTATT	GCTAATTTGA	GTGACAATAT	TAGTTTTGAG	1260
CGTATTATCA	ACGAGCCTAA	ACGTGGAATT	GGTCCAGGTA	CAGTTGAGAA	AATCCGTGAT	1320
TTTGCAAATT	TGCAAAATAT	GTCTATGCTG	GATGCTTCTG	CTAATATTAT	GTTGTCTGGT	1380
ATCAAGGGTA	AGGCAGCCCA	ATCTATCTGG	GATTTTGCCA	ATATGATGCT	TGATTTGCGG	1440
GAGCAGCTAG	ACCACCTTAAG	CATTACAGAG	TTGGTTGAGT	CCGTCCCTAGA	AAAAACAGGT	1500
TATGTCGATA	TTCTTAAACG	CCAAGCGACT	CTAGAAAGCA	AGGCACGGGT	TGAAAATATC	1560
GAAGAGTTTC	TTTCTGTTAC	GAAGAACTTT	GATGACACCA	CGGATGTGAC	AGAAGAGGAA	1620
ACTGGTCTGG	ACAAACTGAG	TCGTTTCTTA	AATGACTTGG	CTTTGATTGC	CGACACAGAT	1680
TCAGGTAGTC	AGGAGACATC	AGAAGTGACC	TTGATGACCC	TGCATGCTGC	CAAAGGTCTC	1740
GAATTTCCAG	TTGTCTTTTT	GATTGGGATG	GAAGAAAATG	TCTTTCCACT	TAGTCGTGCG	1800
ACTGAAGATC	CAGATGAATT	AGAAGAAGAG	CGCCGTCTAG	CCTATGTAGG	TATCACGCGT	1860
GCAGAGAAAA	TTCTCTATCT	GACCAATGCC	AACTCACGCT	TGCTTTTTTG	TCGTACCAAT	1920
TATAACCGTC	CGACTCGTTT	TATTAACGAA	ATCAGTTCAG	ACTTGCTTGA	GTATCAAGGT	1980
CTGGCTCGTC	CTGCAAATAC	AAGCTTTAAG	GCATCATATA	GCAGTGGTAG	TATTTCTTTT	2040
GGTCAAGGTA	TGAGTTTGGC	TCAGGCTCTT	CAAGACCGTA	AACGCGGTGC	TGCCCCAAAA	2100
TCAATCCAGT	CAAGCGGTCT	TCCATTTGGT	CAATTTACAG	CTGGCGCAAA	ACCAGCATCT	2160
AGCGAGGCAA	ATTGGTCCAT	TGGTGATATT	GCTCTCCACA	AGAAATGGGG	AGAGGGAACC	2220
GTTCTGGAAG	TTTCAGGTAG	CGGTGCTAGG	CAGGAATTGA	AAATCAATTT	CCCAGAAGTA	2280
GGTTTGAAAA	AACTTTTAGC	CAGTGTGGCT	CCAATTGAGA	AAAAAATCTA	A	2331

(2) INFORMATION FOR SEQ ID NO:1033:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1356
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

TATAATAGAA	ACATGAACTT	AAAAACTACT	TTGGGCCTTC	TTGCTGGACG	TTCTTCCCAC	60
TTCGTTTTAA	GCCGTCTTGG	ACGTGGAAGT	ACGCTCCCAG	GGAAAGTCGC	CCTTCAATTT	120
GATAAAGATA	TTTTACAAAA	CCTAGCTAAG	AACTACGAGA	TTGTCGTTGT	CACTGGAACA	180
AATGGAAAAA	CCCTGACAAC	TGCCCTCACT	GTCGGCATTT	TAAAAGAGGT	CTATGGTCAA	240
GTTCTAACCA	ATCCAAGCGG	TGCCAACATG	ATTACAGGGA	TTGCAACAAC	CTTCCTAACA	300
GCCAAATCTT	CTAAAACTGG	GAAAAATATT	GCCGTCCTCG	AAATTGACGA	AGCCAGTCTA	360
TCTCGTATCT	GTGACTATAT	CCAGCCTAGT	CTTTTTGTCA	TTACTAATAT	CTTCCGTGAC	420
CAGATGGACC	GTTTCGGTGA	AATCTATACT	ACCTATAACA	TGATATTGGA	TGCCATTCCG	480
AAAGTTCCAA	CTGCTACTGT	TCTCCTTAAC	GGAGACAGTC	CACTTTTCTA	CAAGCCAACT	540
ATTCCAAACC	CTATAGAGTA	TTTTTGGTTT	GACTTGGA	AAAGACCAGC	CCAACCTGGCT	600
CACTACAATA	CCGAAGGGAT	TCTCTGTCCT	GACTGCCAAG	GCATCCTCAA	ATATGAGCAT	660
AATACCTATG	CAAACTTGGG	TGCCTATATC	TGTGAGGGTT	GTGGATGTAA	ACGTCCTGAT	720
CTCGACTATC	GTTTGACAAA	ACTGGTTGAG	TTGACCAACA	ATCGCTCTCG	CTTTGTCTATA	780
GACGGCCAAG	AATACGGTAT	CCAAATCGGC	GGGCTCTATA	ATATCTATAA	CGCCCTAGCT	840
GCTGTGGCCA	TCGCCCCTTT	CCTCGGCGCA	GATTCCCAAC	TCATCAAACA	GGGATTTGAC	900
AAGAGCCGTG	CTGTCTTTGG	ACGCCAAGAA	ACCTTTCATA	TCGGTGACAA	GGAATGTACC	960
CTTGTCTTGA	TTAAAAATCC	AGTCGGTGCA	ACCCAAGCTA	TCGAAATGAT	CAAACCTAGCA	1020
CCTTATCCAT	TAGCCTATC	TGTCCTCCTT	AATGCCAACT	ATGCAGATGG	AATTGACACT	1080
AGCTGGATCT	GGGATGCAGA	CTTTGAGCAA	ATCACTGACA	TGGACATTCC	TGAAATCAAC	1140
GCTGGCGGTG	TTCGTCAATC	TGAAATCGCT	CGTCGCCTCC	GAGTGACTGG	CTATCCAGCT	1200
GAGAAAAATCA	CTGAAACGAG	TAATCTGGAG	CAAGTTCTCA	AGACCATTTGA	GAATCAAGAC	1260
TGCAAGCATG	CCTATATTCT	GGCAACTTAT	ACTGCCATGC	TGGAATTTTCG	TGAACTGCTG	1320
GCTAGTCGTC	AGATTGTTAG	AAAGGAGATG	AACTAA			1356

(2) INFORMATION FOR SEQ ID NO:1034:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

AATTGTAGAA	ATCATCTCCT	AAATGGAGGG	AAAACCGAAA	TGAAATTAAA	TAAATATATA	60
GATCATACGC	TAGGCAAACA	AGATGCACAG	AAAAAACAAA	TTGATAGTTT	GTTGTCTGAG	120
GCTAGAGAAT	ATGACTTTGC	CAGTGTTTGC	GTTAATCCGA	CCTGGGTTGA	ACATGCTAAA	180
AAAGGACTTG	AAGGCACAGA	TGTTAAGGTT	TGCACAGTAG	TAGGTTTCCC	TTTGGGAGCA	240
ACAACTTCAG	CCGTGAAAAGC	ATTTGAGACA	AAAGAAGCTA	TCCAAAATGG	TGCAGATGAG	300
ATTGATATGG	TGATCAATGT	TGGAGCTCTC	AAATCAGGTA	ATTTAGCCTT	GGTTGAGTCA	360
GATATTCGCG	CAGTAGTGGA	AGCAAGTGGT	GATAAGTTAG	TGAAAGTCAT	TATTGAAGCT	420
TGCCTTCTGA	CAGACCAAGA	AAAAATTGTT	GTTTGCCAAT	TGGCCCAAAA	AGCTGGGGCT	480
GACTTTGTTA	AAACATCTAC	TGGCTTTTCA	ACTGGTGGTG	CTACGATAGC	AGATGTTAGA	540
TTAATGCGTG	AAACAGTTGG	ATCTGATATG	GGAGTCAAGG	CTGCTGGTGG	AGCTCGTTCT	600
TATGCAGATG	CTCTTGCCTT	TGTCGAAGCA	GGTGCGACCC	GTATCGGAAC	GTCAGCTGGG	660
GTAGCTATTT	TAAAAGGAGA	ATTGGCAGAT	GGCGACTACT	GA		702

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1029 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

GTTAGTAGAA	ATATGGTTAA	AAAAATTATT	GGAATGGTGC	TAGCTTTACT	TTCTGTAAC	60
GTAGTAGGAG	TAGGTGTTTT	TGCTTATACT	ATTTATCAAC	AAGGGACAGA	AACCTTAGCT	120
AAAACCTATA	AAAAAATCGG	TGAAGAAACC	AAGGTTATTG	AAGCGACTGA	ACCTCTAACC	180
ATTCTGTTAA	TGGGAGTGGA	CACCGGAAAT	GTTGAACGAA	CTGAAACTTG	GGTCGGTAGA	240
AGTGATAGCA	TGATCTTGAT	GACAGTGAAT	CCTAAAACGA	AAAAACAAC	AATGATGAGT	300
TTAGAGCGGG	ATATTCTGAC	GCGCATTGAA	TCAGGGAATG	GTCAGGCTCA	TGAAGCGAAA	360
CTGAACTCAG	CATATGCAGA	TGGTGGAGCA	GAGCTTGCTA	TAGAAACCAT	TCAAAAAATG	420

ATGAATATCC	ATATTGATCG	CTATGTGATG	GTCAATATGA	GAGGGTTGCA	AAAATTAGTG	480
GATGCAGTAG	GAGGTATTAC	AGTCAATAAT	ATCCTAGGTT	TCCCAATTTC	TATCAGTGAC	540
CAAGAAGAAT	TTAATACCAT	TTCTATCGGT	GTTGGGGAGC	AACATATTGG	GGGAGAAGAA	600
GCCCTAGTCT	ATGCACGAAT	GCGTTACCAA	GATCCTGAGG	GGGATTATGG	TCGTCAAAAA	660
CGTCAACGTG	AAGTTATTCA	AAAAGTCATG	GAAAAAGCTC	TCAGTTTAAA	TAGCGTTGGT	720
CATTATCAAG	AGATTCTAAA	AGCTTTGAGT	GACAATATGC	AGACCAATAT	TGATTTGTCT	780
GCAAAAAGTA	TCCCTAACTT	GCTAGGCTAT	AAAGATTCAT	TTAAAACCAT	TGAAACTCAG	840
CAGTTGCAGG	GTGAAGGAGA	GATACTTCAA	GGTGTTCCTT	ACCAGATTGT	TTCGAGAGCA	900
CATATGTTGG	AAATGCAAAA	TATACTCCGA	CGTTCTTTGG	GACAAGAAGA	AGTTACTCAG	960
CTTGAAACCA	ATGCGGTTTT	ATTTGAAGAT	TTATTTGGCA	GAGCACCTGT	TGGTGATGAA	1020
GATAATTAA						1029

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

ATTTTCAGAA	AGGAAAACCT	CAAATTGTTT	TACAAATTTT	TACTCTTCGA	CCTCGACCAC	60
ACTCTTCTTG	ATTTTGATGC	TGCTGAGAA	GTGGCTTTGA	CCCAACTTCT	AAAAGAAGAA	120
GGAGTTGCGG	ATATTCAGGC	TTATAAAGAT	TATTACGTTT	CTATGAACAA	GGCTCTCTGG	180
AAAGACTTGG	AGCTGAAGAA	AATCAGTAAA	CAAGAGCTGG	TTAACACGCG	CTTTTCTCGT	240
TTATTTGCTC	ATTTTGAGCA	GGAAAAAGAC	GGTAGTTTTC	TTGCCCAGCG	TTACCAATTT	300
TACCTCGCCC	AGCAGGGACA	AACACTATCG	GGCGCTCATG	ATCTCTTGGA	CAGCCTCATT	360
GAGCGTGATT	ATAACTTGTA	TGCTGCGACA	AATGGCATT	CTGCCATTCA	GACAGGACGT	420
TTGGCTCAAT	CTGGTCTAGC	ACCTTATTTT	AATCAAGTCT	TTATCTCAGA	ACAGTTGCAA	480
ACTCAAAAGC	CGGATGCTCT	TTTTTATGAA	AAGATTGGCC	AGCAAATTGC	TGGATTTAGT	540
AAAGAAAAGA	CGCTGATGAT	TGGAGATTCT	CTAACC GCCG	ACATTCAAGG	TGGCAATAAT	600
GCGGGGATTG	ACACTATCTG	GTATAATCCT	CATCACCTCG	AAAATCACAC	ACAAGCCCAG	660
CCGACTTACG	AAGTCTATTC	TTACCAAGAC	TTGCTGGATT	GTTTAGATAA	AAATATTCTT	720
GAAAAGATCA	CATTTTAA					738

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

TCAGTCAGAA	ACATCCAACG	GAAGTGCAAG	TTCGACTACC	TTATAAGGAG	AGAAACTAAG	60
ATGAAAGTAT	TAGTCGCAGA	AGATCAAAGT	ATGTTGCGAG	ATGCCATGTG	TCAATTGCTC	120
ACGCTTCAAC	CAGATGTGGA	GTCTGTCCCT	CAAGCCAAGA	ATGGGCAAGA	AGCAATCCAA	180
CTATTAGAAA	AGGAGTCTGT	AGATATCGCC	ATCCTTGACG	TAGAAATGCC	TGTTAAGACA	240
GGTCTTGAAG	TCTTGAGTGT	GATACGATCA	GAAAAGCTTG	AAACAAAGGT	GGTTGTGGTG	300
ACGACCTTCA	AGCGTGCTGG	GTATTTTGAA	CGTGCGGTCA	AGGCTGGAGT	GGATGCTTAT	360
GTATTAAAGG	AACGAAGCAT	TGCAGACCTC	ATGCAAACCT	TGCACACCGT	CCTCGAAGGA	420
CGCAAGGAGT	ATTGCGCTGA	ATTGATGGAA	ATGGTGATGA	CCCGTCCCAA	TCCGTGACA	480
GAACAAGAGA	TTGCTGTCTT	AAAGGGAATC	GCCCGGGGCT	TATCCAACCA	AGAAATCGCA	540
GATCAGCTTT	ACCTCTCAAA	CGGAACTATT	CGAAACTATG	TCACCAATAT	TCTTTCAAAA	600
CTGGATGCTG	GTAATCGAAC	AGAGGCAGCT	AATATCGCAA	AAGAATCTGG	TTGGTTATGA	660

(2) INFORMATION FOR SEQ ID NO:1038:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1296
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GGATCCAGAA	ACAATAATTT	TAAAAAGGAG	AAAAGACACA	TGCACATTTT	TGATGAGCTA	60
AAAGATCGTG	GTTTGATATT	TCAAACGACT	GATGAAGAAG	CTTTGCGTAA	AGCCCTAGAA	120
GAAGGTCAAG	TTTCTTATTA	TACTGGCTAC	GATCCAACTG	CTGACAGCCT	TCACCTAGGC	180
CACCTTGTCG	CAATCTTGAC	AAGTCGTCGC	TTGCAACTAG	CAGGTCACAA	ACCTTATGCG	240
CTCGTTGGCG	GTGCTACAGG	TCTCATCGGA	GATCCGTCCT	TCAAAGATGC	TGAACGTAGT	300

CTCCAAACAA	AAGACACAGT	AGATGGCTGG	GTCAAGTCTA	TCCAAGGACA	ACTTTCTCGT	360
TTTCTTGACT	TTGAAAATGG	CGAAAACAAG	GCTGTCATGG	TCAACAACATA	CGACTGGTTT	420
GGCAGCATCA	GCTTCATTGA	CTTCCTCCGT	GATATTGGAA	AATACTTCAC	GGTCAACTAC	480
ATGATGAGTA	AGGAATCTGT	TAAAAACGG	ATCGAAACAG	GAATTTCTTA	CACTGAGTTC	540
GCTTACCAAA	TCATGCAAGG	GTATGACTTC	TTCGTCCTTA	ACCAAGACCA	TAATGTCACT	600
CTTCAAATCG	GTGTTCTGA	CCAGTGGGGA	AATATGACAG	CTGGTACCGA	ATTGCTTCGT	660
CGTAAGGCGG	ACAAGACTGG	TCACGTTATC	ACTGTTCCAC	TAATCACAGA	TGCAACTGGT	720
AAGAAATTTG	GTAAATCAGA	AGGAAATGCC	GTCTGGCTCA	ATCCCCGAAAA	GACTTCTCCA	780
TACGAAATGT	ACCAATTCTG	GATGAACGTG	ATGGACGCTG	ACGCTGTTCG	CTTCTTGAAA	840
ATCTTTACTT	TCTTGTCACT	TGATGAGATT	GAAGATATTC	GTAAACAATT	TGAAGCAGCG	900
CCACACGAAC	GCTTGGCTCA	AAAAGTCTTG	GCTCGTGAAG	TTGTTACACT	TGTTACCGGA	960
GAAGAAGCCT	ACAAAGAAGC	ACTTAACATC	ACTGAGCAAC	TCTTTGCAGG	AAACATCAAA	1020
AACCTTTCTG	TCAAAGAGCT	CAAACAAGGA	CTTCGTGGTG	TGCCAAACTA	CCAAGTACAG	1080
GCAGACGAAA	ACAACAATAT	CGTGGAAGT	CTCGTCTCAT	CTGGTATAGT	TAACCAAAA	1140
CGCCAAGCCC	GTGAAGACGT	CCAAAACGGA	GCCATCTACG	TAAACGGCGA	CCGCATCCAA	1200
GAGCTTGACT	ATGTCTTGAG	TGACGCTGAT	AAGTTAGAGA	ATGAACTGAC	TGTTATCCGT	1260
CGTGGGAAGA	AAAAATACTT	TGTATTGACT	TACTAA			1296

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

CCTTACAGAA	AGCGGCAACA	AATAATGAAA	ATGTCTACTT	TTTTCAAAAA	AAGTTTCTGG	60
CCAACCTTTA	TGATTGTTAA	CCAAACTGTT	ATACTATTCC	ATCTAAAGGA	TGGCTTGAT	120
CGACAATACC	TAACAACCTGA	GTCCATATAT	TGGGTGATAG	GCACCTTTAT	ATTTGGAAAT	180
ATTCTAGTAG	CTGTGTTTAG	TAATATGAAA	ATTTGGGATA	AAAAGAAAAA	CGGCAGTAAG	240
AAAAAATATA	TCCTGAAAAA	GTAA				264

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

ACTTTAAGAA ATCTTCTCAC TGATAAGATT TTAGCATTAG ACTTCCTGCG AAACAAAATA	60
TGGTATAGTA GTTCTATGAA TTATGAAGCA AGTAAACAAC TAACTGATGC ACGATTTAAA	120
TGTCTTGTTG GTGTTTCAGCG CACCACTTTT GAAGAGATAT TAGCTGTATT AAAAAGTCTT	180
TATCAACTTA AACACACAAA AGGGGGGCGA GAACCTAAAT TAAGCCTAGA AGACCTTCTT	240
ATGGCCACTC TTCAATATGT GCGAGAATAC CGCACTTATG AACAAATTGC GGCTGTTTTT	300
GGTATCCACG AAAGCAACTT ACTCCGTCGG AGCCAATGGG TTGAAGTAAC TCTTGTTCAA	360
AGTATTTTAC AATTTCAAGA ACTCCTCTCA GTTCTGAGGA CACGGTAA	408

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

TTTCTAAGAA ATCAGTCTTT GCCCAGCAGG TTGGACTCAA GGAAGTCGCA AATTACTCTG	60
GGTGAGATTT TCAAGCGTGT TGGAGCTGAA GTGGAGATTG ATGAGAGCTA TACAGCGCCC	120
TTTGTATGAG CACATTTCAA GAGTTCGCGT CCAGATGCCA AGACCTTGAT TTTCTATAAC	180
CACTATGACA CTGTGCCAGC GGATGGGGAT CAGGTCTGGA CAGAGGATCC TTTTACGCTT	240
TCGGTCCGCA ATGGCTTCAT GTATGGGCGT GGGGTTGATG ACGACAAGGG TCATATCACA	300
GCTCGCTTGA GTGCTTTGAG AAAATATATG CAGCACCATG ATGATTTACC TGTCATATC	360
AGCTTTATCA TGGAGGGAGC GGAGGAATCG GCTTCAACAG ACCTAGATAA GTATTTGGAA	420
AAGCATGCAG ACAAACCTCCA TGGGGCGGAT TTGTTGGTCT GGGAAACAAGG GACCAAAAAT	480
GCCTTGGAAC AACTGGAAAT TTCTGGTGGC AATAAGGGGA TTGTGACCTT TGATGCCAAG	540
GTAAAAAGCG CTGATGTGGA TATCCACTCG AGTTATGGTG GCGTTGTGGA ATCAGCTCCT	600
TGGTATCTCC TCCAAGCCTT ACAGTCTCTT CGTGCTGCGG ATGGCCGTAT CTTGGTTGAA	660
GGCTTGATCG AAGAAGTACA TGAGCCCAAT GAACGAGAAA TGGCCTTGCT AGAACTTAT	720
GGTCAACGAA ACCCAGAGGA AGTTAGTCGG ATTTATGGAT TGGAGTTGCC TCTCTTACAG	780

GAGGAGCGGA TGGCCTTTCT AAAACGTTTC TTTTTCGAGC CAGCGCTTAA TATCGAAGGA	840
ATCCAGTCTG GTTATCAAGG TCAGGGTGTT AAGACTATTG TGCCTGCAGA AGCCAGTGCC	900
AAGCTAGAGG TT	912

(2) INFORMATION FOR SEQ ID NO:1042:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...447
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

AATAAAAGAA AGAAGCTGAC AAAGGAGACG GGTATGGAAC ACACATTCTT TATCATCAAA	60
CCAGATGGTG TAAAAAGAGG GCTAGTGGGT GAAGTGTTAA AGCGCATCGA ACAACGTGGA	120
TTTACAATCG AAAAATTGGA GTTTCGTTCA CAGGTTTCAG AAGAGTTGAT TGACCAGCAC	180
TATCAGGACT TGTTTGGTCA GAGTTTTTAC CCACCGATTC GTGAATTCAT GACTTCAGGT	240
CCAGTTCTTG TGGGTGTCAT TTCTGGTCCC AAAGTAATCG AAAGTTGGCG GACCATGATG	300
GGTGCAACTC GTCCAGAAGA AGCTTTACCA GGCATATTC GAGGTGATTT TGCAAAAGCT	360
GCTGGAGAAA ATGAGATTAT CCAAAATGTT GTACATGGTT CAGATTCAGA AGAGTCAGCT	420
AAGCGAGAAA TTGCTCTTTG GTTTTAA	447

(2) INFORMATION FOR SEQ ID NO:1043:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

CAAAAAAGAA	AACAGTTTAC	AAAGAAAAAT	GATGGAGGAG	CAAACATGGC	ACAAAAAGGA	60
GTAAGCCTTA	TCAAGGCAGC	ATTTGATACA	GATAACTTTC	TCATGCGTTT	TAGTGAGAAA	120
GTCTTGGACA	TCGTGACAGC	CAATCTTCTT	TTTGTCTCT	CTTGTTTGCC	CATCGTGACG	180
ATTGGAGTGG	CTAAAATCAG	CCTCTACGAG	ACCATGTTTCG	AAGTTAAGAA	GAGCAGACGG	240
GTGCCTGTTT	TTAAAATCTA	TCTAAGATCT	TTCAAGCAAA	ATCTGAAACT	AGGTCTTCAG	300
CTGGGTTTAA	TGGAGTTAGG	AATTGTGTTT	CTTACCCTTT	CAGATCTCTA	TCTTTTCTGG	360
GGTCAAACAG	CTCTGCCCTT	CCAATTGCTG	AAAGCCATTT	GTTTAGGTAT	TCTGATTTTT	420
CTTACTATCG	TGATGCTGGC	TAGTTACCCT	ATCGCGGCAC	GTTATGACCT	ATCTTGGAAA	480
GAAATTCTTC	AAAAAGGATT	GATGTTGGCT	AGTTTTAACT	ATCCCGCTCT	TCACCACGAA	540
TGGAAC						546

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

AAAAAAAGAA	AGATTTGGCC	AGCCAGGTTT	TTGATAATAA	TGGCAATCAG	AACCAGCTTC	60
TTAATCAAGT	GCATATCCTT	CTTGAGGGAG	GTAGGCAAGA	TGACAGAGAT	TAACTGGAAG	120
GATAATCTGC	GTATTGCCTG	GTTTGGTAA	TTTCTGACAG	GAGCCAGTAT	TTCTTTGGTT	180
GTACCTTTTA	TGCCCATCTT	CGTGGAAAAT	CTATGTGTAG	GGAGTCAGCA	AGTCGCTTTT	240
TATGCAGGCT	TAGCAATTTT	TGTCTCTGCT	ATTTCCGCGG	CGCTCTTTTC	TCCTATTTGG	300
GGTATTCTTG	CTGACAAATA	CGGCCGAAAA	CCCATGATGA	TTCTGGGCAG	GTCTTGCTAT	360
GAATATCACT	ATGGGAGGCT	TGGCCTTTGT	CCCAAATATC	TATTGGTTAA	TCTTTCTTCG	420
TTTACTAAAC	GGTGTATTTG	CAGGTTTTGT	TCCTAA			456

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

TATCGAAGAA	AAGGAATAAG	AAAGAATATG	GCTAACGTAA	TTATTGAAAA	AGCTAAAGAG	60
AGAATGACCC	AGTCTCACCA	ATCACTTGCT	CGTGAATTTG	GTGGTATCCG	TGCTGGTCGT	120
GCCAATGCAA	GCTTGCTTGA	CCGTGTACAT	GTAGAATACT	ATGGAGTCGA	AACTCCTCTT	180
AACCAAATCG	CTTCAATTAC	GATTCCAGAA	GCGCGTGTTT	TGTTGGTAAC	ACCATTTGAC	240
AAGTCTTCAT	TGAAAGACAT	CGAACGTGCC	TTGAACGCTT	CTGATCTTGG	TATCACACCG	300
GCTAATGACG	GTTCTGTGAT	TCGCTTGGTT	ATCCCAGCTC	TTACAGAAGA	AACTCGTCGT	360
GACCTTGCTA	AAGAAGTGAA	GAAGGTCGGC	GAAAATGCTA	AAGTGGCTGT	CCGCAATATC	420
CGTCGCGATG	CTATGGACGA	AGCTAAGAAA	CAAGAAAAAG	CACAAGAAAT	CACTGAAGAC	480
GAATTGAAGA	CTCTTGAAAA	AGATATTCAA	AAAGTAACAG	ACGATGCTGT	TAAACACATC	540
GACGACATGA	CTGCTAACAA	AGAGAAAGAA	CTTTTGGAAG	TCTAA		585

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GGAGGAAGAA	AGATGAAATC	AAAAGAAGAA	ATAAATATGC	TTGGTTTTAC	AATTGTCGCT	60
TACGCAGGAG	ATGCAAGGTC	AGATTTGATG	GATGCTTTGG	CGTTTGCGAG	AGATGGATAT	120
TTTGAACAGG	CAAGAGAAAT	GGTTGAGTCT	GCAAACGACT	CAATAGTGTC	TGCCCATCGA	180
GAACAGACTA	ATTTATTAGC	GGAGGAGGCA	TCTGGAGATA	ATTTTGAAGT	GAGTTTTTATC	240
ATGATTTCATG	GTCAGATAC	TTTGATGACA	ACGATGCTAT	TGTATGATCA	GGTCAAGTTT	300
TTTATTGATG	AATATGAACG	AATTCGAAAG	ATTGAAGAAC	ATATTGGTTT	GCAATGA	357

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

AATAAGAGAA	AGAACTCTAT	CAAGGAGGAA	ATCATGGAAA	AACAAACCGT	CGCCGTCTTG	60
GGGCCTGGTT	CTTGGGGAAC	CGCCCTTTCA	CAAGTCTTAA	ATGACAATGG	ACACGAGGTA	120
CGTATTTGGG	GAAATCTTCC	CGAGCAAATC	AATGAAATTA	ATACACACCA	TACTAATAAG	180
CACTACTTTA	AAGATGTCGT	TCTAGACGAA	AATATCATTG	CCTACACCGA	CTTAGCAGAA	240
ACATTGAAAG	ATGTGGATGC	GATTTTGTTT	GTTGTCCCAA	CAAAAGTGAC	ACGACTTGTT	300
GCCCAACAAG	TTGCACAAAC	CTTGGACCAT	AAGGTTATCA	TCATGCACGC	ATCAAAGGGA	360
TTAGAACCTG	ATAGCCATAA	ACGATTATCA	ACCATTCCTG	AAGAAGAAAAT	TCCTGAACAT	420
CTCCGTAGTG	ATATCGTCGT	TGTTTCAGGG	CCTAGTCATG	CAGAAGAGAC	CATTGTGCGT	480
GACCTAACTT	TAATAACTGC	TGCTTCTAAA	GATTTACAAA	CAGCTCAATA	CGTTCAGGAG	540
CTATTTAGTA	ATCACTACTT	CCGACTTTAT	ACCAATACGG	ATGTTATCGG	GGTTGAAACT	600
GCTGGTGCTC	TTAAAAATAT	TATTGCTGTC	GGTGCTGGAG	CTTTACATGG	TCTTGATTTT	660
GGTGATAATG	CTAAGGCAGC	CATCATCGCT	CGAGGTTTAG	CAGAAATCAC	CCGCCTAGGG	720
GTAGCACTCG	GGGCCAGTCC	ATTGACCTAT	AGCGGCTTAT	CTGGTGTGGG	AGATTTGATC	780
GTAACGGGAA	CTTCCATCCA	CTCTCGTAAC	TGGAGAGCTG	GAGATGCTCT	CGGACGAGGA	840
GAATCCTAG						849

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG AAGTCTTTAT GAGGGAGGCT	60
TTGAGAGAGG CTGAGATTGC TCTTGAACAC GATGAAATTC CAATTGGTTG TGTGATTGTC	120
AAAGATGGGG AAATCATTTG TCGTGGGCAT AATGCGCGTG AGGAATTACA GCGAGCGGTT	180
ATGCATGCCG AAATTATGGC TATAGAGGAT GCGAACTTGA GTGAGGAGAG CTGGCGCTTG	240
CTGGATTGCA CACTTTTTGT GACCGTCCAA CAC	273

(2) INFORMATION FOR SEQ ID NO:1049:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

AAAGAGAGAA AGATGGTCTA TTTAGTCCTA GGAATTTTAC TGCTCCTACT CTATGTATTT	60
GCGACACCAG AAAGCATTAAG AGGGACAGTC AATATCGTCG CTATGGTATG TATTTTAGTG	120
GCACTCTTGA TTTTATTGGT TCTATCTTTT CTGAAAATTT TTCAATTACC AACAGAAATA	180
TTCTAGCAA TAGCCATGTT GATCCTAGCT TACTTTAGTG TTAGAGACAT TACTCATG	240
CCAGTCAAAA AAAGTAAAAG AAGATAA	267

(2) INFORMATION FOR SEQ ID NO:1050:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

GCAAGGAGAA	AATTGACTAC	GAACAAGAAC	TCCCGTATCC	AGGCAGAGAA	AGAACGCAAG	60
AAGAGGGATA	AAATCGCCAA	GCAATATGCA	GACAATCTGG	TTCTAGCCAT	GGGACCCGCA	120
GAGCGTGCTT	ATCAAGATTA	CTTTGGCTTT	ACAGAGACCC	TGACTCAAGA	AGAACGCAAG	180
TGGGAAAAAA	TTCTTTTTTG	TAAAAATAGA	GCAGAACGGG	CTATCAAGGC	CAAACAATAC	240
CAAAAAGAGC	TGGAAAAAGA	CCAACGAATT	GCCAGTCAGG	ATCCAATTGA	AAGAAAACAG	300
AAACAGACTT	GGCTCCTCAA	TTCTATTTTT	CGTGAGCTTC	CTGAAGAAAA	AGCTCGATTT	360
TCTAGGCTCT	TATTAGAATA	TCGAAAAAAT	GGTGAAGTAC	CCTTTTCAAC	TGAATACCTG	420
TCAGATCATC	TCATCGACTT	TTTCTATAAA	ATGAAAGCCT	TTGAATTTGA	AATCGCACCA	480
GAACAAGTCC	GAGATTTTCT	AAAAAAAAGC	CTGCAGGAAG	ACTATCGCTC	ATCAGCACAA	540
GGAAGCTGGA	TAGAAGGAAT	TCTCCTCAAC	TGCCTCAAAC	CATTTTTTAGA	ACGATTAGTG	600
ATATGA						606

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

AAAAGGAGAA	ATAAAATGGT	TAAAGTATTA	GCAGCGTGCG	GAAATGGAAT	GGGTTCATCA	60
ATGTTTATCA	AGATGAAGGT	TGAAAATGCT	CTCCGTAAGC	TTAATCAAAC	AGATTTTACA	120
GTCAATTCAT	GCAGTGTCGG	TGAAGCTAAA	GGTTTAGCAG	TAGGATATGA	CATCGTAATC	180
GCTTCTCTTC	ATTTGATTCA	AGAATTGGAA	GGGCGAACTA	ATGGGAAGTT	AATTGGGCTT	240
GATAACTTGA	TGGATGATAA	AGAAATCACC	GAAAACTCA	GTCAAGCACT	ACAGTAA	297

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

AAGGAGAAAG	AAAATGAAAA	AATTTGTTGC	TGAGTTAATC	GGTACGTTCA	TGCTTGTATT	60
CGTCGGGACA	GGAGCTGTTG	TTTTTGGA	TGGTCTTGAT	GGCCTTGGTC	ACCTTGGAAT	120
CGCCTTTGCC	TTTGTTTGG	CAATCGTGGT	GGCAGCCTAC	TCAATCGGAA	CTGTTTCAGG	180
TGCTCACTTG	AACCCGGCTG	TTTCGATTGC	TATGTTTGTA	AACAAACGTT	TGTCATCTTC	240
AGAACTTGTA	AACTACATCC	TTGGTCAGGT	TGTTGGAGCT	TTCATCGCTT	CTGGCGCTGT	300
CTTCTTCCTC	TTGGCTAACT	CAGGTATGTC	AACTGCTAGT	CTTGGTGAAA	ATGCCTTGGC	360
AAACGGTGTC	ACTGTCTTTG	GTGGTTTCTT	GTTTGAAGTC	ATCGCAACTT	TCTTGTTTGT	420
ATTGGTTATC	ATGACTGTGA	CTTCAGAAAG	CAAGGGCAAT	GGCGCGATTG	CTGGTTTGGT	480
AATCGGTTTG	TCATTGATGG	CGATGATTCT	TGTCGGATTG	AAGATTACTG	GACTTTCAGT	540
AAACCCAGCT	CGTAGCTTGG	CACCAGCTGT	CTTGGTAGGC	GGCGCAGCCC	TTCAACAAGT	600
TTGGATTTTC	ATCCTTGAC	CAATCGCTGG	TGGAGTTCTT	GCAGCCCTTG	TTGCAAAAAA	660
TTTCCTTGGA	ACAGAAGAAT	AA				682

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

TACAAATGGAA	AAAATAAAAT	CAAAAGGAGT	TTTTTTATGA	CTTATCCAAA	TCTCTTGGAC	60
CGCTTCTTAA	CCTATGTTAA	GGTCAACACG	CGCTCTGATG	AACACTCTAC	TACTACTCCA	120
AGTACACAGA	GTCAGGTTGA	CTTCGCAACA	AATGTCCTAA	TTCTGAAAT	GAAACGTGTT	180
GGACTGCAAA	ATGTTTACTA	TCTACCGAAT	GGTTTTGCTA	TTGGAACCTT	GCCAGCCAAC	240
GATCCGTCTT	TAACACGTAA	GATTGGTTTT	ATATCGCACA	TGGATACTGC	TGATTTTAAAT	300
GCTGAAGGAG	TCAATCCACA	GGTAATTGAA	AACTACGATG	GTGGTGTGAT	TGAACTAGGG	360
AATTCTGGTT	TCAAACTCGA	TCCAGCTGAC	TTCAAGAGTC	TTGAAAAATA	TCCAGGACAA	420
ACGCTCATCA	CAACAGATGG	AACAACCTTG	CTAGGTGCTG	ATGACAAGTC	AGGAATTGCT	480
GAAATTATGA	CAGCCATTGA	ATATCTAACT	GCTCATCCTG	AAATTAAGCA	CTGTGAGATT	540
CGTGTGTTGG	TTGGTCCAGA	TGAAGAAATC	GGTGTGTTGG	CCAATAAAAT	TGATGCAGAA	600
GATTTTGATG	TGGATTTTGC	CTACACTGTT	GATGGTGGTC	CACTAGGTGA	ACTTCAGTAC	660

GAGACTTTCT	CAGCCGCTGG	TGCTGAATTG	CATTTCCAAG	GCCGTAATGT	CCACCCCTGGT	720
ACTGCCAAAG	GGCAGATGGT	CAATGCCCTT	CAGCTAGCAA	TTGATTTTCA	TAATCAACTT	780
CCAGAAAATG	ACCGACCTGA	GTTAACTGAA	GGTTACCAAG	GTTTTTACCA	TCTAATGGAT	840
GTGACAGGTA	GTGTTGAGGA	GGCGCGTGCA	AGCTACATCA	TTCGTGATTT	TGAAAAAGAT	900
GCCTTTGAAG	CGCGTAAAGC	ATCCATGCAA	TCTATCGCTG	ATAAGATGAA	TGAAGAACTT	960
GGGAGCAACC	GTGTCACCTC	CAACTTGACA	GACCAGTACT	ACAATATGAA	AGAAGTCATT	1020
GAAAAAGATA	TGACTCCAAT	TACCGTTGCT	AAAGCCGTTA	TGGAAGATCT	AGGTATCACG	1080
CCTATTATCG	AACCAATCCG	GGGTGGAACA	GACGGCTCTA	AGATTTCCCT	TATGGGAATC	1140
CCAACCTCCG	ATATCTTTGC	AGGTGGCGAA	AATATGCACG	GACGTTTTGA	ATACGTTAGC	1200
CTTCAGACTA	TGGAACGTGC	AGTTGATACC	ATCATTGGCA	TCGTAGCTTA	TAAAGGCTAA	1260

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

GAGGATGGAA	ACATGAAAAA	AAATAGTTTA	TATATCATAT	CCTCACTCTT	TTTTGCTTGT	60
GTCTTATTTG	TCTATGCTAC	GGCGACGAAT	TTTCAAAACA	GTACCAGTGC	TAGGCAGGTA	120
AAAACGGAAA	CCTATACTAA	TACAGTAACA	AATGTCCCCTA	TTGACATACG	CTATAATAGT	180
GATAAGTATT	TTATTAGCGG	TTTTGCTTCA	GAAGTATCAG	TGGTCTTGAC	TGGTGCAAAT	240
CGCCTATCGC	TAGCTAGTGA	AATGCAAGAA	AGTACACGTA	AATTCAAGGT	TACTGCTGAC	300
CTAACAGATG	CCGGTGTTGG	AACGATTGAA	GTTCCCTTTGA	GCATTGAAGA	TTTACCCAAT	360
GGGCTGACCG	CTGTGGCGAC	TCCGCAAAAA	ATTACAGTCA	AGATTGGTAA	GAAGGCTCAG	420
AAGGATAAGG	TAAAGATTGT	ACCAGAGATT	GACCCTAGTC	AAATTGATAG	TCGGGTACAA	480
ATTGAAAAATG	TCATGGTGTC	AGATAAAGAA	GTGTGATTTA	CGAGTGACCA	AGAGACATTG	540
GATAGAATTG	ATAAGATTAT	CGCTGTCTTG	CCAAC TAGCG	AACGTATAAC	AGGTAATTAC	600
AGTG GTTCAG	TACCTTTGCA	GGCAATCGAC	CGCAATGGTG	TTGTCTTACC	GGCAGTTATC	660
ACTCCGTTTG	ATACAATAAT	GAAGGTGACT	ACAAAACCAG	TAGCACCAAG	TTCAAGCACA	720
TCAAAATCAA	GTACAAGCAG	TTCATCGGAG	ACATCTTCGT	CAACGAAAGC	AACTAGTTCA	780
AAAACGAATT	AA					792

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

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AATAAAGGAA AAGGAGAAAAG AAGAATGAAA GTAATCTTTT TAGCAGATGT TAAAGGAAAA    60
GGTAAAAAAG GCGAAATTAA GGAAGTACCA ACAGGGTATG CGCAAAACTT TCTTATCAAA    120
AAGAATCTAG CCAAAGAAGC GACTGCTCAA GCTGTAGGTG AACTTCGTGG TAAACAAAAA    180
TCGGAAGAAA AAGCTCACGC TGAGATGATT GCAGAAGGAA AAGCAATTAA AGCACAACTT    240
GAAGCAGAAG AAAGTGTGTT AGAATTTGTT GAAAAAGTTG GTCCAGATGG TCGTACCTTT    300
GGTTCTATTA CCAATAAGAA GATTGCAGAA GAATTGCAAA AGCAATTTGG AATTAAGATT    360
GATAAACGTC ATATTCAAGT ACAAGCTCCG ATTCGAGCGG TTGGTTTGAT TGATGTGCCA    420

GTGAAAATCT ATCAAGATAT CACAAGTGTA ATCAATCTTC GTGTGAAAGA AGGATAA      477

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(2) INFORMATION FOR SEQ ID NO:1056:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

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TTGAAAGGAA ATACCATGGA GGAACAGTCG GAAATAGTCC GTTCTAAGAA AGAATTCGCC    60
TTTGCACTCTA GCACTATACT ATCCCAAGTT GGTCGAGGAA TCATTGTCGG CCTCATCGTT    120
GGAATTATCG TCGGATCCTT TCGTTTCTTA ATTGAAAAGG GATTCCACCT GATACAAGGA    180
GTTTATCAAG ATCAAGGGTA CTTAGTGCGC AATCTTTTGT TACTGGTTTT GTTTTATATA    240
CTCATCTGTT GGCTCAGTGC CAAACTAACA CGGTCAGAAA AAGATATTAA AGGCTCAGGA    300
ATTCTCAAG TCGAAGCCGA ACTGAAAGGC CTCATGTCCC TCAACTGGTG GGGCATTCCT    360
TGGAAAAAAT ATGTGCTAGG TATTCTTGCT ATTGCCAGTG GACTCATGCT GGGTCGAGAA    420
GGACCCAGTA TTCAACTTGG AGCAGTTGGT GGTAAAGGAA TTGCCAAGTG GCTCAAATCC    480

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AGTCCAGTAG	AGGAACGTTT	CTTGATTGCC	AGTGGAGCTG	CAGCAGGTTT	AGCCGCAGCC	540
TTTAATGCTC	CTATTGCAGC	ACTTCTCTTT	GTTGTAGAAG	AAGTCTATCA	CCATTTTTCG	600
CGCTTTTCT	GGGTCTCAAC	TCTAGCAGCC	AGCATCGTAG	CAAACTTTGT	GTCTCTACTC	660
ATGTTTCGGT	TGACACCAAT	ATTGGATATG	CCAGATAACA	TTCCCTCCCAT	GACCCTAGAT	720
CAGTATTGGA	TATATCTCGT	CATGGGAATT	TTCCCTGGAT	TTTCAGGTTT	TCTCTATGAG	780
AAAGCTGTAT	TAAACGTTGG	AAGAGTTTAT	GACTTGATTG	GTCAAAAAAT	CCATTTGGAT	840
AGGGCTTATT	ATCCCATCTT	GGCTTTTATC	CTTATCATAC	CAGTCGGAAT	CTTCTTACCT	900
CAAATCCTTG	GTGGCGGAAA	TCAGCTTGTC	CTTTCTTTAA	CTGAACAAAA	TTTTAGTTTT	960
CAAGTTTTAT	TAGCTTACTT	TTTGATCCGC	TTTATTTGGA	GTATGATTAG	CTATGGAAGT	1020
GGACTGCCAG	GAGGAATTTT	CCTCCCCATT	TTAGCTCTTG	GTTCTTTGCT	TGGTGCCTTA	1080
GTTGGTGTTA	TCTGTGTCAA	TCTTGGACTT	GTCAGTCAAG	AGCAATTCCC	TATATTTGTC	1140
ATTCTAGGAA	TGAGTGGCTA	TTTTGGATCC	ATATCAAAAG	CTCCCTTAAC	CGCTATGATC	1200
CTCGTAACTG	AGATGGTAGG	AGATATTTCG	AACCTCATGC	CACCTGGTCT	TGTCACCTCT	1260
GTTTCTTATA	TTATCATGGA	TTTGCTCAAA	GGTACGCCAG	TCTATGAAGC	CATGCTGGAA	1320
AAAATGCTTC	CAGAAGAAGT	ATCTAGCGAA	GGAGAAGTTA	CACCTATCGA	AATACCAGTT	1380
TCTGATAAAA	TTGCTGGGAA	ACAAGTTCAT	GAACCTCACT	TACCACACAA	CGTCCTCATC	1440
ACAACTCAAG	TCCATAATGG	CAAGAGCCAA	ACAGTTAACG	GCTCAACCAG	AATGTATCTG	1500
GGTGATATGA	TTCACCTGGT	TATTCCAAAA	AGTGAAATTG	GAAAAGTCAA	AGATTTGTTG	1560
TTGTAG						1566

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

GTAGGAGGAA	ACATGAAAGC	AGAAATCATT	GCTGTTGGAA	CAGAGATTTT	GACAGGACAG	60
ATTGTCAACA	CCAATGCCCA	GTTTTTGTCG	GAAAAACTAG	CTGAGATTGG	GGTAGATGTA	120
TATTTTCAGA	CGGCTGTAGG	AGACAATGAA	GTTCGTCTCT	TGTCTTTGCT	TGAGATTGCC	180
AGTCAACGTA	GCACTCTGGT	GATTTTGACA	GGCGGTTTGG	GGCCAACTGA	GGACGACCTA	240
ACCAAACAAA	CCCTAGCTAA	ATTTTTAGGG	AAAGCATTAG	TCTTTGATCC	TCAGGCTCAG	300
GAGAAAGTTG	ATATCTTTTT	TGCCCTGCGA	CCAGACTATG	CCCGAACACC	GAATAACGAA	360
AGACAAGCTC	AAATTGTTAG	AGGAGCGATT	CCACTGCCAA	ACGAAACAGG	ACTGGCTGTT	420
GGAGGAAAAA	TAGAAAGTAG	CGGAGTGACC	TATGTCGTCC	TTCCAGGTCC	GCCAAGTGAA	480
TTGAAACCCA	TGGTCTTAAA	CCAACCTTCT	CCCAAGTTGA	TGACAGGGAG	CAAGCTGTAT	540
TCCCGAGTTC	TTCTGTTCTT	TGGGATTGGC	GAGAGCCAGC	TGGTTACGAT	TTTGGCTGAT	600
TTAATTGATA	ATCAGATCGA	TCCTACCTTG	GCCCCCTTAT	CCAAGACAGG	AGAAGTCACT	660
CTACGTCTGT	CAACAAAGGC	TAGCAGTCAA	GAAGAGCGCA	ATCAAGCGCT	GGATATCTTG	720
GAAAAATCAA	TCTTGGACTG	CCAGACTTTC	GAAGGAATTT	CTTTACGAGA	CTTTTGCTAT	780
GGTATATGGG	AAGAAACTAG	TTTAGCCAGC	ATTGTGGTAG	AAGAACTGAA	AAGGCAAGGG	840

AAAACCATCG	CGGCTGCAGA	GAGTTTAACG	GCAGGTCTTT	TCCAAGCTAC	CGTGGCGAAT	900
TTTCTGGAG	CTTCAAGTAT	ATTTAAGGGT	GGTTTGTGA	CCTATAGCTT	GGAGGAAAAA	960
TCAAGGATGT	TGGATATTCC	TGCCAAGAAT	TTGGAAGAAC	ATGGTGTGGT	GTCTGAATTT	1020
ACAGCTCAGA	AGATGGCTGA	GCAGGCACGA	AGCAAGACCC	AGTCTGATTT	TGGAATTAGT	1080
TTGACCGGAG	TGGCAGGACC	AGATAGCCTA	GAAGGACACC	CAGTTGGGAC	AGTCTTCATA	1140
GGCTTGGCGC	AAGAGCAAGG	AACTGAGGTT	ATCAAGGTTA	ATATTGGAGG	CAGAAGCCGA	1200
GCAGATGTAC	GTCATATTGC	GGTTATGCAT	GCCTTTAACC	TAGTTCGCAA	GGCTTTATTA	1260
AGTGACTAA						1269

(2) INFORMATION FOR SEQ ID NO:1058:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

AAGATGGGAA	AAAAGAAGGA	AAATCAAATA	GAGAAATTGC	CTCTCTACTT	GGAAAAAGCTC	60
CTCAAACTAT	CCATACTGAA	ATCAAGTATG	GGACAGTCCG	AAAATGTCTT	GGAAAAAGGGC	120
GCTTCAAAGA	GGTTTATTCT	GCCGACTATG	CTCAACAGTC	TTATGAAAAAT	AATCGCAAGC	180
ACTCGGTCAA	GAGATCAAGC	TTGA				204

(2) INFORMATION FOR SEQ ID NO:1059:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

GTTGGGGGAA AGAGTAGAGC CTTTATCCTG GCAGAAGGTA CAAGAATGGG GCATATTCAT	60
CTTTCCGTCA AGGATAGTCG AAAGTCCAGC CAGTTTTATC AAAAGGTGTT AGGGCTAGAG	120
AATAAATTCA GTGTGCCTGG CGCTAGTTGG ATTGCGGCTG GAGATTACCA TCATCATTTA	180
GCAGTTAACG AATGGGGAGG AAAAGGTCTG GCTTCGCGTA AGCAAGGCTT ACCAGGTTTA	240
GCCTAN	246

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

AAACAGTGTT TTGAGCAACC TGCGGCTAGC TGCCTAGTTT GTTCTTTGAT TTTCATTGAG	60
TTTCACTCCA CTGTGACTTA TGGTCAGATG CTGATACTTT TATTCTTTTA TGCAATATCA	120
AATTTTAACT GGCCTGCTTT GACACCAATC TTAAGTGTGC TGCCTGCCAC TAAATCTCCC	180
TTAAGAAGAA GTTCTGCCAA CTTGTCTCTC ACTTCTGTTT GCAGGGTTCT GCGAAGTGGG	240
CGAGCTCCCA TCTCTGGGTC ATATCCTTGA	270

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

GGAGAGTGTT	TGGGTATCTT	GGGAATCAAC	GGTGCTGGCA	AAACATCCAC	TTTAAAGATG	60
ATTTACTCAC	TGACCTCAAT	TTCCTCAGGA	GAGATTGATA	TCTTGGGGCA	AAATATTGAA	120
ACCAATCGTC	GTAAGAGTAA	ATCTTGCTCG	GGTATTGTAG	GGCAGGAGGA	TATGCTGGAC	180
ATGACCTTGA	ATGTTTATGA	TAATCTTTTT	GCTCACGGTC	TATGTTATGG	TATCTCATCT	240
GTCGAACTTA	GGAAGAGAAT	CGATTCTCTC	TTGGATTTTG	TTCAACTGAG	CAAACATGCG	300
CAAAAGATGG	TGAATCAGCT	GTCGAGTGGG	ATGCGACGAC	GTCTTGTCTT	GGCAAGAGCT	360
CTCATCAATC	GACCTGATAT	TATCATTTTA	GATGAACCGA	CAGTTGGTTT	AGACATTCAA	420
TCCCGCAATA	TTATTTGGGA	TAAACTTTTG	GAGTTGAAGG	AATTAGGTGT	TTCCATCATT	480
ATTACTTCCC	ACTATATGAA	TGAGATTGAA	TATTTGACAG	ATAGGGTGCT	GATGCTCCAC	540
CAAGGGACTA	TCAAAGAAGA	AGGAACTGTA	GAAGACTTGC	TCATCAAGTA	TGATGCTGAC	600
AACCTTGAGA	CGCTTTTTTT	GGGTTGACT	GGGACAGAGA	AGGAGGACTT	GCATGTTTAA	660

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

AGTTCTTTGA	AAATTTTTTC	ATCTTTCAAT	ATTAATGCAC	GATCAGTTTT	CGAGGCCAAT	60
TCTATATCGT	GCGTTACCAT	AATTACACAC	TTACCCGCCC	CTACTAACTC	TCTCAATAAA	120
TCAAAAATTA	CTTCACGAGA	AACGCTGTCT	AAAGCACCAG	TTGGCTCATC	AGCAAATATT	180
ATATCACTAT	CAGCAATAAA	CGCTCTAGCT	ATAGCAACCT	TCTGTTGTTC	TCCACCAGAC	240
AGAGTTCCAA	CAAAATCGTT	TAAGCCAGCA	TTAAACTTCA	TTCTTTTGAG	TAAGTTTTCT	300
ACATTTTTAA	TAGTTAATTT	TTTTTGTGAT	AATCGCAAAG	GAAGTGCTAT	ATTTTCTATT	360
ACCGGCAGGG	AAGGTATTAA	ATTATATGCT	TGA			393

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

AAAAC'TTTGA	AAGAAAGAAA	AAAGATGAAT	TTAAAAGATT	ACATTGCAAC	AATTGAAAAT	60
TATCCAAAGG	AAGGCATTAC	CTTCCGTGAT	ATTAGTCCTT	TGATGGCTGA	TGGAAATGCT	120
TATAGCTACG	CTG'TTCGTGA	AATCGTTCAG	TATGCTACTG	ACAAGAAAAGT	CGACATGATC	180
GTGGGACCTG	AAGCTCGTGG	ATTTATCGTG	GGTTGTCCAG	TTGCC'TTTGA	GTTGGGAATT	240
GGTTTTGCGC	CTG'TTCGTAA	GCCAGGTAAA	TTGCCACGTG	AAGTTAT'TTC	TGCTGACTAT	300
GAAAAAGAGT	ACGGTGTCGA	TACCTTGACT	ATGCACGCGG	ATGCCAT'TAA	GCCAGGTCAA	360
CGTGTTC'TTA	TTGTAGATGA	CCTTTTGGCG	ACAGGTGGAA	CTGTTAAGGC	AACTATCGAG	420
ATGATTGAAA	AACTTGGTGG	TGTTATGGCA	GGTTGTGCCT	TCCTTGT'TGA	ACTGGTTGAA	480
TTGAACGGCC	GTGAAAAAAT	TGGTGACTAC	GACTACAAAG	TTCTTATGCA	TTATTAA	537

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

CGAAGTTTGA	ATTGGATTTT	CGCAGAGTGT	AAATTGTTGA	AACTAGGTTG	TCATACCATG	60
TATACCACTT	GGGCTTTAGT	AGTAGCTAAC	TGCACTAAAT	ATAATATAAG	GAGGGTTTTA	120
TGGGGAAAGG	CCATTGGAAT	CGGAAAAGAG	TTTATAGCAT	TCGTAAAGTTT	GCTGTGGGAG	180
CTTGCTCAGT	AA					192

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

CGTGGTTTGA AGAGATTTTC GAAGAGTATT AGAAGAAAAA GAATGAAAGA AATAGCCTTT	60
GACGCATTTT ACCAGCTTTA CCAAAACGAC CAGCTTTCTT TAGTGATGT GAGAGAAAGTG	120
GATGAGTTTG CAGCTCTTCA TTTAGAAGGT GCCCACAACC TACCGCTTAG TCAATTGGCT	180
GATAGTTATG ATTAA	195

(2) INFORMATION FOR SEQ ID NO:1066:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

CGTGGTTTGA AGAGATTTTT GAAGAGTATT AATAAAGGTG TACAAGAAGT GAGATTAATT	60
TTGTATGAAA AACAAGGAGA GAAATTTATG AAAGTAGAAC TACAGATTAG TGAGACTTAC	120
GAGGAGGAAA AGCTGATTGT CCAAGCACCT CAGCCGACAG ATAAAGTCCA GAAAGTCATC	180
GAGTTCGCAG AAAATCTGGA CCAAAGAGAA AAAATCAAAG GGAAAAGCGA TGATCAGGTC	240
TATCTAGTTG AGATTGGCAA GATTCAGCGC TTCTATATCG AGAATCGGAA GGTTCAGCA	300
GAAACCGCGA GTCAGACCTA CAGCATTGAT TTGCGACTCT ATCAGGTTCC TAAACTCTTG	360
CCAAGCAATT TTATCCAAAT TTCCCAATCA GAAATCATCA ATATCGATTG CATCTCTCAC	420
CTCAAGCTCA CGCCAAACGG TCTGGTAGAA ATTTTCTTGA AAAACGAAAG CTTCACCTAC	480
TCTTCACGCC GTTATCTAAA AACCATCAAG GAGAAATTAG AACTATGA	528

(2) INFORMATION FOR SEQ ID NO:1067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...420
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

CGCGGTTTGA	AGAGATTTTC	GAAGAGTATA	ATACTAGACT	CAAATCAAAA	AGCATTATAC	60
AATAGTAATA	TGAAATCAAC	TAAAGAAGAA	ATCCAAACCA	TCAAAACACT	TTTAAAAGAC	120
TCTCGTACAG	CTAAATATCA	TAAACGCCTT	CAAATCGTTC	TATTTCTGCT	GATGGGCAAA	180
TCTTATAAAG	AGATTATAGA	GCTTTTAGAC	TGTAATCAAA	CAACGATTG	GCGAAATGTA	240
AAAAAATATG	AGGAGTTCGG	ACTCGACTCT	CTCCTTCAAG	AAACACGTGG	TGGTCGTAAC	300
CATGCATATA	TGACAGTTGA	GGAAGAGAAA	GCCTTTCTTG	CCCGCCATTT	GAAGGCTACA	360
GAGGCAGGAG	AATTTGTTAC	AATACCTTAT	TTCAGGCTTA	TATCGTTCCT	ACACACGTGA	420

(2) INFORMATION FOR SEQ ID NO:1068:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 687 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...687
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

CGCGGTTTGA	AGAGATTTTC	GAAGAGTATT	AGTACATTCT	TTGAGATTGG	AGCTAGTATG	60
AAAATCCATA	AAACCGTGAA	TCCTGTTGCC	TATGAAAATA	CCTATTATCT	AGAAGGCGAA	120
AAGCACCTCA	TCGTCGTCGA	TCCTGGTAGT	CATTGGGAAG	CCATTCGTCA	GACAATCGAG	180
AAGATCAACA	AACCGATCTG	TGCTATTCTC	TTGACCCACG	CCCATTATGA	CCATATCATG	240
AGTCTGGACT	TGGTTCGCGA	GACGTTTGGC	AATCCTCCTG	TCTATATCGC	AGAGAGCGAA	300

GCCAGCTGGC	TCTACACTCC	TGTCGATAAT	CTCTCCGGTC	TCCCTCGCCA	CGATGATATG	360
GCAGATGTGG	TCACAAAACC	TGCAGAACAC	ACCTTTGTCT	TTCACGAAGA	ATACCAACTA	420
GAGGAATTTT	GTTTTAAGGT	TCTACCGACC	CCAGGGCACT	CTATCGGTGG	TGTTTCCCTA	480
GTCTTTCCTG	ATGCTCACCT	AGTCTTGACG	GGAGATGCTC	TATTCCGCGA	AACTATCGGA	540
CGGACCGACC	TTCCGACTGG	TAGCATGGAG	CAACTCCTTC	ATAGTATCCA	GACCCAACTC	600
TTCAACCCTAC	CAAACCTACG	TGTCTATCCA	GGACATGGTC	CAGCTACTAC	TATCGCTCAC	660
GAAAAGGCCT	TCAATCCCTT	TTTTTAG				687

(2) INFORMATION FOR SEQ ID NO:1069:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

GTTCTCTTGA	AGTTTTTTTGT	AAGCCAGATC	AATTGCTGGC	AGAGGTGCAT	GAGAAGGGGG	60
GCCCATCAGC	TATTCTTTTT	GGATATTGAG	ATTGACATG	AGGAGATGAA	GGGTCTGGAT	120
GTGGCTAGAA	AGATTCGGGA	TCGGGATTCG	TATGCCCTGA	TTGTCTTGGT	GACGAGCTCA	180
CTCGAGGTTT	ATGCCCTGT	CCTTTCGCTA	CCAAGTGTCT	GCTCTGGATT	ATATTGA	237

(2) INFORMATION FOR SEQ ID NO:1070:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

TTGCTCTTGA AATGGAACGG TGCCAGAGAA AAATTGAGCA CAAAGACTGT TCCAAGATTG	60
ACCAAAAAAT CAAAGAGCAG AAGGAGATAT TTGAATCCTG TTGTAAAAAA GATTAAGGAG	120
GACGTGCGTG GAATTACTGA TTTACCTCAT CCTATTTTGA CTGGTTTTGA TTGTCTCAAG	180
TACAACCAAT AA	192

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

TTTTCATTGA ATANNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NTGGGGGNAA	60
NNNAATANNN NNAANNNNNN NNNAAAAAAA AAAAAANNNA NNNNNNNNAA AAGGGAAANN	120
AAAAAAAAGA GGGAAANNNG AAGGGGGGGG AGAAAANGGG GAGGGAGGGA AAGGAGGAAG	180
AAGGNGGGGT GA	192

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

AACGCGCTGA	AGAAATTGCT	GCCCTTCGTG	GTATTTCACT	TTCTGATTG	GCATAAGAAA	60
GGGGATAAAA	TGGCTCAAAT	TAAAATTACT	TTGACTAAGT	CTCCAATCGG	ACGCATTCCA	120
TCACAACGTA	AAACTGTTGT	AGCACTTGGA	CTTGGCAAAT	TGAACAGCTC	TGTTATTAAA	180
GAAGATAACG	CTGCTATCCG	TGGTATGATT	ACAGCAGTAT	CTCACTTAGT	AACAGTTGAA	240
GAAGTAAACT	AA					252

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...5310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

AAGTTTATGA	ATAAAGGATT	ATTTGAAAAA	CGTTGTAAAT	ATAGTATTCG	GAAATTTTCA	60
TTAGGTGTTG	CTTCTGTTAT	GATTGGAGCT	GCATTCCTTG	GGACAAGTCC	GGTTCCTGCA	120
GATAGCGTGC	AGTCTGGTTC	CACGGCGAAC	TTACCAGCTG	ATTTAGCTAC	TGCTCTTGCA	180
ACAGCAAAAG	AGAATGATGG	GCGTGATTTT	GAAGCGCCTA	AGGTGGGAGA	AGACCAAGGT	240
TCTCCAGAAAG	TTACAGATGG	ACCTAAGACA	GAAGAAGAAC	TATTAGCACT	TGAAAAAGAA	300
AAACCGGCTG	AAGAAAAACC	AAAAGAGGAT	AAACCTGCAG	CTGCTAAACC	TGAAACGCCCT	360
AAGACGGTAA	CCCCTGAATG	GCAAACGGTA	GAGAAAAAAG	AACAACAGGG	AACAGTCACT	420
ATCCGAGAAG	AAAAAGGTGT	CCGCTACAAC	CAACTATCCT	CAACTGCTCA	AAATGATAAC	480
GCAGGTAAAC	CAGCTCTGTT	TGAAAAGAAG	GGCTTGACCG	TTGATGCCAA	TGGAAATGCA	540
ACTGTTGATT	TAACCTTCAA	AGAAGATTCT	GAAAAGGGCA	AATCACGCTT	TGGTGTCTTC	600
TTGAAATTTA	TAAGATCCAA	TAATAATGTT	TTTGTTCGGT	ATGACAAGGA	TGGCTGGTTC	660
TGGGAGTATA	AATCTCCAAC	AAC TAGCACT	TGGTATAGAG	G TAGTCGTGT	TGCTGCTCCT	720
GAAACAGGAT	CAACAAACCG	TCTCTCTATC	ACTCTCAAGT	CAGACGGTCA	GCTAAATGCC	780
AGCAATAACG	ATGTCAATCT	C TTTGACACA	GTGACTCTAC	CAGCTGCGGT	CAATGACCAT	840
C TTA AAAATG	AGAAGAAGAT	TCTTCTCAAG	GCGGGCTCTT	ATGACGATGA	GCGAACAGTT	900
GTTAGCGTTA	AAACGGATAA	CCAAGAGAGG	GTAAAAACAG	AGGATACCCC	TGCCCAGAAA	960
GAAACAGGTC	CGGTGTTGA	CGATAGAAAG	GTGACTTATG	ATACGATCCA	GTCTAAGGTA	1020
CTTAAGGCAG	TAATTGACCA	AGCCTTCCCT	CGTGTCAAGG	AATACACCTT	GAATGGACAT	1080
ACTTTGCCAG	GACAGGTGCA	ACAATTCAAC	CAAGTCTTTA	TCAATAACCA	CCGAATCACC	1140
CCTGAAGTCA	CTTATAAAAA	AATCAATGAG	ACAACAGCAG	AGTACTTGAT	GAAGCTTCGC	1200
GATGATGCTC	ACTTAATCAA	TGCGGAAATG	ACAGTACGCT	TGCAAGTTGT	GGACAAATCAA	1260
TTGCACTTTG	ATGTGACCAA	GATTGTCAAC	CACAATCAAG	TCACTCCAGG	TCAAAAAGATT	1320
GATGACGAAA	GAAAACTACT	TTCTTCTATT	AGTTTCCTCG	GCAATGCTTT	AGTCTCTGTT	1380
TCTAGTGATC	AAACTGGTGC	TAAGTTTGAT	GGGGCAACCA	TGTCAAAACAA	TACGCATGTC	1440
AGCGGAGATG	ATCATATCGA	TGTAACCAAT	CCAATGAAGG	ATTTGGCTAA	GGGTTACATG	1500
TATGGATTTG	TTTCTACAGA	TAAGCTTGCT	GCTGGTGTTT	GGAGTAACTC	TCAAAATAGC	1560
TATGGTGGTG	GTTCGAATGA	CTGGACTCGT	TTGACAGCTT	ATAAAGAAAC	AGTCGGAAAT	1620

GCCAACTATG	TAGGAATCCA	CAGCTCTGAA	TGGCAATGGG	AAAAAGCTTA	TAAGGGCATT	1680
GTTCCTCCAG	AATACACGAA	GGAACCTCCA	AGTGCTAAGG	TTGTTATCAC	TGAAGATGCC	1740
AATGCAGACA	AGAAAGTTGA	TTGGCAAGAT	GGTGCCATTG	CTTATCGTAG	CATTATGAAC	1800
AACCCCTCAAG	GTGGGAAAA	AGTTAAGGAT	ATCACAGCTT	ACCGTATCGC	GATGAACTTT	1860
GGTTCTCAAG	CACAAAACCC	ATTCCCTTAG	ACCTTGGATG	GTATCAAGAA	AATCAATCTC	1920
CACACAGATG	GTCTTGGGCA	AGGTGTTCTC	CTTAAAGGAT	ATGGTAGCGA	AGGCCATGAC	1980
TCTGGTCACT	TGAACTATGC	TGATATTGGT	AAGCGTATCG	GTGGTGTCTG	AGACTTCAAG	2040
ACCCTAATTG	AGAAGGCTAA	GAAATATGGA	GCTCATCTAG	GTATCCACGT	TAACGCTTCA	2100
GAAACTTATC	CTGAGTCTAA	ATACTTCAAT	GAAAAAATTC	TCCGTAAGAA	TCCAGATGGA	2160
AGCTATAGCT	ATGGTTGGAA	CTGGCTAGAT	CAAGGTATCA	ACATTGATGC	TGCCATATGAC	2220
CTAGCTCATG	GTCTTTTGGC	ACGTTGGGAA	GATTTGAAGA	AAAAACTTGG	TGACGGTCTC	2280
GACTTTATCT	ATGTGGACGT	TTGGGGTAAT	GGTCAATCAG	GTGATAACGG	TGCCCTGGGCT	2340
ACCCACGTTT	TTGCTAAAGA	AATTAACAAA	CAAGGCTGGC	GCTTTGCGAT	CGAGTGGGGC	2400
CATGGTGGTG	AGTACGACTC	TACCTTCCAT	CACTGGGCAG	CTGACTTGAC	CTACGGTGGC	2460
TACACCAATA	AAGGTATCAA	CAGTGCCATC	ACCCGCTTTA	TCCGTAACCA	CCAAAAAGAT	2520
GCTTGGGTTG	GGGACTACAG	AAGTTATGGT	GGTGCAGCCA	ACTATCCACT	GCTAGGTGGC	2580
TACAGCATGA	AAGACTTTGA	AGGCTGGCAA	GGAAGAAGTG	ATTACAATGG	CTATGTAACC	2640
AACTTATTTG	CCCATGACGT	CATGACTAAG	TACTTCCAAC	ACTTCACTGT	AAGTAAATGG	2700
GAAAATGGTA	CACCGGTGAC	TATGACCGAT	AACGGTAGCA	CCTATAAATG	GACTCCAGAA	2760
ATGCGAGTGG	AATTGGTAGA	TGCTGACAA	AATAAAGTAG	TTGTAACTCG	TAAGTCAAAT	2820
GATGTCAATA	GCCCACTATA	CCGTGAACGT	ACAGTAACGC	TCAACGGACG	TGTCATCCAA	2880
GATGGTTTCA	CTTACTTGAC	TCCTTGGAAC	TGGGATGCAA	ATGGTAAGAA	ACTTCTTACT	2940
GATAAGGAAA	AGATGTACTA	CTTCAATACG	CAGGCCGGTG	CAACAACCTT	GACCCCTTCCA	3000
AGCGATTGGG	CAAAAGACAA	GGTTTACCTT	TACAAGCTAA	CTGACCAAGG	TAAGACAGAA	3060
GAGCAAGAAC	TAACTGTAAA	AGATGGTAAA	ATTACCCTAG	ATCTTCTAGC	AAATCAACCA	3120
TACGTTCTCT	ATCGTTCGAA	ACAAACCAAT	CCTGAAATGT	CATGGAGTGA	AGGCATGCAC	3180
ATCTATGATC	AAGGATTTAA	TAGCGGTACT	TTGAAACATT	GGACCATTTC	AGGCGATGCT	3240
TCTAAGGCAG	AAATTGTCAA	GTCTCAAGGG	GCAAACGATA	TGCTTCGTAT	TCAAGGAAAC	3300
AAAGAAAAAG	TTAGTCTCAC	TCAGAAATTA	ACTGGCTTGA	AACCAAATAC	CAAGTATGCC	3360
GTTCATGTCG	GTGTCGATAA	CCGTAGTAAT	GCCAAGGCAA	GTATCACTGT	GAATACTGGT	3420
GAAAAAGAAG	TGACTACTTA	TACCAATAAG	TCTCTCGCCC	TCAACTATGT	AAAAGCCTAC	3480
GCCCACAATA	CACGTTCGTAA	CAATGCTACA	GTTGACGATA	CAAGTTACTT	CCAAAACATG	3540
TACGCCTTCT	TTACAACCTG	ATCGGACGTC	TCAAATGTTA	CTCTGACATT	GAGTCGTGAA	3600
GCTGGTGATC	AAGCAACTTA	CTTTGATGAA	ATTTCGTACCT	TTGAAAACAA	TTCAAGCATG	3660
TACGGAGACA	AGCATGATAC	AGGTAAAGGC	ACCTTCAAGC	AAGACTTTGA	AAATGTTGCT	3720
CAGGGTATCT	TCCCATTTGT	AGTGGGTGGT	GTCGAAGGTG	TCGAAGACAA	CCGCACTCAC	3780
TTGTCTGAAA	AACACGATCC	ATATACACAA	CGTGGTTGGA	ACGGTAAGAA	AGTTGATGAT	3840
GTTATCGAAG	GAAATTGGTC	ACTCAAGACA	AATGGACTAG	TGAGCCGTCT	TAACCTGGTT	3900
TACCAAATA	TTCCGCAAAA	CTTCCGTTTT	GAAGCAGGTA	AGACCTACCG	TGTAACCTTT	3960
GAATACGAAG	CAGGTTTCAA	CAATACCTAT	GCTTTTGTAG	TCGGTAAGGG	AGAATTCCAG	4020
TCAGGTTCGT	GTGGTACTCA	AGCAAGCAAC	TTGGAAAATG	ATGAATTGCC	AAATACCTGG	4080
ACAGATTCTA	AGAAAAGCCAA	GAAGGCAACC	TTCCTCGTGA	CAGGTGCAGA	AACAGGGGAT	4140
ACTTGGGTAG	GTATCTACTC	AACTGGAAAT	GCAAGTAATA	CTCGTGGTGA	TTCTGGTGGA	4200
AATGCCAACT	TCCGTGGTTA	TAACGACTTC	ATGATGGATA	ATCTTCAAAT	CGAAGAAATT	4260
ACCCTAACAG	GTAAGATGTT	GACAGAAAAT	GCTCTGAAGA	ACTACTTGCC	AACGGTTGCC	4320
ATGACTAACT	ACACCAAAGA	GTCTATGGAT	GCTTTGAAAG	AGGCGGTCTT	TAACCTCAGT	4380
CAGGCCGATG	ATGATATCAG	TGTGGAAGAA	GCGCGTGCAG	AGATTGCCAA	GATTGAAGCC	4440
TTGAAGAATG	CTTTGGTTCA	GAAGAAAACG	GCTTTGGTAG	CAGATGACTT	TGAAAGTTTG	4500
GATGCGCCAG	CTCAACCAGG	TGAAGGCCTA	GAGAATGCTT	TTGATGGCAA	TGTGCTTAGT	4560
CTATGGCATA	CATCTTGGA	TGGTGGAGAT	GTAGGCAAGC	CTGCAACCAT	GGTCTTGAAA	4620
GAACCAACTG	AAATCACTGG	ACTTCGTTAC	GTTCCACGTG	GATCGGGTTC	AAATGGTAAC	4680
TTGCGTGATG	TGAAACTTGT	TGTGACAGAT	GAGTCTGGCA	AGGAGCATAC	CTTTACTGCA	4740
ACTGATTGGC	CAGATAACAA	TAAGCCAAAA	GACATTGATT	TTGGTAAGAC	AATTAAGGCT	4800
AAGAAAAATT	TCCTTACAGG	TACTAAGACT	TACGGAGATG	GTGGCGATAA	ATACCAATCT	4860
GCAGCGGAAC	TTATCTTTAC	TCGTCCACAG	GTAGCAGAAA	CACCTCTTGA	CTTGTTAGGC	4920
TATGAAGCAG	CTTTGGCTAA	GGCTCAGAAA	TTAACAGACA	AAGACAATCA	AGAGGAAGTA	4980

GCTAGCGTTC	AGGCAAGCAT	GAAATATGCG	ACGGATAACC	ATCTCTTGAC	GGAAAGAATG	5040
GTGGAATACT	TTGCAGATTA	TCTCAACCAA	TTAAAAGATT	CTGCTACGAA	ACCAGATGCT	5100
CCAACTGTAG	AGAAACCTGA	GTTTAAACTT	AGCTCTTTAG	CTTCCGAGCA	AGGTAAGACG	5160
CCAGATTATA	AGCAAGAAAT	AGCTAGACCA	GAAACACCTG	AACAAATCTT	GCCAGCAACA	5220
GGTGAGAGTC	AATCTGACAC	AGCCCTCTTC	CTAGCAGGTG	TTAGCCTAGC	CCTATCTGCT	5280
CTCTTTGTAG	TAAAAACGAA	GAAAGACTAG				5310

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

ATTTCTATGA	ATAAAAAACT	AACAGATTAT	GTGATTGATC	TGGTGAAAT	TTTAAATAAA	60
CAACAAAAGC	AGGTTTTCTG	GGAATATTT	GATATTTTCA	GTATGGTGGT	TTCCATCATT	120
GTATCTTATA	TTTTATTTTA	TGGGCTGATT	AATCCAGCAC	CTGTTGACTA	CATTATCTAT	180
ACGAGTTTGG	CCTTCTTGTT	CTATCAATTG	ATGATTGGTT	TTTGGGGGTT	GAACGCGAGC	240
ATTAGTCGTT	ACAGCAAGAT	TACGGATTTT	ATGAAAAATCT	TTTTTGGTGT	GACTGCTAGC	300
AGTGTCTTGT	CATATAGTAT	CTGTTATGCC	TTCTTGCCAC	TCTTCTCCAT	CCGTTTTCATC	360
ATTCTCTTTA	TCTTGTGAG	TACCTTCTTG	ATTTTATTGC	CACGGATTAC	TTGGCAGTTA	420
ATCTACTCCA	GACGCAAAAA	AGGTAGTGGT	GATGGAGAAC	ACCGTCGGAC	CTTCTTGATT	480
GGTGCCGGTG	ATGGTGGGGC	TCTCTTTATG	GATAGTTACC	AACATCCAAC	CAGTGAATTA	540
GAACTGGTCG	GTATTTTGGA	TAAGGATTCT	AAGAAAAAGG	GTCAAAAACT	TGGTGGTATT	600
CCTGTTTGGG	GCTCTTATGA	CAATCTGCCT	GAATTAGCCA	AACGCCATCA	AATCGAGCGT	660
GTCATCGTTG	CGATTCCGTC	GCTGGATCCG	TCAGAATATG	AGCGTATCTT	GCAGATGTGT	720
AATAAGCTGG	GTGTCAAAATG	TTACAAGATG	CCTAAGGTTG	AAACTGTTGT	TCAGGGCCTT	780
CACCAAGCAG	GTA CTGGCTT	CCAAAAAATT	GATATTACGG	ACCTTTTGGG	TCGTCAGGAA	840
ATCCGTCTTG	ACGAATCGCG	TCTGGGTGCA	GAAC TGACAG	GTAAGACCAT	CTTAGTCACA	900
GGAGCTGGAG	GTTCAATCGG	TTCTGAAATC	TGTCGTCAAG	TTAGTCGCTT	CAATCCTGAA	960
CGCATTGTCT	TGCTCGGTCA	TGGGGAAAAC	TCAATCTACC	TTGTTTATCA	TGAATTGATT	1020
CGTAAGTTCC	AAGGGATTGA	TTATGTACCT	GTGATTGCGG	ACATTCAAGA	CTATGATCGT	1080
TTGTTGCAAG	TCTTTGAGCA	GTACAAACCT	GCTATTGTTT	ATCATGCGGC	AGCCCACAAG	1140
CATGTTCCTA	TGATGGAGCG	CAATCCAAAA	GAAGCCTTCA	AAAACAATAT	CCGTGGAAC	1200
TACAATGTTG	CTAGAGCCGT	TGATGAAGCT	AAAGTGCTTA	AGATGGTTAT	GATTTTCGACA	1260
GATAAGGCAG	TCAATCCACC	AAATGTTATG	GGAGCAACCA	AGCGCGTGGC	GGAGTTGATT	1320
GTCACTGGCT	TTAACCAACG	TAGCCAATCA	ACCTACTGTG	CAGTTCGTTT	TGGGAATGTT	1380
CTTGGTAGCC	GTGGTAGTGT	CATTCCAGTC	TTTGAACGTC	AGATTGCTGA	AGGTGGGCCCT	1440
GTAACGGTGA	CAGACTTCCG	CATGACCCGT	TACTTTATGA	CCATTCCAGA	AGCTAGTCGT	1500
CTGGTTATCC	ATGCTGGTGC	TTATGCCAAA	GATGGGGGAA	TCTTTATCCT	TGATATGGGC	1560
AAACCAGTCA	AGATTTATGA	CTTGGCCAAG	AAGATGGTGC	TTCTAAGTGG	CCACACTGAA	1620

AGTGAAATTC	CAATCGTTGA	AGTTGGAATC	CGCCCAGGTG	AAAAACTCTA	CGAAGAACTC	1680
TTGGTATCAA	CCGAACTCGT	TGATAATCAA	GTTATGGATA	AGATTTTCGT	TGGTAAGGTT	1740
AATGTCATGC	CTTTAGAATC	CATCAATCAA	AAGATTGGAG	AGTTCCGCAC	TCTCAGTGGA	1800
GATGAGTTGA	AGCAAGCTAT	TATCGCCTTT	GCTAATCAAA	CAACCCACAT	TGAATAA	1857

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

TATCCTATGA	AAGGAGTTAA	TATGGAAAAG	CAACAACCTA	GTAAAGCAGC	CCTGCTGTCT	60
ATCATTCCTG	GGTTAGGACA	GATTTACAAT	AAACAAAAAG	CCAAAGGTTT	TATCTTCCTT	120
GGTGTAACCA	TCGTATTTGT	CCTTTACTTC	CTAGCACTTG	CAACCCCTGA	ATTGAGCAAC	180
CTCATCACTC	TTGGTGACAA	ACCAGGTCGT	GATAATTCCC	TCTTTATGCT	GATTCGTGGT	240
GCCTTCCATC	TAATCTTTGT	AATCGTTTAT	GTACTCTTTT	ATTTCTCAAA	TATCAAAGAT	300
GCACATACGA	TTGCAAAACG	CATTAACAAT	GGAATTCCAG	TTCCACGCAC	ACTCAAAGAC	360
ATGATCAAAAG	GGATTTATGA	AAATGGCTTC	CCTTACCTCT	TGATCATTCC	ATCTTATGTT	420
GCCATGACCT	TCGCGATTAT	CTTCCCAGTT	ATCGTAACCT	TGATGATCGC	CTTTACCAAC	480
TACGACTTCC	AACACTTGCC	ACCAAACAAG	TTGTTGGACT	GGGTGGGTTT	GACCAACTTT	540
ACAAACATTT	GGAGCTTGAG	TACCTTCCGT	TCTGCCTTTG	GTTCTGTTC	TTCTTGGACT	600
ATCATTGCGG	CTTTGGCAGC	TTCTACTTTA	CAAAATCGTAA	TTGGTATCTT	CACAGCTATC	660
ATTGCTAACC	AACCATTAT	CAAAGGAAAA	CGTATCTTTG	GTGTTATTTT	CCTTCTTCCT	720
TGGGCTGTCC	CAGCCTTCAT	CACTATCTTG	ACATTCTCAA	ACATGTTTAA	CGATAGTGTC	780
GGTGCTATCA	ACACTCAAAG	ATTGCCAATC	TTGGCTAAAT	TCCTTCCTTT	CCTTGATGGA	840
GCTCTTATTC	CTTGGAACAA	AGACCCAACT	TGGACTAAGA	TTGCCCTTGAT	TATGATGCAA	900
GGTTGGCTCG	GATTCCCAT	CATCTACGTT	CTGACCTTGG	GTATCTTGCA	ATCTATTCCT	960
AACGACCTTT	ACGAAGCAGC	TTATATTGAC	GGTGCCAACG	CTTGGCAAAA	ATTCCGCAAC	1020
ATCACTTTCC	CAATGATTTT	GGCTGTTGCG	GCACCTACTT	TGATTAGCCA	ATACACCTTC	1080
AACTTTAACA	ACTTCTCTAT	CATGTACCTC	TTCAATGGTG	GAGGACCTGG	TAGTGTGCGA	1140
GGTGGAGCTG	GTTCAACCGA	TATCTTGATC	TCATGGATCT	ACCGTTTGAC	AACAGGTACA	1200
TCTCCTCAAT	ACTCAATGGC	GGCAGCTGTT	ACCTTGATTA	TCTCTATCAT	TGTCATCTCA	1260
ATCTCTATGG	TTGCATTCAA	GAAACTACAC	GCATTTGATA	TGGAGGACGT	CTAA	1314

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

AACACTATGA	AAGATAAACA	AACATTTTTTA	ATGAAGGGCA	GTTTTGCCCT	TTTACTTTTC	60
GTTATTCTTG	GCTATATGGT	CAAATTTTAC	CCTGAAATGT	TGGTCAATTT	TGACCAATCG	120
ATTCAGACTG	CCATTCGAGG	AAACTTACCA	AATTATTTGA	CTATTCTTTT	TCGATCCCTC	180
ACACGTCTGA	TTGATATCCC	AGTGATTATC	ACTTGGGTTG	TCATTACAGC	TTTTGTCTTT	240
TATCGTAAGC	GATGGAAAAT	AAAAAGTTTC	TTCATGCTGG	GAAATCTGGC	TTTGGCAGGT	300
CTTTTAATCG	TGACCTTTAA	AAATATCTAC	CAGCGCCAC	AACCAGCTAT	CTTACATCTG	360
GTGGAGGAGA	AGGGATTTTC	CTTCCCAAGT	GGGCATTCTC	TGGCTGTAAC	CTTGATGGTA	420
GGTACTTTGA	TTGTTATTCT	TAGTCAGCGG	ATTAAAGATC	CAGTCTGGAG	AAAAATCGTA	480
CAAATCGTCC	TTGGCCTCTA	CCTAGTCAGT	GTGCTGGTAT	CAAGAGTCTA	TCTGGGAGTT	540
CATTACCCAT	CAGACGTCCT	TGCCAGTCTC	TGTGTGGGCT	TGGGAGTCCT	GTTTATCGAG	600
TTTCCCTTCT	ATGACAAGCT	CCGCTTCCAA	TGGCGATTTA	AAGGCAAACA	GAAGTGA	657

(2) INFORMATION FOR SEQ ID NO:1077:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

AATCATATGA	ATATTACCAA	TTTGTTTTCT	ATCAAGACAG	GATGTGATGA	AACTGATAGG	60
CAACTGCAAA	AACTATTTTT	TCAGTTGGAT	TTACAATTGG	GAGAAATTGAC	AGATCAACTA	120
AGAAAAATTAG	ATTCTAATTT	TGTTCCCTCGT	AGTCAATTTG	TAGACACGTT	GGATTTGAAT	180
GATGTAGAAT	ATAAAGAAAT	TTTAAACTAT	TTTATCTTCC	ATCGTAATGA	TAGTGAAGAA	240

AGTTTGGTAG AATGGTTATA TGATTGGATT TCCACAAATC GTTATGAACT TCCTAAAGAG	300
TTTTCGATTC GTATGGCTCA TAAATACCAT GAAAGTGTTA CTGAAGTTTT CGGAGATGAA	360
TAA	363

(2) INFORMATION FOR SEQ ID NO:1078:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

ACCAATATGA AACGTATTGC TGTCTTGACT AGTGGCGGAG ACGCACCTGG TATGAACGCT	60
GCCATCCGTG CAGTTGTTTCG TCAAGCAATT TCAGAAGGAA TGGAAGTGTT TGGTATCTAT	120
GACGGATATG CTGGTATGGT TGCCGGTGAA AATTCATCCC CTAAATGCAG CTTCAGTAGG	180
GGACATCATT TCTCGTGGTG GTACTTTTCT TCACTCAGCT CGTTATCCAA ATTTTCGCTCA	240
ACTTGA	246

(2) INFORMATION FOR SEQ ID NO:1079:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...468
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

GACAATATGA AGCAAACAAA AACAACTAAA ATCGCCCTTG TATCCCTATT AACCGCCCTT	60
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TCTGTGGTTC	TAGGTTATTT	CTTAAAATTC	CCAACACCTA	CAGGAATTCT	AACTCTTTTA	120
GATGCTGGTG	TCTTCTTTGC	GGCCTTTTAC	TTTGGTAGTC	GTGAAGGAGC	GGTAGTCGGA	180
GGACTAGCAA	GTTTCTTGAT	TGACCTCTTA	TCAGGCTACC	CTCAGTGGAT	GTTCTTTAGC	240
TTGGTCAACC	ATGGCTTGCA	GGGATTTTTC	GCAGGATTTA	AAGGAAAAAG	TCAGTGGTTA	300
GGCCTTATTT	TAGCAACTAT	TGCCATGGTA	GGAGGCTACG	CCTTGGGTTC	TACTTTGATG	360
AATGGCTGGG	CAGCAGCCCT	CCCAGAAATT	CTACCGAATT	TTATGCAAAA	TATGGTAGGG	420
ATGATTGTAG	GATTTATTCT	TAGTCAAAGT	ATCAAGAAGA	TTAAGTAA		468

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

ATAAGTATGA	ATTTAAACGA	TATTAAAGAC	TTGATGACTC	AATTTGACCA	GTCAAGTTTG	60
AGAGAATTTT	CTTATAAAAA	TGGGACGGAT	GAGTTGCAGT	TTAGCAAGAA	TGAAGCGAGA	120
CCTGTGCCTG	AAGTTGCAAC	TCAAGTCGCT	CCAGCACCCG	TTCTAGCAAC	ACCGAGTCCA	180
GTAGCTCCTA	CATCTGCTCC	AGCAGAGACT	GTAGCAGAAG	AAGTTCCAGC	TCCAGCTGAA	240
GCAAGTGTGG	CTAGTGAGGG	AAATCTTGTA	GAGAGTCCAC	TTGTTGGAGT	GGTTTACTTG	300
GCTGCTGGAC	CAGATAAACC	TGCCTTCGTT	ACAGTTGGTG	ATAGTGTCAA	AAAAGGTCAA	360
ACATTGGTAA	TTATCGAAGC	CATGAAAGTC	ATGAATGAAA	TCCCAGCTCC	TAAGGATGGT	420
GTGGTAACGG	AAATTCTCGT	CTCTAACGAA	GAAATGGTTG	AGTTTGGTAA	AGGATTGGTA	480
CGTATCAAAT	GA					492

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

AGAAGTATGA	AAGTAAATTT	AGATTATCTC	GGTCGTTTAT	TTACTGAGAA	TGAATTAACA	60
GAAGAAGAAC	GTCAGTTGGC	GGAGAAACTT	CCAGCAATGA	GAAAGGAGAA	GGGGAAACTT	120
TTCTGTCAAC	GTTGTAATAG	TACTATTCTA	GAAGAATGGT	ATTTGCCCAT	CGGTGCTTAC	180
TATTGTGCGAG	AGTGCTTGCT	GATGAAGCGA	GTCAGAAGTG	ATCAAACCTT	ATACTATTTT	240
CCGCAGGAGG	ATTTTCCGAA	GCAAGATGTT	CTCAAATGGC	GCGGCCAATT	AACTCCTTTT	300
CAAGAGAAGG	TGTCAGAGGG	ACTGCTTCAA	GCAGTAGACA	AGCAAAAAGCC	AACCTTAGTT	360
CATGCGGTAA	CAGGAGCTGG	AAAGACAGAA	ATGATTTATC	AAGTAGTGGC	TAAAGTGATC	420
AATGCGGGTG	GTGCACTGTG	TTTGGCTAGT	CCTCGCATAG	ATGTTTGTTT	GGAGCTGTAC	480
AAGCGCCTGC	AACAGGATTT	TTCTTGCGGG	ATAGCTTTGC	TACATGGAGA	ATCGGAACCT	540
TATTTTCGAA	CACCACTAGT	TGTTGCAACA	ACCCATCAGT	TATTGAAGTT	TTATCAAGCT	600
TTTGATTTGC	TGATAGTGGA	TGAAGTAGAT	GCTTTTCCCT	ATGTTGATAA	TCCCATGCTT	660
TACCACGCTG	TCAAGAATAG	TGTAAAGGAG	AATGGATTGA	GAATCTTTTT	AACAGCGACT	720
TCGACCAATG	AGTTAGATAA	AAAGGTCCGT	TTAGGAGAAC	TAAAAAGACT	GAATTTACCG	780
AGACGGTTTC	ATGGAAATCC	GTTGATTATT	CCAAAACCAA	TTTGGTTATC	GGATTTTAAT	840
CGCTACTTAG	ACAAGAATCG	TTTGTACCA	AAGTTAAAGT	CCTATATTGA	GAAGCAGAGA	900
AAGACAGCTT	ATCCGTTACT	CATTTTTGCT	TCAGAAATTA	AGAAAAGGGA	GCAGTTAGCA	960
GAAATCTTAC	AGGAGCAATT	TCCAAATGAG	AAAATTGGCT	TTGTATCTTC	TGTAACAGAG	1020
GATCGATTAG	AGCAAGTACA	AGCTTTTTCGA	GATGGAGAAC	TGACAATACT	TATCAGTACG	1080
ACAATCTTGG	AGCGTGGAGT	TACCTTCCCT	TGTGTGGATG	TTTTCGTAGT	AGAGGCCAAT	1140
CATCGTTTGT	TTACCAAGTC	TAGTTTGATT	CAGATTGGTG	GACGAGTTGG	ACGAAGCATG	1200
GATAGACCGA	CAGGAGATTT	GCTTTTCTTC	CATGATGGGT	TAAATGCTTC	AATCAAGAAG	1260
GCGATTAAGG	AAATTCAGAT	GATGAATAAG	GAGGCTGGTC	TATGA		1305

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 942 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

AGAAGTATGA	AGTGGACCAA	GATTATTAAA	AAAATAGAAG	AACAAATCGA	GGCAGGAATT	60
TATCCCGGAG	CCTCTTTTGC	GTATTTTAAAG	GACAATCAAT	GGACAGAGTT	CTATTTAGGC	120
CAGAGTGACC	CAGAGCATGG	CTTGCAGACT	GAGGCAGGAC	TAGTTTATGA	CCTAGCTAGT	180

GTCAGCAAGG	TTGTTGGGGT	TGGCACAGTT	TGTACCTTCT	TGTGGGAAAT	AGGTCAATTA	240
GATATTGATA	GACTGGTAAT	AGATTTTTTA	CCTGAGAGTG	ATTATCCAGA	CATCACTATT	300
CGCCAGCTCT	TGACTCATGC	AACAGACCTT	GATCCTTTTA	TTCCTAATCG	TGATCTTTTA	360
ACAGCCCCTG	AATTAAAGGA	AGCGATGTTT	CATCTCAACA	GACGAAGTCA	GCCAGCCTTT	420
CTTTATTTCG	ATGTCCATTT	TTTGCTGTTG	GGCTTTATTT	TGGAAAGAAT	TTTAAATCAA	480
GATTTGGATG	TGATTTTAAA	GGATCAAGTC	TGGAAACCTT	GGGGAATGAC	GGAAACCAAG	540
TTTGGGCCAG	TTGAGCTTGC	TGTTCCAACA	GTTAGAGGTG	TAGAGGCAGG	CATAGTGCAT	600
GATCCCAAGG	CTCGTCTCCT	GGGTAGACAT	GCTGGGAGTG	CTGGTTTATT	TTCGACTATA	660
AAGGATTTAC	AAATCTTTTT	AGAACTACTAT	TTAGCAGATG	ATTTTGCAAG	AGACTTAAAT	720
CAAAATTTTT	CTCCTTTGGA	TGACAAGGAA	CGTTCCTTAG	CATGGAATTT	GGAAGGAGAT	780
TGGCTAGACC	ATACGGGCTA	TACAGGTACC	TTTATCATGT	GGAATCGTCA	GAAGCAAGAA	840
GCCACTATTT	TCCTATCGAA	TCGTACCTAT	GAAAAGGACG	AGAGAGCTCA	ATGGATATTA	900
GACCGCAATC	AAGTGATGAA	CTTGATTTCGT	AAAGAAGAGT	AA		942

(2) INFORMATION FOR SEQ ID NO:1083:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...483
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

CTGCTCATGA	AGTGGACCGC	GCTGCCCCGTG	AGGTCATCGA	AAAAGCTGGT	TATGGTGAGT	60
ACTTCAACCA	CCGTCTCGGG	CATGGTATCG	GTATGGATGT	CCATGAATTC	CCATCTATCA	120
TGGAAGGAAA	CGACATGGTC	ATCGAAGAAG	GCATGTGCTT	CTCTGTTGAA	CCAGGTATCT	180
ATATCCCTGG	TAAAGTCGGT	GTTTCGTATTG	AAGACTGCGG	TGTTGTTACC	AAGGATGGCT	240
TCGACCTCTT	TACAAGCACC	AGCAAAGATT	TGCTTTATTTT	TGATTAAACT	ATATAGCCCC	300
TATGCTTTCC	TTTCAAAATA	TCTAGGGGCT	ATTTTATTGT	CATTTTCTG	CTATTATGCT	360
AAAGAAATTG	GCTGCAATAA	TCTAACCCTA	AGTGCTGGA	ATGATAACGA	GGGTGCTCTC	420
CGCTTTTATC	AAAGACAAGG	GATGAAACCC	CAAGAAACAA	CAATGGAAAT	GATAATTGAT	480
TAA						483

(2) INFORMATION FOR SEQ ID NO:1084:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1965 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

TCTTTAATGA	AAAAACAAAA	TAATGGTTTA	ATTAAAAATC	CTTTTCTATG	GTTATTATTT	60
ATCTTTTTTC	TTGTGACAGG	ATTCCAGTAT	TTCATTCTG	GGAATAACTC	AGGAGGAAGT	120
CAGCAAATCA	ACTATACTGA	GTTGGTACAA	GAAATTACCG	ATGGTAATGT	AAAAGAATTA	180
ACTTACCAAC	CAAAATGGTAG	TGTTATCGAA	GTTCCTGGTG	TCTATAAAAA	TCCTAAAACA	240
AGTAAAGAAG	GAACAGGTAT	TCAGTTTTTC	ACGCCATCTG	TTACTAAGGT	AGAGAAATTT	300
ACCAGCACTA	TTCTTCCTGC	AGATACTACC	GTATCAGAAT	TGCAAAAAC	TGCTACTGAC	360
CATAAAGCAG	AAGTAACTGT	TAAGCATGAA	AGTTCAAGTG	GTATATGGAT	TAATCTACTC	420
GTATCCATTG	TGCCATTTGG	AATTCATATC	TTCTTCCTAT	TCTCTATGAT	GGGAAATATG	480
GGAGGAGGCA	ATGGCCGTAA	TCCAATGAGT	TTTGGACGTA	GTAAGGCTAA	AGCAGCAAAT	540
AAAGAAGATA	TTAAAGTAAG	ATTTTCAGAT	GTTGCTGGAG	CTGAGGAAGA	AAAACAAGAA	600
CTAGTTGAAG	TTGTTGAGTT	CTTAAAAGAT	CCAAAACGAT	TCACAAAAC	TGGAGCCCGT	660
ATTCCAGCAG	GTGTTCTTTT	GGAGGGACCT	CCGGGGACAG	GTAAGACTTT	GCTTGCTAAG	720
GCAGTCGCTG	GAGAAGCAGG	TGTTCCATTC	TTTAGTATCT	CAGGTTCTGA	CTTTGTAGAA	780
ATGTTTGTCG	GAGTTGGAGC	TAGTCGTGTT	CGCTCTCTTT	TTGAGGATGC	CAAAAAAGCA	840
GCACCAGCTA	TCATCTTTAT	CGATGAAATT	GATGCTGTTG	GACGTCAACG	TGGAGTCGGT	900
CTCGGCCGAG	GTAATGACGA	ACGTGAACAA	ACCTTGAACC	AACTTTTGAT	TGAGATGGAT	960
GGTTTTGAGG	GAAATGAAGG	GATTATCGTC	ATCGCTGCGA	CAAACCGTTC	AGATGTACTT	1020
GATCCTGCCC	TTTTGCGTCC	AGGACGTTTT	GATAGAAAAG	TATTGGTTGG	CCGTCCTGAT	1080
GTTAAAGGTC	GTGAAGCAAT	CTTGAAAGTT	CACGCTAAGA	ACAAGCCTTT	AGCAGAAGAT	1140
GTTGATTTGA	AATTAGTGGC	TCAACAAACT	CCAGGCCTTG	TTGGTGCTGA	TTTAGAGAAT	1200
GTCTTGAATG	AAGCAGCTTT	AGTTGCTGCT	CGTCGCAATA	AATCGATAAT	TGATGCTTCA	1260
GATATTGATG	AAGCAGAAAG	TAGAGTTATT	GCTGGACCTT	CTAAGAAAGA	TAAGACAGTT	1320
TCACAAAAAG	AACGAGAATT	GGTTGCTTAC	CATGAGGCAG	GACATACCAT	TGTTGGTCTA	1380
GTCTTGTCGA	ATGCTCGCGT	TGTCCATAAG	GTTACAATTG	TACCACGCGG	CCGTGCAGGC	1440
GGATACATGA	TTGCACTTCC	TAAAGAGGAT	CAAATGCTTC	TATCTAAAGA	AGATATGAAA	1500
GAGCAATTGG	CTGGCTTAAT	GGGTGGACGT	GTAGCTGAAG	AAATTATCTT	TAATGTCCAA	1560
ACTACAGGAG	CTTCAAACGA	CTTTGAACAA	GCGACACAAA	TGGCACGTGC	AATGGTTACA	1620
GAGTACGGTA	TGAGTGAAAA	ACTTGGCCCA	GTACAATATG	AAGGAAACCA	TGCTATGCTT	1680
GGTGACACGA	GTCTTCAAAA	ATCAATTTCA	GAACAAACAG	CTTATGAAAT	TGATGAAGAG	1740
GTTCTGTTTCA	TATTAAATGA	GGCACGAAAT	AAAGCTGCTG	AAATTATTCA	GTCAAATCGT	1800
GAAACTCATA	AGTTAATTGC	AGAAGCATTA	TTGAAATACG	AAACATTGGA	TAGTACACAA	1860
ATTAAAGCTC	TTTACGAAAC	AGGAAAGATG	CCTGAAGCAG	TAGAAGAGGA	ATCTCATGCA	1920
CTATCCTATG	ATGAAGTAAA	GTCAAAAATG	AATGACGAAA	AATAA		1965

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

CAACTAATGA	ACTTTGAAAC	AGTCATCGGA	CTTGAAGTCC	ACGTAGAGCT	CAACACCAAT	60
TCAAAAATCT	TCTCACCTAC	TTCTGCCCAC	TTCGGAAATG	ATCAAAATGC	CAACACTAAC	120
GTGATTGACT	GGTCTTTCCC	AGGAGTTCTG	CCAGTTCTCA	ATAAAGGGGT	TGTTGATGCC	180
GGTATCAAGG	CTGCTCTTGC	CCTCAACATG	GACATCCACA	AAAAAATGCA	CTTTGACCGC	240
AAGAACTACT	TCTACCCTGA	TAATCCCCAA	GCCTACCAAA	TTTCTCAGTT	TGATGAGCCA	300
ATCGGTTATA	ACGGCTGGAT	TGAAGTCGAG	CTAGAAGACG	GTACGACCAA	GAAAAATTGGT	360
ATCGAACGCG	CCCACTTAGA	GGAAGACGCT	GGTAAAAACA	CCCACGGTAC	AGACGGCTAC	420
TCTTACGTTG	ACCTTAACCG	CCAAGGGGTA	CCTTTGATTG	AGATTGTATC	TGAAGCCGAT	480
ATGCGTTCGC	CAGAGGAGGC	CTATGCTTAT	CTGACAGCAC	TCAAGGAAGT	TATCCAGTAT	540
GCTGGCATT	CTGACGTTAA	GATGGAGGAA	GGTTCGATGC	GTGTGGATGC	CAACATCTCC	600
CTCGTCCTTA	TGGTCAAGAG	AAATTCGGTA	CCAAGACTGA	ATTGA		645

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1299 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

CCTATAATGA	AAAGCGACAA	AACCATCATT	AGAAAGATTC	ATATGGAACA	ATTACATTTT	60
ATCACAAAAC	TGCTCGATAT	TAAAGACCCA	AACATCAAGA	TTCTAGATAT	CATCAATATG	120
GATACCCACA	AAGAAATTAT	CGCTAAGCTG	GATTATGAGG	CTCCATCTTG	CCCTGATTGT	180
GGAAGTCTAA	TGAAGAAATA	TGACTTTCAA	AAACCGTCTA	AGATCCCCTTA	CCTCGAAACA	240
ACTGGTATGC	CTTCTAGAAT	TCTCCTTAGA	AAACGCCGTT	TCAAGTGCTA	TCACTGTTCA	300
AAAATGATGG	TTGCTGAGAC	TCCCCTGGTA	AAGAAAAATC	ACCAAATCCC	TCGTATCATC	360
AACCAAAAAA	TTGCTCAAAA	GTTAATTGAA	AAAATTTCTA	TGACTGATAT	TGCCCATCAG	420
CTGGCCATTT	CAACTTCAAC	TGTCATTTCG	AAGCTCAATG	ACTTTCACTT	TGAGCATGAT	480
TTTCTCGGC	TTCCAAAGAT	TATGTCTTGG	GATGAGTATG	CCTTCACTAA	GGGAAAGATG	540

AGTTTCATTG	CGCAAGATTT	TGATAATCTT	AATATTATCA	CTGTTCTTGA	AGGCAGAACA	600
CAAGCTGTCA	TCCGAAATCA	CTTTCCTTCG	TACGATAGAG	CCGTTTCGTTG	TCAAGTGAAA	660
ATCATTACGA	TGGATATGTT	TAGTCCTTAC	TATGACTTGG	CTAAACAGCT	TTTTCCGTGT	720
GCTAAAATCG	TTCTAGATCG	TTTCCATATT	ATCCAACATC	TCAGCCGTGC	CATGAGTCGT	780
TTTCGTGTTT	AAATTATGAA	TCAGTTTGAA	CGAAAATCTC	ATGAATACAA	GGCTATCAAA	840
CGTTACTGGA	AACTCATCCA	ACAGGATAGT	CGTAAATTGA	GCGATAAACG	TTTTTATCGC	900
CCTACTTTTC	GCATGCACCT	AACAAATAAA	GAAATTCCTG	ACAAGATTTT	AAGCTATTCA	960
GAAGACTTGA	AACACCACTA	TCAGATCTAT	CAACTCTTAC	TTTTTCACTT	TCAGAACAAA	1020
GACCCTGAGA	AATTTTTTCGG	ACTCATTGAG	GACACTCTGA	AGCAGGTTCA	TCCTATTTTT	1080
CAGACTGTCT	TTAAAACCTT	TCTAAAGAAC	AAAGAAAAAA	TCGTCAACGC	TCTTCAATTA	1140
CCTTATTCCA	ACGCAAAATT	GGAAGCGACC	AATAATCTCA	TCAAACCTAT	CAAACGAAAC	1200
GCCTTTGGAT	TTCGGAACTT	TGAAAACCTC	AAAAAAAGGA	TTTTTATCGC	TCTGAACATC	1260
AAAAAAGAAA	GGACGAATTT	TGTCCTTTCT	CGAGCTTAG			1299

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

AAAATAATGA	AGATAAGTTG	GAATGGATTT	TCTAAAAAAT	CATACCAAGA	GCGCCTCGAG	60
CTGCTAAAAG	CTCAGGCGCT	CCTTAGTCCT	GAGAGACAAG	CTAGTCTGGA	GAAGGATGAA	120
CAGATGAGTG	TGACTGTGGC	AGACCAGCTG	AGTGAGAATG	TGGTGGGAAC	TTTTTCTCTG	180
CCTTATTTCG	TGGTTCCGGA	GGTACTTGTC	AACGGTCAGG	AATACACCGT	TCCCTATGTG	240
ACAGAAGAAC	CCTCTGTGGT	TGCGGCGGCC	AGCTATGCCA	GCAAAATCAT	CAAGCGTGCA	300
GGTGGTTTTA	CTGCACAAGT	CCATCAGCGC	CAGATGATTG	GGCAGGTAGC	CCTTTATCAA	360
ATTGCTAATC	CTAAACTAGC	GCAAGAGAAG	ATTGCCAGCA	AGAAAGCGGA	GCTCTTGAGG	420
CTTGCCAATC	AAGCCTATCC	TTCTATCGTT	AAACGTGGGG	GTGGGGCGCG	TGATCTGCAT	480
GTCGAGCAGA	TAAAAGGCGA	ACCAGACTTT	CTCGTTGTTT	ATATTCTATG	CGATACCCAG	540
GAAGCCATGG	GTGCCAATAT	GCTCAACACC	ATGCTGGAAG	CCTTGAAACC	AGTCTTAGAA	600
GAAGCTCAGT	AGGGACAGAG	TCTCATGGGA	ATCCTGTCCA	ACTACGCGAC	TGATTCTCTG	660
GTGACTGCAA	GCTGTCGCAT	CGCCTTTTCG	TACTTGAGCC	GCCAAAAGGA	TCAAGGACGA	720
GAGATTGCGG	AGAAAATTGC	GTTGGCTAGT	CAGTTTGCGC	AGGCTGATCC	TTACCGAGCT	780
GCTACTCATA	ATAAAGGAAT	TTTTAATGGT	ATTGATGCGA	TTTTGATTGC	CACTGGTAAT	840
GAATGGCGTG	CCATCGAAGC	TGGGGCCCAT	GCCTTTGCCA	GTCGAGATGG	ACGCTATCAA	900
GGTCTTAGCT	GCTGGACGCT	GGACCTTGAA	AGAGAAGAAT	TGGTCGGTGA	GATGACCCCTG	960
CCCATGCCCTG	TAGCGACTAA	GGGTGGCTCT	ATCGGCCCTCA	ACCCACGTGT	AGCTCTCAGT	1020
CATGATCTAC	TAGGAAATCC	TTCTGCCAGA	GAATTAGCCC	AGATTATCGT	GTCCATCGGT	1080
CTTGCTCAAA	ATTTTGCAAG	CCTCAAAGCC	TTGGTAAGTA	CGGGCATCCA	GCAAGGCCAC	1140
ATGAACTAC	AGGCCAAATC	CCTAGCTCTC	CTAGCTGGGG	CTAGTGAATC	TGAAGTTGCT	1200

CCCCTAGTAG AGCGCCTCAT CTCAGATAAA ACCTTTAACC TAGAGACAGC CCAGCGCTAT	1260
CTCGAAAATT TAAGATCATA A	1281

(2) INFORMATION FOR SEQ ID NO:1088:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 840 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

AAAATAATGA AGAAGAAATC CAGTATTTAT TTAGATATTC TCTCACATGT ACTCTTAGTT	60
GGTGCACCA TTGTTGCAAT TTTCCCATTG GTATGGATTA TCATATCTTC TGTCAAAGGG	120
AAGGGGGAAT TAACTCAGTA TCCAACACGA TTTTGGCCTG AACAAATTAC ATTAGATTAT	180
TTCATCATG TTATCAACGA TTTGCACTTC ATTGATAACA TTCGAAACAG TTTAATCATT	240
GCCTTGGCTA CAACCTTAT TGCATTATT ATTTCTGCTA TGGCAGCCTA TGGTATTGTT	300
CGATTCTTTC CTAAATTGGG AGCAATCATG TCGAGACTAC TCGTCATTAC CTACATTTTC	360
CCACCAATT TGTAGCAAT TCCCTATTCA ATTGCCATTG CTAAAGTTGG GTTAACAAAT	420
AGTTTATTTG GCTTGATGAT GGTTTATCTA TCTTTTAGTG TTCCATATGC AGTTTGGCTC	480
TTAGTTGGAT TTTTCCAAAC AGTTCCAATT GGAATTGAAG AAGCGGCTAG AATTGATGGT	540
GCAAAATAAT TTGTTACGTT TTATAAAGTT GTGCTACCGA TTGTAGCACC AGGTATTGTA	600
GCAACAGCTA TTTATACATT TATCAATGCT TGGAAATGAAT TCCTGTATGC CTTGATTTTG	660
ATTAACAATA CAGGAAAGAT GACAGTAGCA GTAGCCCTTC GTTCACTTAA TGGTTCAGAA	720
ATACTAGACT GGGGAGATAT GATGGCAGCG TCTGTTATTG TAGTTCTTCC ATCAATTATT	780
TTCTTCTCTA TCATCCAAA TAAGATTGCA AGTGGATTAT CAGAAGGATC TGTGAAGTAG	840

(2) INFORMATION FOR SEQ ID NO:1089:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

GAAATAATGA AACGAATTTT AATAGCGCCT GTGCGCTTTT ACCAACGTTT TATCTCACCA	60
GTCTTTCCAC CCTCTTGTCG CTTTGAGCTG ACTTGTTCCA ACTACATGAT TCAGGCTATT	120
GAAAAACATG GTTTTAAGGG GGTATTGATG GGCTTGGCTC GGATTTTACG TTGTCATCCC	180
TGGTCGAAAA CAGGTAAGGA CCCC GTTCCA GACCACTTTT CCCTTAAACG AAATCAAGAA	240
GGGGAATGA	249

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

TACTCAATGA AAATCAAAGA GCAAAC TAGG AAGTTAGCCG CAGGTTGCTC AAAACAGTGT	60
TTTGAGGTTG TAGATGAAAC TGACGAAGTC AGCTCAAAC AGTGTTTTGA GGTGTAGAT	120
GAAACTGACG AAGTCAGTAA CCATACCTAC GGCAAGGCGA AACTGACGTG GTTTGAAGAG	180
ATTTTCGAAG AGTATAAAAT GATGGGGAAG GCTGGGCAAC TAGTCTTTTT CGATGTTTAT	240
AGATTAGTTA GGCAAGTAAG CTAG	264

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

TACTCAATGA	AAATCAAAGA	GCAAACCTAGG	AACTAGCCG	CAGGTTGCTC	AAAACACCGT	60
TTTGAGGTTG	CAGATAGAAC	TGATGAAGTC	AGCTCAAAAC	ACTGTTTTGA	GGTTGTGGAT	120
AGAACTGACG	AAGTCAGCTC	AAAACACCGT	TTTGAGGTTG	TGGATAGAAC	TGACGAAGTC	180
AGTAACCATA	CCTACGGCAA	GGTGAAGCTG	ACGTGGTTTG	AAGAGAGTTT	CGAAGAGTAT	240
AAGTAG						246

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

TACTCAATGA	AAATCCAAGA	GCAAACCTAGG	AACTAGCCG	CAAGCTGTTC	AAAGCACTGC	60
TTTGAGGTTG	TAGATAAGAC	TGACAAAGTC	AGTCACATAT	ATACGGTAAG	GCGACGTTGG	120
CGCGGTTTGA	AGAGATTTTT	GAAGAGTATA	AAAATCCTCA	AGATACTTTC	TTCTATCCTT	180
TAG						183

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

TACTCAATGA AAATCAAAGA GCAAAC TAGG AAGCTAGCCG CAGGTTGTTC AAAACACAGT	60
TTTGAGGTTG TAGATGAAAC TGACGAAGTC AGCTCAAAAC ATGGTTTTGA GGTTGTAGAT	120
GAAACTGACG AAGTCAGCTC AAAACATGGT TCTGAGGTTG TAGATGAAAC TGACGAAGTC	180
AGCTCAAAAC ATGGTTTTGA GGTTGTAGAT GAAACTGACG AAGTCAGCTC AAAACATGGT	240
TTTGAGATTG TAGATGAAAC TGACGAAGTC AGTAACCATA CATACGGTAA GGCGACGCTG	300
ACGTGGTTTG AAGAGATTTT CGAAGAGTAT AAAAATAA	339

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

TACTCAATGA AAATCAAAGT GCAAAC TAGG AAGTTAGCCG CAGGCTGCTC AAAACACTGT	60
TTTAAGGTTG TGGATGGAAC TGACGAAGTC AGCTCAAAAC ACTGTTTTGA GGTTGTGGAT	120
AGAACTGACG AAGTCAGTAA CCATATCTAC GGCAAGGTGA AGCTGACGTG GTTTGAAGAG	180
ATTTTCGAAG AGTATAAGTC TCTACATAAT AAAACGCATA TTACCAAGGT TCTTATGAAC	240
TGCACCCCAA AAGTTAGACA GAAAAAATCT AACTTTTGGG GGTCAGTACA TTCAACACCT	300
GATACTATGC GTTTTTTTAA TTTTAAAGAT TTTTACAAC TTCCTTTTGAC TCACATTAAA	360
CTATTCTAA	369

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

TACTCAATGA	AAATCAAAGA	GCAAAC TAGG	AAACTAGCCG	CAGGCTGCTC	AAAACACTGT	60
TTTGAGGTTG	CAGATAGAAC	TGACGAAAGTC	AGCTCAAAAC	ACTGTTTTGA	GGTTGCAGAT	120
AGAACTGACG	AAGTCAGTAA	CCATACCTAC	GATAAGGCGA	CGTTGACGCG	GTTTGAAGAG	180
ATTTTCGAAG	AGTATAAAGG	TGTACCGAGA	TGA			213

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

CTCCAAATGA	AACTGACTGA	TTACGTCAAG	CAGGTTTCAC	TAGAAGACTT	CGGCAGACCT	60
TTTATCCATC	ATGTCCAGTG	GAATAGGCGT	CTACGTTTCGA	CAGGTGGGCG	ATTTTTCCCC	120
AAAGATGGGC	ATTTGGATTT	TAATCCCAAG	GTTTATCAGG	AACTGGGGTT	GGACGTTTTT	180
AGGAAAATTG	TCCGACATGA	ACTCTGTCAT	TATCACCTTT	ATTTCCAAGG	GAAGGGCTAT	240
CAACACAAGG	ATCGGGATTT	TAAGGAACTT	TTGAAAGCAG	TGGATGGATT	ACGGTTTGTA	300
CCATCCTTGC	CCAATAGTAA	CTCCAAACCA	CTCAAGCTCT	ATCGTTGCCA	ATCCTGCCAG	360
CAAAC TTATC	AGCGCAAGCG	TAGGATTGAT	ACCAAACGCT	ATCGCTGTGG	ACTTTGTCGA	420
GGTAAATTGC	TTCTGATAAA	TCAGCCTGAG	GACTGA			456

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1986 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1986
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

GAGGGAATGA	ATGTGTTAAA	CATTAAAGAG	AAAGATATCC	TTCAATTTTT	AATAAAAAAT	60
AAGGAACGTT	TTGTTACAAG	CAAAGAACTA	GCAGAATATT	TATCCTGTTC	AGATAGAACT	120
GTCCGTAATG	TACTGAAATT	AATTGAGAAG	ACAATGATTA	TTCAAGGAGT	CCGGTTGATT	180
TCAAAACAAAG	GTCAAGGGTA	TCAAATATTT	TTTGAGAATC	AAGGCGCTTA	CCAGGAGTTT	240
AGACAAACTT	ATGAACTGGA	AGAAGACTAT	ACGAAAAC TG	CGGTTTCAAA	AGGTGATGAT	300
CGTTTAGTAT	TTATCTTAAA	TAAATTATTA	TTTGAGCAAG	TTCCAGTTCT	TTTTGATGAT	360
TTAGCTGATG	AACTTTACGT	TAGTCGTTCA	ACATTATCTC	ATGATTTTCA	AAAGATACGA	420
GTGATGTTAT	CAGAGTATAA	TTTGTCCATT	GAGAGTAGGG	CGAATAAAGG	AGTTTATGTC	480
TCAGGCGAGG	AACGTGATAA	ACGACGTTTT	ATCATAAATT	ATTTCCTAGA	GAATCAATTT	540
TTTAAAACAA	TACATTGCTA	TGTAAAATTT	AACTTTTTTG	ATCAAAC TGT	TCCATTAGAA	600
GAATTTGCTA	GAATTGTTTT	GGATGAATGC	CAAGAGGCCA	ACCTAAACT	ATCTGATTTT	660
GTACTACAGA	ATTTAGTAGT	TCACATAGCA	TTGTCTGTGA	TTCTGTTAAA	ATCCGGATTT	720
GAAATAAAAA	ATATAGACTG	TCAGATGACT	GATGATGCAA	CAGAGAGAAA	GGTTGCCCAA	780
AGAATTC TTT	CTAAAGTAAG	AGAAGTAACA	AATCAGGAAT	TTCCAGTTCA	GGAAATAGAC	840
TACATTACTT	TGCATTTGTT	AGCTAAGAGT	CAACAATGTC	AAAAAAATCA	GAAGAATATT	900
TCTGAAGAAG	TTTTAAAAAA	ATCTTTATTT	AAAACATTTT	AGAATTTAGG	ATTAGATGAT	960
ATGTATAACT	TTTCTTCAGA	TTTCCAAC TA	ATTGAAGGAT	TGATAACTCA	TCTAATGACA	1020
CTACAAGTAC	GTTTAGAAAG	CCGGATTACC	TTAAATAACC	CTTTAGTAGA	TGAAATTA AA	1080
CAGAATTATA	GTGATATATT	CTTTATGACT	AGAGAAATTC	TTGCAAATAT	GGACAAGTTC	1140
TTGGAGTGGA	CAATATCAGA	TGATGAAGTA	GCATATGTAA	GTCTTCACTT	TTTAGCTGCT	1200
ATGGAACGTA	GCAAAGAGAG	TACTAAGTTT	AATATTCTTG	CTATTTGTGC	AACAGGATTT	1260
GGTGCAGCCC	AAATGTTAAG	AAATCGTTTG	GAAACGGAGT	TTGGGAAGCG	AGTAGAAGTT	1320
GTTGATGTAA	TAGGCTATTA	TGAATTGAAT	CAAGAAAAAC	TTAAAGGAAT	AGATTTTATA	1380
GTGTCAGCTG	TTGATTTATC	AAATCTATAT	TTTCAAATCC	CAGTTTTTAA	AGTTAGTGTG	1440
TTTCTTAAGA	TGATGAGAT	GGAAATGATT	AGAAAAGCTA	TGGATCAGAT	GCAAGTTTCT	1500
AGTTATGTAC	CATCATCAAA	GATTAACAAA	TTTGAAAACA	ACGGCTTTAG	ACAGTATTTT	1560
AGTAAAGAAA	ATTTT TTAAT	ATGTACTGAA	TCAGACAAGG	TAAATTTACT	TGAAAAGATG	1620
GTTGAGGGTT	TATCTGTTGG	TGAATCAAAT	GAGTTTGAAC	AATCTTTACT	TTATGGAATT	1680
AAACAGCGCG	AAGAATTAAG	TTCAGTTGTT	TTTTCTGAAA	AAATTGCAGT	TCCGCATCCT	1740
ATTCAGCCCT	TTGGTACAGA	GGGAAAGGTT	TCGGTTGCAA	TCTGTAAAGA	TTCGTTACTC	1800
TGGGATAATC	AAAGTTCATA	TGTCCAGCTA	GTATTTCTTC	TATCTCCATC	AATATATGGG	1860
AACGAAGGTT	TGGCAACTGT	GACTAAAAAG	ATAGTCTCTC	TGACAGAGAA	TGATGAGTTG	1920
CAAAATCAGC	TAATATCTTG	CAATAACTTT	GAAGATTTTA	TTAACATATT	TGAGAAGATA	1980
AAATAG						1986

(2) INFORMATION FOR SEQ ID NO:1098:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...708
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

AGGCTGATGA	AGCAACTAAT	TAGTCTAAAA	AATATCTTCA	GAAGTTACCG	TAATGGTGAC	60
CAAGAACTGC	AGGTTCCTCA	AAATATCAAT	CTAGAAGTGA	ATGAGGGTGA	ATTTGTAGCC	120
ATCATGGGAC	CATCTGGGTC	TGGTAAGTCC	ACTCTGATGA	ATACGATTGG	CATGTTGGAT	180
ACACCAACCA	GTGGAGAATA	TTATCTTGAA	GGTCAAGAAG	TGGCTGGGCT	TGGTGAAAAA	240
CAACTAGCTA	AGGTCCGTAA	CCAACAAATC	GGTTTTGTCT	TTCAGCAGTT	CTTCTCTCTA	300
TCGAAGCTCA	ATGCTCTGCA	AAATGTAGAA	TTGCCCTTGA	TTTACGCAGG	AGTTTCGTCT	360
TCAAAACGTC	GCAAGTTGGC	TGAGGAATAT	TTAGACAAGG	TTGAATTGAC	AGAACGTAGT	420
CACCATTTAC	CTTCAGAATT	ATCTGGTGGT	CAAAAGCAAC	GTGTAGCCAT	TGCGCGTGCC	480
TTGGTAAACA	ATCCTTCTAT	TATCCTAGCG	GATGAACCGA	CAGGAGCCTT	GGATACCAAA	540
ACAGGTAACC	AAATTATGCA	ATTATTGGTT	GATTTGAATA	AAGAAGGAAA	AACCATTATC	600
ATGGTAACGC	ATGAGCCTGA	GATTGCTGCC	TATGCCAAAC	GTCAGATTGT	CATTCGGGAT	660
GGGGTCATTT	CGTCTGACAG	TGCTCAGTTA	GGAAAGGAGG	AAAACTAA		708

(2) INFORMATION FOR SEQ ID NO:1099:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1113
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GTGCCGATGA	ATATAATTCT	AATCGCCAAA	CTTTTGAGAG	AGAATACAAA	TACAAAAGCA	60
AATGCCCTTA	ATAATGGTTG	GGCTAGATCT	GGTCTGAAG	AGTTCAAAAA	GTTCTCCAC	120
TTTGTAGGGG	TAGACAAAGG	GATTGTGCGA	ACGAATGTAC	TGACTGGTAA	AAAACTATCT	180

GATAAGATTA	GGAAAGAAGT	GGGCTCTGGA	GATAGCAAAC	TAGGAAAAGG	CGGCTATTTT	240
TCTACTGGGG	ATGTTCTATT	AGGAAAAGAT	GTTGTTTCTT	ATACCGTACA	AGTATTTTCA	300
GAGAATAATG	AAAGAGTAGG	AGTAAACACT	CAAAGTCACC	GTGTTTCAGT	TAATCTCCCA	360
ATTCTAGCTG	ACTTTTCAGT	CATCCAAGAT	ACTGTGGAAC	CATCACGAAC	CGTTGTTGAA	420
AAAATCATT	CAAAACATAA	TATTTCCGAA	GAAGAGAAAG	GGAAAATAAC	CGAAGAAATC	480
AAGAAAAAGA	AAAAAACCTC	AGAATTGGCA	GAACTAATCT	CAGAAAATGT	GAAAGTTCGC	540
TATGTTGATG	AACAAGGGCG	TTTGCTATCA	TTGAAAAATG	ATACTGGAAT	TGGAGAAAAA	600
GAAAGTGACG	GAACCTACAT	TACCAATAAA	AAACAACCTG	TTGGTACCAG	CTACAATGTC	660
ACAGATAAAA	AACTCAGTAG	CATGACTACT	ACTGACGGAA	AATATTATAC	TTTTAAAGAA	720
GCAGATACAA	ATTCTGCAAG	TTTAACTGGG	AATATTGTAA	GCGAAGGTAG	AACAGTGACC	780
TTAGTTTATA	GAGAAAGCGA	AGCGCCAACC	ACTGCTACAG	TAACAGCCAA	TTACTATAAA	840
GAAGGTAGCC	AAGAGAAGTT	GGCAGAGTCT	GTTATAAAAG	CTGATTTAGC	GATAGGTTCT	900
GAGTATACCA	CAGAATCAAA	AACTATTGAA	GGGAAAACAA	CAACTGAGGA	CAAAGAAGAC	960
CGAGTTATCA	CAAGGAAAAC	AACATACACC	TTGGTAGCAA	CTCCTGCAAA	TGCGTACCAG	1020
AAGACGGTGC	AACAGTTGAC	TATTACTACC	GTGAGAATGT	TGAGGAAACA	GTGGTTCCCA	1080
AAACAGCAAC	CTCTACTGAG	ACGAAGACTA	TAA			1113

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

CAACAGATGA	AGATTGATAA	ATATTCTGCC	ATTTTAGGAA	ACTACCACGT	TGGTTTTTCAC	60
AATATGTCGA	CATTGACGGA	CCACCGTCCA	GTAGCAAGTT	TGCCATTTGG	TGGGAAATAT	120
CGTTTGATTG	ACTTCCCACT	TTCAAGCCTT	GCTAATGCAG	GTGTTTCGTAG	TGTCTTTGGT	180
ATTTTCCAGC	AGGATAATAT	CAGCTCAGTA	TTTGACCATA	TTCGTTTCAGG	ACGCGAGTGG	240
GGCTTATCAA	CCCTTCTTAG	TCATTACTAT	CTAGGAATTT	ACAATACCCG	TGTAGAAAGT	300
AGTACAGTTG	GAAAAGAATA	CTACCAACAG	CTTCTTACTT	ATTTGAAACG	TTCTGGCTCA	360
AACCAAACGG	TTGCCCTCAA	CTGCGATGTT	CTTATTAACA	TTGATTTGAA	CCAAGTTTTT	420
CACCTACATA	GTACAACAAA	AGAGCCTATC	ACTGTAGTTT	ATAAAAAACT	AGCTAAGAAA	480
GATATTTTCA	AAGTAAATGC	AATCTTGGAT	GTAGATGAAA	CAGACCATGT	TCTTTCTCAT	540
AAACTCTTTG	ATAGCAAGTC	AACAGCTGAA	ACGTTCAATA	TGTCTACAGA	TATCTTTGTC	600
GTTGATACAC	CTTGTTTGAT	TGAACACTTG	GAAGAAGAAG	CTAAAAAGA	ACATCCAGAG	660
AAATTGCGCT	ATGTTTTACG	GGATTTGGCT	GTAAAAGAGG	GAGCTTTCGC	CTACGAGTAC	720
ACGGGCTATC	TAGCCAATAT	TCACTCTGTT	AAATCTTATT	ATCAAGCGAA	TATCGATATG	780
CTTGAATCAC	AAAAATTCTA	TTCTCTTTTC	TCACCAAACC	AAAAGATTTA	TACAAAGGTC	840
AAAAACGAAG	AGCCAACTTA	CTATGCTAAT	ACATCTAAGG	TAAGCACTTC	TCAGTTTGCC	900
TCTGGTAGTA	TTATTGAAGG	TCAAGTAGCT	AATTCTGTTC	TATCACGTAA	TATTCATGTC	960

CATAAGGATA	GCTTGGTAA	AGATAGCCTG	CTCTTCCCTC	GTGTTGTTAT	TGGAGAAGGG	1020
GCTCAGGTCG	AATATGCTAT	CTTGGACAAA	GGGGTTGAAG	TTGAGCCTGG	TGTTGTGATT	1080
CGAGGAACTG	CAGAACATCC	AGTTGTGGTT	AAGAAAGGTG	CTAAAGTAAC	AGAGGATATT	1140
CATTCATGA						1149

(2) INFORMATION FOR SEQ ID NO:1101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...711
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

TGTAAGATGA	ATCAAGTAAT	CAATGCTATG	CGTAAACGAG	TCTGTGATGC	CAATCAATCA	60
TTGCCAAAAC	ATGGACTTGT	CAAATTTACC	TGGGGGAATG	TATCTGAAGT	CAATCGCGAA	120
CTCGGTGTCA	TTGTTATCAA	ACCATCAGGC	GTGGATTATG	ACGAATTGAC	ACCTGAAAAC	180
ATGGTAGTGA	CTGATCTAGA	TGTAAGATC	CTAGAAGGGG	ATTTAAGACC	ATCTTCCGAC	240
CTCCCAACTC	ATGTGCAATT	ATATAAGGCT	TGGTCAGAAA	TTGGTAGTGT	GGTTCACACC	300
CATTCGACAG	AAGCTGTTGG	TTGGGCTCAG	GCAGGTCGTG	ATATTCCTTT	CTACGGAACA	360
ACCCATGCAG	ATTATTTCTA	CGGTTCAATC	CCTTGCGCCC	GTAGTTTGAC	CAAGGACGAA	420
GTAGAAGTGG	CCTATGAAAA	AGATACTGGC	CTGGTTATCG	TAGAAGAGTT	TGAACATCGC	480
GGACTTAACC	CGGTTGAAGT	ACCAGGAATT	GTTGTACGCA	ATCACGGTCC	ATTCACCTGG	540
GGCAAAAATC	CAGAGGATGC	TGTTTATCAC	TCTGTTCGTAC	TAGAGGAAGT	ATCAAAGATG	600
AATCGCTTTA	CAGAACAAAT	CAATTCAAGA	GTTGAACCTG	CTCCCCAGTA	CATACTAGAG	660
AAACACTACC	AACGTAAACA	TGGACCAAAT	GCTTATTATG	GTCAAAAGTA	A	711

(2) INFORMATION FOR SEQ ID NO:1102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

AACAAGATGA	ACAAACCAAC	GATTCTGCGC	CTAATCAAGT	ATCTGAGCAT	TAGCTTCTTA	60
AGCTTGGTTA	TCGCAGCCAT	TGTCTTAGGC	GGAGGAGTTT	TTTTCTACTA	CGTTAGCAAG	120
GCTCCTAGCC	TATCCGAGAG	TAAACTAGTT	GCAACAACCT	CTAGTAAAAT	CTACGACAAT	180
AAAAATCAAC	TCATTGCTGA	CTTGGGTTCT	GAACGCCGCG	TCAATGCCCA	AGCTAATGAT	240
ATTCCCACAG	ATTTGGTTAA	GGCAATCGTT	TCTATCGAAG	ACCATCGCTT	CTTCGACCAC	300
AGGGGGATTG	ATACCATCCG	TATCCTGGGA	GCTTTCTTGC	GCAATCTGCA	AAGCAATTCC	360
CTCCAAGGTG	GATCAACTCT	CACTCAACAG	TTGATTAAGT	TGACTTACTT	TTCAACTTCG	420
ACTTCCGACC	AGACTATTTT	TCGTAAGGCT	CAGGAAGCTT	GGTTAGCGAT	TCAGTTAGAA	480
CAAAAAGCAA	CCAAGCAAGA	AATCTTGACC	TACTATATAA	ATAAGGTCCT	CATGTCTAAT	540
GGGAACATATG	GAATGCAGAC	AGCAGCTCAA	AACTACTATG	GTAAAGACCT	CAATAATTTA	600
AGTTTACCTC	AGTTAGCCTT	GCTGGCTGGA	ATGCCTCAGG	CACCAAACCA	ATATGACCCC	660
TATTCACATC	CAGAAGCAGC	CCAAGACCGC	CGAAACTTGG	TCTTATCTGA	AATGAAAAAT	720
CAAGGCTACA	TCTCTGCTGA	ACAGTATGAG	AAAGCAGTCA	ATACACCAAT	TACTGATGGG	780
CTACAAAGTC	TCAAATCAGC	AAGTAATTAC	CCTGCTTACA	TGGATAATTA	CCTCAAGGAA	840
GTCATCAATC	AAGTTGAAGA	AGAAACAGGC	TATAACCTAC	TCACAAC TGG	GATGGATGTC	900
TACACAAATG	TAGACCAAGA	AGCTCAAAAA	CATCTGTGGG	ATATTTACAA	TACAGACGAA	960
TACGTTGCCT	ATCCAGACGA	TGAATTGCAA	GTCGCTTCTA	CCATTGTTGA	TGTTTCTAAC	1020
GGTAAAGTCA	TTGCCCAGCT	AGGAGCACGC	CATCAGTCAA	GTAATGTTTC	CTTCGGAATT	1080
AACCAAGCAG	TAGAAACAAA	CCGCGACTGG	GGATCAACTA	TGAAACCGAT	CACAGACTAT	1140
GCTCCTGCCT	TGGAGTACGG	TATCTACGAT	TCAACTGCTA	CTATCGTTCA	CGATGAGCCC	1200
TATAACTACC	CTGGGACAAA	TACCCCTGTT	TATAACTGGG	ATAGGGGCTA	CTTTGGCAAC	1260
ATCACCTTGC	AATACGCCCT	GCAACAATCG	CGAAACGTCC	CAGCCGTGGA	AACTCTAAAC	1320
AAGGTCGGAC	TCAACCGCGC	CAAGACTTTC	CTAAATGGTC	TCGGAATCGA	CTACCCAAGT	1380
ATTCACTACT	CAAA TGCCAT	TTCAAGTAAC	ACAACCGAAT	CAGACAAAAA	ATATGGAGCA	1440
AGTAGTGAAG	AGATGGCTGC	TGCTTACGCT	GCCTTTGCAA	ATGGTGGAAC	TTACTATAAA	1500
CCAATGTATA	TCCATAAAGT	CGTCTTTAGT	GATGGGAGTG	AAAAAGAGTT	CTCTAATGTC	1560
GGAACTCGTG	CCATGAAGGA	AACGACAGCC	TATATGATGA	CCGACATGAT	GAAAACAGTC	1620
TTGACTTATG	GAAC TGACG	AAATGCC TAT	CTTGCTTGGC	TCCCTCAGGC	TGGTAAAACA	1680
GGAACCTCTA	ACTATACAGA	CGAGGAAATT	GAAAACCACA	TCAAGACCTC	TCAATTTGTA	1740
GCACCTGATG	AACTATTTGC	TGGCTATACG	CGTAAATATT	CAATGGCTGT	ATGGACAGGC	1800
TATTTCTAAC	GTCTGACACC	ACTTG TAGGC	AATGGCCTTA	CGGTCGCTGC	CAAAGTTTAC	1860
CGCTCTATGA	TGACCTATCT	GTCTGAAGGA	AGCAATCCAG	AGGATTGGAA	TATACCAGAG	1920
GGGCTCTACA	GAAATGGAGA	ATTCTGATTT	AAAAATGGTG	CTCGTTCTAC	GTGGAAC TCA	1980
CCTGCTCCAC	AACAACCCCC	ATCAACTGAA	AGTTCAAGCT	CATCATCAGA	TAGTTCAACT	2040
TCACAGTCTA	GCTCAACCAC	TCCAAGCACA	AATAATAGTA	CGACTACCAA	TCCTAACCAAT	2100
AATACGCAAC	AATCAAATAC	AACCCCTGAT	CAACAAAATC	AGAATCCTCA	ACCAGCACAA	2160
CCATAA						2166

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 948 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

AAGAAGATGA	AACAAACAAA	ACGAATTAAG	CGGTGGCGCT	ATTATCTGCG	CCGCTTTGCT	60
TATCAGATAA	AAATTTTACG	TGTCTTACAA	AGTATCTCTC	GAGAAAAGTA	TGATGAGAAG	120
ATTTCGGCCT	CTCTGGTCTA	TGGTTTTTTA	TCAGCAGTAG	CAGTTAATTT	CTTTTTCCAA	180
CCAGGGCATG	TGTATTCGAG	TGGTGCAACA	GGTCTGGCAC	AGATTATCTC	TGCCTTGAGT	240
AATCACTGGT	TTGGTTTTCA	TATTCGGATT	TCGCTAACCT	TCTACGCCAT	TAACCTCCCT	300
TTGATGGTCT	TAGCTTG GTA	TCAGATTGGC	CATAAGTTCA	CCGTCTTTAC	CTTTATCACG	360
GTATCTATGA	GTTCCCTCTT	TATCCAGTTT	GTCCCTGTGG	CAACCTTGAC	GGAGGATCCC	420
ATTATCAATG	CCCTTTTGG	TGGTGTGTG	ATGGGTTTGG	GGATTGGTTT	TGCTCTTCGA	480
AACAATATCT	CCAGTGGTGG	GACGGATATC	GTCAGCCTGA	CTATTCGCAA	GAAAACGGGT	540
AAGAATGTCG	GTAGTATTTT	TTTCTTG GTA	AATGGAACTA	TCATGCTGAT	AGCAGGTTTG	600
ACCTTTGGTT	GGAAATACGC	TCTTTATTCT	ATGATTACCA	TCTTTGTCTC	TAGCCGTGTG	660
ACAGACGCAG	TCTTTACTAA	GCAAAAGCGT	ATGCAGGCCA	TGATTGTGAC	AAATCATCCA	720
GAGAAGGTAA	TTGAAAAAAT	CCATAAAAAA	TTGCACCGCG	GAGCAACCAT	GATCCACGAT	780
GCAGAAGGAA	CCTATAATCA	CGAGAGAAAG	GCAGTTTTAA	TCACTGTCAT	TACACGTGCA	840
GAGTTTAATG	AATTTAAACA	GATTATGACA	CAAGTGGATC	CAAGCTCCTT	TGTCTCTGTC	900
TCGAAAAATG	TTCATATTCT	AGGAAGATTT	GTGGAGATAG	ATAATTAG		948

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 933 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

AAAACAGTGA	AATCTATTAA	ACGTTTTGCA	CTCTCGGCTA	TGGGAGTGGC	TATGTTGCTT	60
GTCTTGACTG	GCTGTGTCAA	TGTCGATAAA	ACCACAGGTC	AGCCAACAGG	ATTTATTTGG	120
AATACGATCG	GAGCGCCTAT	GGCTGAAGCC	ATCAAGTACT	TCGCTACTGA	TAAAGGTCTA	180
GGCTTTGGTG	TCGCTATCAT	TATCGTAACC	ATTATCGTAC	GCTTGATTAT	CTTACCACTT	240
GGTATCTACC	AATCATGGAA	GGCAACGCTT	CACTCTGAAA	AGATGAACGC	CCTCAAGCAC	300
GTCTTGAGC	CACACCAAAC	GCGTCTCAAA	GAAGCGACTA	CTCAAGAAGA	AAAACCTCGAA	360

GCCCAACAAG	CTCTCTTTGC	TGCTCAAAAA	GAGCACGGTA	TCAGCATGTT	TGGCGGTGTA	420
GGATGTTTCC	CTATCCTCCT	TCAAATGCCT	TTCTTCTCTG	CTATCTACTT	TGCTGCCCAA	480
CATACTGAAG	GGGTGCTCA	AGCAAGCTAC	CTAGGCATTG	CTCTAGGTTT	TCCAAGTATG	540
ATTTTGGTTG	CCTGTGCTGG	TGTCCTTTAC	TATCTTCAAT	CGCTCCTTTT	ACTTCACGGA	600
GTAAAAGATG	AAATGCCAAG	AGAACAAATC	AAGAAAATGA	TTTACATGAG	CCCACTCATG	660
ATCGTCGTCT	TCTCCCTCTT	CTCACCAGCT	AGTGTCACAC	TTTACTGGGT	TGTCGGTGGT	720
TTCATGATGA	TTCTCCAACA	GTTTATCGTC	AACTATATCG	TTCGTCCAAA	ACTTCGCAAA	780
AAAGTCCGTG	AAGAAGTAGC	CAAGAACCCA	CCAAAAGCAA	GTGCTTTCTC	TAAACCAAGT	840
GGACGAAAAG	ACGTTACCCC	TGAACAACCA	ACTGCTATCA	CAAGCAAGAA	AAAACACAAA	900
AATCGTAACG	CTGGAAAACA	ACGTTTCGAGA	TAA			933

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

ATAATGGTGA	AGGAATTTAA	GGAGGGAAGT	ATGAAAAATT	CGATTATGGA	TACAAAATTT	60
GATAGACGTA	TCTTACTCTT	AAATAAAATC	ATTATTGTCT	TTATCGTTTT	GATGACTTTG	120
CTTCCTTTAC	TTTATATCGT	CGTAGCATCC	TTTATGGATC	CTAAGGTTCT	GGTTAGTAGA	180
GGGATTAGCT	TTAATCCAGC	CGATTGGACT	GTAGAAGGTT	ATCAGCGTGT	ATTCAAGTGAC	240
CAATCTATTC	TAAGAGGTTT	TATCAATTCT	CTACTATACT	CTTTTGGATT	TGCAGCTTTA	300
ACAGTCTTGC	TATCTGTGTT	TACAGCTTAT	CCTCTTTCTA	AGAAAGACTT	GGTTGGACGT	360
CGTTGGATTA	ACTACTTCTT	GATTGTAAC	ATGTTCTTTG	GTGGTGGTTT	AGTCCCAACT	420
TACTTGCTCG	TAAAAGAATT	GGGAATGCTC	AATACTCCAT	GGGCAATCAT	TGTTCCAGGT	480
GCTGTCAATG	TTTGGAATAT	TATTCTTGCT	AGGGCCTATT	TCCAAGGATT	GCCTGAAGAA	540
TTAGTTGAAG	CTGCTGTCAT	TGATGGTGCA	AATGATTTAC	AGATTTTCTT	CAAAATCATG	600
CTTCCTCTTG	CAAAACCAAT	TATGTTTGTT	CTCTTCCTCT	ATGCTTTTGT	AGGACAGTGG	660
AACTCATACT	TTGATGCAAT	GATTTATATC	AAGGATCCAA	ACTTGGAACC	ATTGCAACTT	720
GTACTTCGTA	AAATTCTCAT	TCAGAGCCAA	CCAGGTCAAG	ACATGATTGG	AGCACAAGCG	780
GCTATGAATG	AAATGAAACG	TTTAGCTGAA	TTGATTAAAT	ACGCAACTAT	TGTCATTTCC	840
AGCTTGCCAT	TGATTGTTAT	GTATCCATTC	TTCCAAAAAT	ACTTTGATAA	AGGAATTATG	900
GCTGGTTCAC	TTAAAGGATA	A				921

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

CTCGTGGTGA	AGATAATCCA	AAAAGGAATA	TTTATCATGT	CGCAAGCTAT	TTCCTTAAAT	60
CAATCAACCT	GGGCAAGCAA	GCTAAAAGCA	ATGGGACCTG	GAATCCTAAT	GGCAACTGCC	120
GCTGTTGGAG	GTTCCACAT	TGTATCCCTCA	ACTCAAGCTG	GCGGTTCTTA	CGGTTGGTCT	180
CTACTTCTCT	TGGTCATCTT	AGCCAATGTC	TTTAAATATC	CATTTTTCCG	TTTTGGTGCT	240
GAATACACAG	CTGATACTGG	AAAGACTTTG	GTTGAAGGTT	ATGCCGAAAA	AGGAAAACCTC	300
TATCTCTGGA	TTTTCTTTAT	CCTCAATGTC	TTTTTCGGCTA	TGGTCAACAC	GGCTGGTGTT	360
GCCATTCTGT	GCTCAGCTAT	CATCGCCAGT	GCCTTCCCAA	TGATTGGACT	TAGCATTACT	420
CAGTGGTCCC	TCATTCTCGT	TGCAATCATT	TGGGCTATGC	TACTCTTTGG	AGGCTACAAA	480
CTTTTAGACG	GCATGGTCAA	ATGGATTATG	TCTGCCTTAA	CCATTGCGAC	TGTTCTTGCA	540
GTTATCATTG	CGGCGGTCAA	GCATCCAGAA	TACAGTTCTG	ATTTTGTCTGA	GAAGACACCT	600
TGGCAAATGG	CAGCTCTGCC	TTCATCGTCT	CCCTCCTAG			639

(2) INFORMATION FOR SEQ ID NO:1107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

TACTCTTCGA	AAATCTCTTC	AAACCACGTC	AGCGTCGCCC	TACCGTATGT	ATGGTTACTG	60
ACTTCGTCAG	TTTCATCTAC	AACCTCAAAG	CAGTGCTTTG	AGCTGACTTC	GTCAGTTTCA	120
TCTACAACT	CAAAAACATG	TTTTGAGCTG	ACTTCGTCAG	TTCTATCTAC	AACCTCAAAG	180
CAGTGCTTTG	AGCAACCCGC	GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	240

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

TACTCTTCGA AAATCTCTTC AAACCACGTC AGCGTCACAT TACCGTATAT ATGGTTACTG	60
ACTTCGTCAG TTCTATCCAC AACCTCAAAA CAGTGTTTTG AGCAGCCTGC GGCTAGCTTC	120
CTAGTTTGCT CTTTGATTTC CATTGAGTAT GAGAAGAAAT ATAGTGGATA CTCTTTAACA	180
TTAACCACTC CACCTGACTA G	201

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

CTTTTATCGA AAATTGGATT AACAACTACC CTAAAAAATG CTTGGACTAC AAGTCGCCAA	60
GTGAATTTCT TTTGGGTGGC TAACTTCAAC TTGAAATTTG GGATACCGAC ACTATATACA	120
TTAAGTAGTG GAAGAGTTCT ATCAAGTATT GATGCACGTT ATGGTGGGAC TCATGATTCT	180
AAAAGTAAGA TTAATATTGC CACTTCTTAT AGTGATGATA ATGGGAAAAC GTGGAGTGAG	240

CCAATTTTGT	CTATGAAGTT	TAATGACTAT	GAGGAGCAGT	TAGTTTACTG	GCCACGAGAT	300
AATAAAATTAA	AGAATAGTCA	AATTAGTGGA	AGTGCCTTCAT	TCATAGATTTC	ATCCATTGTT	360
GAAGATAAAA	AATCTGGGAA	AACGATATTA	CTAGCTGATG	TTATGCCTGC	GGGTATTGGA	420
AATAATAATG	CAAATAAAGC	CGACTCAGGT	TTTAAAGAAA	TAAATGGTCA	TTATTATTTA	480
AAACTAAAGA	AGAATGGAGA	TAACGATTTT	CGTTATACAG	TTAGAGAAAA	GGGTGTCGTT	540
TATGATGAAA	CAACTAATAA	ACCTACAAAT	TATACTATAA	ATGATAAGTA	TGAAGTTTTG	600
GAGGGAGGAA	AGTCTTTAAC	AGTCGAACAA	TATTCGGTTG	ATTTTGATAG	TGGCTCTTTA	660
AGAGAAAGGC	ATAATGGAAA	ACAGGTTTCCT	ATGAATGTTT	TCTACAAAGA	TTCGTTATTT	720
AAAGTGACTC	CTACTAATTA	TATAGCAATG	ACAAC TAGTC	AGAATAGAGG	AGAGAGTTGG	780
GAACAATTTA	AGTTGTTGCC	TCCGTTCTTA	GGAGAAAAAC	ATAATGGAAC	TTACTTATGT	840
CCCGGACAAG	GTTTAGCATT	AAAATCAAGT	AACAGATTGA	TTTTTGCAAC	ATATACTAGT	900
GGAGAACTAA	CCTATCTCAT	TTCTGATGAT	AGTGGTCAAA	CATGGAAGAA	ATCCTCAGCT	960
TCAATTCGGT	TTGAAAATGC	AACAGCAGAA	GCACAAATGG	TTGAACTGAG	AGATGGTGTG	1020
ATTAGAACAT	TCTTTAGAAC	CAC TACAGGT	AAGATAGCTT	ATATGACTAG	TAGAGATTCT	1080
GGAGAAACAT	GGTCGAAAAGT	TTCGTATATT	GATGGAATTC	AACAAACTTC	ATATGGCACA	1140
CAAGTATCTG	CAATTAATAA	CTCTCAATTA	ATTGATGGAA	AAGAAGCAGT	AAATTTGAGT	1200
ACACCAAATT	CTAGAAGTGG	CCGTAAGGGA	GGCCAATTAG	TTGTCGGTTT	GGTCAATAAA	1260
GAAGATGATA	GTATTGATTG	GAGATACCAC	TATGATATTG	ATTTGCCCTTC	GTATGGTTAT	1320
GCCTATTCTG	CGATTACAGA	ATTGCCAAAT	CATCACATAG	GTGTACTGTT	TGAAAAATAT	1380
GATTCGTGGT	CGAGAAATGA	ATTGCATTTA	AGCAATGTAG	TTCAGTATAT	AGATTTGGAA	1440
ATTAATGATT	TAACAAAATA	A				1461

(2) INFORMATION FOR SEQ ID NO:1110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1071 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1071
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

ATTAAATCGA	AAAATCTGAA	GAAAGGAGAG	ACGATGCTAG	CCATTGAAGA	AAGTCAGAAG	60
TTGACTTTAT	CAAATTTACC	GAGCCTGAGC	CTATTTACAG	GGACAGATCA	GGGTCAGTTT	120
GAAGTGATGA	AGAGTCAAGT	GTTGAAACAG	ATTGGGTATG	ATTCTGCTGA	CCTCAACTTT	180
GCCTACTTTG	ATATGAAAGA	AGTAGTTTAC	AAGGATGTGG	AACTGGAGTT	GGTCAGCCTT	240
CCTTTCTTTG	CGGATGAGAA	AATCGTGATA	TTAGATTATT	TTATGGATAT	CACGACTGCT	300
AAGAAACGCT	TTTTGACAGA	TGATGAGCTT	AAGTCATTTG	AGGAATACCT	TGACAATTCT	360
TCTCCAACAA	CCAAGTTGAT	AATCTTTGCA	GAAGGAAAGC	TGGATAGCAA	AAGACGGTTA	420
GTCAAATTAC	TTAAGCGTGA	TGCCAAGGTC	TTCGATGCAG	TAGAAGTAAA	AGAACAAGAA	480
TTGCGCCAGT	ATTTCCAAAA	GTGGAGTCAG	AAACAAGGTC	TGCAGTTTAC	CAATCATTCT	540
TTTGAAAATC	TCCTCATCAA	GTCGGGGTTT	CAATTTAGCG	AAATCCAGAA	AAATCTTCTC	600
TTTTTACAGT	CCTATAAGGC	GAATTCTGTT	ATTGAGGAAG	AGGATATTGT	TAACGCAATT	660
CCCAAGACCT	TGCAGGACAA	TATTTTTTGAT	TTAACTCAGT	TTATTCTGAC	TAAAAAGATG	720

GATCAGGCGC	GCGATTTGGT	GAGAGACTTG	ACCTTGCAAG	GGGAAGATGA	AATCAAACCTG	780
ATTGCAGTCA	TGCTGGGACA	ATTTTCGGACT	TTTACTCAGG	TGAAGATTTT	GGCGGAGTCT	840
GGCCAAACAG	AATCGCAGAT	TGCAAGTAGT	TTAGGTAGTT	ATCTGGGACG	TAACCCAAAT	900
CCTTATCAAA	TCAAGTTTGC	ATTAAGAGAT	TCGAGAGGAC	TTTCTTTGAG	CTTTTTGAAG	960
CAAGCTATTT	CCTATTTGAT	TGAGACAGAC	TATCAGATTA	AGACAGGTCT	TTATGAAAAA	1020
GGTTTCCTTT	TTGAAAAGGC	ACTCTTACAG	ATTGCTAGTC	AGGTCAATTG	A	1071

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

CAATTTCCGA	AAGGATCTAA	CCACAGCTTT	TTGTTTCAAT	TGGTCATGAG	TTTGATAACG	60
CATAAACGTT	TTATCTCGTG	TAATGAAAAC	ATCAAACATT	ACAAGAGGCT	CATTGACAAG	120
GCGGAAACAT	GTGTCAATGA	CTTGATGGCT	GAGTTCAACT	CGATCATAAC	GACGGTTACT	180
GGGATTGGGA	ATCGTTTAGG	GGCGGTCATT	TTAGCCGAGA	TTCGAAATAT	TCATGCCTTT	240
GATAATCCTG	CTCAATTACA	AGCTTTCGCT	GGACTGGATT	CTTCTATTTA	TCAGTCAGGT	300
CAGATTGATT	TAGCTGGAAG	AATGGTCAAA	CGGGGTTCCT	CTCATCTGCG	G TAG	354

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

ATGTATACGA	AAAGTAGGAC	GATAAAATCG	CTTATCACTC	AGTTTACGGC	TATCCTGTTG	60
TATGAGCTTC	CAGTAGCGCT	TGATAGCCTT	GTATTCATGG	GATTTTCGAT	GAAACTGATT	120
CATGATTTGA	ACACGCACAC	GACTCATAGC	ACAGCTAAGA	TGTTGTACAA	TGTGAAAGCG	180
AAGCTGTTTA	GCCAAGCCAT	AGTAAGGGCT	AAACATATCC	ATAGTAATAA	TTTTGACGCG	240
ACATCGGACA	ACTCTATCGT	AGCGAAGAAA	GTGATTTCTGA	ATGATAGCTT	GTGTTCTACC	300
CTCAAGAACA	GTGATGATAT	TGAGATTGTT	AAAATCTTGC	GCAATGAAGC	TCATCTTTCC	360
CTTTGTAAAA	GCATACTCAT	CCCAAGACAT	AATCTCAGGA	AGACAAGAAA	AATCATGTTT	420
AAAGTGAAAA	TCATTGAGCT	TACGAATAAC	AGTTGA			456

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

TTAATCACGA	AGGAAAGGAG	AAGTATAATG	GCAAATCGTT	TAAAAGAAAA	ATATCTTAAT	60
GAAGTAGTTC	CTGCTTTGAC	AGAACAATTC	AACTACTCAT	CAGTGATGGC	TGTGCCTAAA	120
GTAGATAAGA	TTGTTTTGAA	CATGGGTGTT	GGTGAAGCTG	TATCAAACGC	TAAAAGCCTT	180
GAAAAAGCTG	CTGAAGAATT	GGCACTTATC	TCAGGTCAAA	AACCACTTAT	CACTAAAGCT	240
AAAAAATCAA	TCGCCGGCTT	CCGTCTTCGT	GAAGGTGTTG	CGATCGGTGC	AAAAGTTACC	300
CTTCGTGGTG	AACGTATGTA	CGAATTCTTG	GATAAATTGG	TATCAGTTTC	ACTTCCACGT	360
GTACGTGACT	TCCACGGTGT	TCCAACAAAA	TCATTTGATG	GACGCGGGAA	CTACACACTT	420
GGTGTGAAAG	AACAATTAAT	CTTCCCAGAA	ATCAACTTCG	ATGACGTTGA	CAAAACTCGT	480
GGTCTTGACA	TCGTTATCGT	AACAACCTGCT	AACACTGACG	AAGAGTCACG	TGCATTGCTT	540
ACAGGCCTTG	GAATGCCTTT	TGCAAAATAA				570

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GAGAGAACGA	ACACTATGTA	CGCATATTTA	AAAGGAATCA	TTACCAAAAT	TACTGCCAAA	60
TACATTGTTC	TTGAAACCAA	TGGTATTGGT	TATATCCTGC	ATGTGGCCAA	TCCTTATGCC	120
TATTCAGGTC	AGGTTAATCA	GGAGGCTCAG	ATTTATGTGC	ATCAGGTTGT	GCGTGAGGAC	180
GCCCATTTGC	TTTATGGATT	TCGCTCAGAG	GATGAGAAAA	AGCTCTTTCT	TAGTCTAATT	240
TCGGTCTCTG	GGATTGGTCC	TGTATCAGCT	CTTGCTATTA	TCGCTGCTGA	TGACAATGCT	300
GGCTTGTTTC	AAGCCATTGA	AACCAAGAAC	ATCACCTACT	TGACCAAGTT	CCCTAAAATT	360
GGCAAGAAAA	CAGCCCAGCA	GATGGTGCTG	GACTTGGAAG	GCAAGGTAGT	AGTTGCAGGA	420
GATGACCTTC	CTGCCAAGGT	CGCAGTGCAA	GCAAGTGCTG	AAAACCAAGA	ATTGGAAGAA	480
GCTATGGAAG	CCATGTTGGC	TCTGGGCTAC	AAGGCAACAG	AGCTCAAGAA	AATCAAGAAA	540
TTCTTTGAAG	GAACGACAGA	TACAGCTGAG	AACTATATCA	AGTCGGCCCT	TAAAATGTTG	600
GTCAAATAG						609

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1005 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

TGGATGACGA	AAATATTACT	GTTTGGAGAA	CCATTAATTC	GAATCTCACC	ATTAGATGCC	60
ACCAGTATCG	GCGATCATGT	TGCCAGTTCG	ACTTATTTTG	GCGGATCAGA	AATTAACATC	120
GCTTGTAATT	TGCAAGCCCT	GGGTATCTCA	ACGAAAGTCT	TTACCGCACT	CCCTGCCAAC	180
GAGATTGGAG	ATCGTTTTCT	CACATTCTTG	AAACAGCACC	AAATCGATAC	CAGTTCAATC	240
TGTCGGCTTG	GCGATCGAAT	CGGCCCTAC	TATTTGGAGA	ACGGCTTTGG	TTGTCGTCAA	300
AGTGAAGTTT	TCTACGATCG	TAAGCATACG	AGTATCAGCC	AGATTCGGCC	AAACATGCTA	360
GATATGGATT	CTCTCTTTCA	GGGGATTAGC	CATTTTCATT	TTAGTGGAAT	CACCGTAGCT	420
ATCGGTCAAG	AGGTCCGTGC	GATCCTTCTC	CTACTCTTGG	AAGAAGCCAA	GCGCCGAGGA	480
ATTGTCGTTT	CAATGGATCT	CAATCTGAGA	ACAAAGATGA	TTTCAGTCCT	AGAAGCCAAG	540
TATGAATTTT	CTAAGTTTGC	ACGTTTACT	GACTATTGCT	TCGGTATTGA	TCCTCTCATG	600

ATTGATGACC	AAAATCTAGA	GATGTTTCCA	AGAGACAGTG	CTAGCCTAGA	AGAGGTGGAA	660
AATCGCATGC	GACTTTTAAA	AGAAGCCTAT	GGTTTCAAGG	CCATTTTCCA	TACCCTCCGA	720
TCTAGTGATG	AGCAAGACAA	AAATGTCTAT	CAAGCCTATG	CTCTGGAAGA	ACGATTTGAA	780
GAGTCTGTCC	AACTAAAAAC	TGCAGTCTAT	CAACGAATTG	GTAGCGGGGA	TGCCTTTATA	840
TCTGGTGCCC	TTTACCAACT	ACTCCATCAT	TCCTCCCTAA	AAACTACCAT	TGACTTTGCA	900
GTTGCGAGCG	CAACTCTCAA	ATGCACTCTT	CCAGGAGACC	ATCTCTCCAC	TTCCGCAACT	960
AGTATTGAAA	ATTTACTGGC	AAATGCACAA	GATATCATTC	GTTAG		1005

(2) INFORMATION FOR SEQ ID NO:1116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 975 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...975
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

CTCTTTGCGA	ATAGTATAGG	TGAGGAGGTA	AGTATGGTTC	AAGAAATTGC	ACAAGAAATC	60
ATTCGTTCAG	CTCGGAAAAA	AGGGACGCAG	GATATCTATT	TTGTCCCTAA	GTTAGACGCC	120
TATGAGCTTC	ATATGAGGGT	AGGAGACGAG	CGCTGTAAAA	TTGGTAGCTA	TGATTTTGAA	180
AAGTTTGCA	CCGTTATCAG	TCACTTTAAG	TTTGTGGCGG	GTATGAATGT	GGGAGAAAAA	240
AGACGTAGTC	AACTGGGTTC	CTGTGATTAT	GCCTATGACC	ATAAGATAGC	GTCTCTACGT	300
TTATCTACTG	TAGGCGATTA	TCGGGGGCAT	GAGAGTTTGG	TTATCCGTTT	GTTGCACGAT	360
GAGGAGCAGG	ACCTGCATTT	TTGGTTTCAG	GATATTGAAG	AATTAGGCAA	GCAGTACAGG	420
CAACGGGGAC	TCTATCTTTT	TGCTGGTCCG	GTTGGGAGTG	GTAAGACGAC	CTTGATGCAT	480
GAATTGTCCA	AGTCACTCTT	TAAAGGACAG	CAAGTTATGT	CCATCGAAGA	TCCTGTGCGA	540
ATCAAGCAGG	ACGACATGCT	TCAATTGCAG	TTGAACGAAG	CAATCGGCCT	AACCTATGAA	600
AATCTAATCA	AACTTTCCTT	GCGTCATCGA	CCAGATCTCT	TGATTATCGG	AGAAATTCGT	660
GACAGCGAGA	CGGCGCGTGC	AGTGGTCAGA	GCTAGTTTGA	CAGGTGCGAC	AGTCTTTTCA	720
ACCATTACAG	CCAAGAGTAT	CCGAGGTGTT	TATGAGCGTC	TGCTGGAGTT	GGGTGTGAGT	780
GAAGAAGAAT	TGGCAGTTGT	TCTGCAAGGA	GTCTGCTACC	AGAGATTAAT	CGGGGGAGGA	840
GGAATCGTTG	ACTTTGCAAG	CAGAGATTAT	CAAGAACACC	AAGCAGCCAA	GTGGAATGAG	900
CAAATTGACC	AGCTTCTTAA	AGATGGACAT	ATCACAAGTC	TTCAGGCTGA	GACGGAAAAA	960
ATTAGCTACA	GCTAA					975

(2) INFORMATION FOR SEQ ID NO:1117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

ATTGGAGCGA	AAATGAAACG	AACAGGTTTA	TTTGCAAAGA	TATTTATCTA	TACCTTCTCG	60
ATATTTAGTG	TTCTGGTTAT	CTGCC TTCAT	TTAGCTATTT	ATTTTCTTTT	TCCTTCGACT	120
TATCTGAGTC	ATCGTCAGGA	AACCATTTGGT	CAAAAGGCAA	CAGCCATTGC	CCAGTCCCCTA	180
GAAGGGAAAAG	ATAGGCAGAG	TATCGAGCAA	GTGTTAGACT	TGTATTCCCA	GACTAGTGAT	240
ATCAAGGGGA	CCGTCAAAGG	TGAGATGACC	GAGGACAAGT	TAGAGGTCAA	GGACAGTCTT	300
CCTCTGGACA	CAGACCGCCA	GACAACCTCT	CTCTTTATTG	AGGAGCGCGA	GGTGAAAACG	360
CAAGACGGTG	GTACTATGAT	TCTCCAGTTT	CTAGCTTCCA	TGGATTTACA	AAAGGAAGCG	420
GAGCAAATCA	GTCTCCAGTT	TCTTCCCTAT	ACCTTGCTGG	CCTCCTTTCT	GATTTCCCTC	480
TTGGTGGCCT	ACATCTACGC	TCCGACTATT	GTTGCACCGA	TTTTGGAAAT	CAAGCGGGTG	540
ACCCGTCGGA	TGATGGACCT	GGATTCCCAA	GTGCGATTGC	GCGTGGATTC	TAAGGATGAG	600
ATAGGTAATC	TCAAGGAACA	AATCAATAGC	CTTTACCAGC	ATCTCTTGAC	TGTTATTGCG	660
GACTTG CATG	AAAAGAATGA	AGCCATTCTC	CAGCTGGAGA	AGATGAAGGT	CGAATTCCCTA	720
CGAGGAGCTT	CTCATGAATT	GAAAAACCCG	CTGGCTAGTT	TGAAAATCCT	AATCGAAAAT	780
ATGAGAGAGA	ATATCGGTCG	TTATAAGGAT	AGAGACCAGT	ATCTGGGAGT	TGCCTTGGGG	840
ATTGTGGATG	AACTCAATCA	CCATGTTCTG	CAGATACTTT	CCCTCTCTTC	TGTGCAGGAA	900
TTGCGAGATG	ATAGGGAAAC	AATTGACCTC	CTCCAGATGA	CGCAAAATCT	GGTCAAAGAT	960
TATGCCTTGC	TAGCCAAGGA	AAGAGAGCTC	CAGATAGACA	ATAGTTTGAC	CCATCAGCAG	1020
GCTTATCTAA	ACCCATCAGT	TATGAAGTTG	ATTCTTTCTA	ATCTCATCAG	CAATGCCATT	1080
AAGCACTCTG	TTCCAGGTGG	CTTAGTTCTGA	ATTGGAGAAA	GAGAAGGAGA	ACTTTTTTATC	1140
GAAAATAGCT	GTAGCTCAGA	GGAACAAGAA	AACTAGCCC	AGTCTTTTTC	TGACAAATGCT	1200
AGTCGCAAGG	TCAAGGGGTC	TGGTATGGGG	CTCTTTGTGG	TTAAGAGTCT	ATTAGAACAT	1260
GAAAAATTAG	CTTATCGTTT	CGAGATGGAG	GAGAATCGTT	TAACCTTCTT	TATAGATTTT	1320
CCAAAAGTCG	CCCAAGACTA	G				1341

(2) INFORMATION FOR SEQ ID NO:1118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

AGATCGGCGA	ATACCAGAAA	GGCCAGGACA	GCGAAGCCGA	CCAGGCCATC	GAGAAGATCG	60
CGGCGATCCG	CCAGTGGCTG	CGCCAGGGTA	CCCACGAAAC	CAGCGATTAC	GCACAGGCCT	120
GCGCGCAGTT	GCGGAGCCTC	TGCGCATGAG	CCTGGCGCTG	CTGTTGCGCG	TCCGACGCCT	180
GCGCCTGGAC	CGGGCCGAGC	GCGCCCAGGG	CCGCCAATTG	CTACGGGTTC	GCGCCGCGGC	240
GCAGGAACAC	ACCGAGCGCC	AGGCGGCGCA	ACGGGACTAC	CGCGACTGGC	GA CTGGCCGA	300
AGAGCAACGG	CTGTTTCTCG	CCTGCCAGGC	GGCCATGCTC	GACCGCCGGC	GCCTGGAAGC	360
CTGGCAGCAG	CAGGTAGGAC	TGCTGCGGGA	AAAGGAAGCC	GGCCTGGAAC	AGGACTGCGC	420
CGAGACCGCG	CAGCGCCTCG	AAGGGGAGCG	CGAGCGCCTG	CGGCAGTGCC	GGCGAGAACT	480
GCTGGAACGC	CAGCGGCAAC	TGGAGAAATT	CGCCGAAC TG	GAGCGCCACG	TCGACGCCGA	540
GCGCCAGGGG	CTGCGCGAAC	GCAGCGAGGA	AGGCGAAC TG	GAAGAATTCA	CCCGCCACGA	600
GACCTGGCCA	TGCTCAAGCT	GAACGCCGTG	GATACGGCTC	CGCTCGTGTC	GTCCGACACC	660
CCTGCCCCCC	TTCCGCCGCT	GCGCGCGCAG	CAGATCGCCT	TCGAACAGGC	CCTGCCCGCG	720
CACCGACCGC	CGGCGCCCAG	GCCACCGTTC	GACAAGGGCG	ACGAAACGAC	AGAGGCCGAA	780
GAGCCCGCCG	CGAACAGCGA	CGCGCCGACC	TCGACGCCTC	TCGCCGACCA	GCCCGCGGCG	840
CCTGCCGCCG	ACCGGCCGCC	GACCAATNGG	CAAGCCCCCG	TGCCAGTTGC	CGCGGAAGCA	900
ACGCCAACGC	CAACGCCAAC	GCCAACGCCA	ACGCCAACGC	CAACGCCAAC	GCCAACAGTG	960
TTGCCGTCCG	GATCGGTAGC	ACGGCAAGCG	CCGGCGGTTT	CCGCGCGCGT	CGCGGCGTCC	1020
ACGCAAGCCC	GGGAGCCGGC	CAGCGTTTCG	GCGCCTCCGG	TCGACGAACC	GCCGCTGGTG	1080
CCGCTGTCCCT	CCCACCCGCA	AATCGCAGGT	CGGACGCATG	AGCGGCCACA	GCCCGGCCCC	1140
GGCTTCCCCG	CGAAAACCGC	AGCCGAGGTC	GCGTCCACGG	CGCAGGCCAG	TGTCCAGGTC	1200
TCGCCGCCCC	CGCCGACAGC	GGGCGGCGAA	GGCCGCGGAG	AGGAGCGTCG	GCAACCCGGA	1260
GAAACCGATC	CATCCGCACT	GCCCCCCGAC	GACCAAGCGC	CTGTGCCATT	GCCTGCCATG	1320
CAAACCCCCG	GCGACCGCCT	GCTGGCACGC	CTGCTGGCAT	CGAGCGGGAG	CCGGCCACTG	1380
CCGCTGGCCG	ATCTCGCGCG	CCTGCTAGAT	GCCGTGCAGG	GGCGCATCCA	GGTCGCCAGC	1440
GCAGCCGAAA	GCCATGCGGC	GCGCCTGCAG	GTGCGACTGC	CCCAGCTCGG	CGCCGTGGAG	1500
GTGCAGGTCC	TGCATGGCCA	TGGCCAGTTG	CAGGTCGTCT	TCACCACGAG	CCGGGAGGTC	1560

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

ATAAATCAGA	ATAGAAAGAG	AAGTATGTAT	AAGACAAAGT	GTTTACGAGA	GAAGTTAGTA	60
TTATTTTAA	AAATTTTCTT	CCCAATCCTG	ATCTACCAAT	TTGCCAATTA	TTCTGCCTCT	120

TTTGTGATA	CTGCAATGAC	AGGTCAATAC	AACACTATGG	ACTTGGCTGG	TGTATCTATG	180
GCAACCAGTA	TCTGGAATCC	TTTCTTTTACA	TTTCTAACAG	GGATTGTGTC	AGCCTTGGTG	240
CCTATCATTG	GTCACCATCT	TGGTCGAGGC	AAAAAGGAAG	AAGTTGCGTC	TGATTTTTTAC	300
CAATTTATTT	ATTTGGCCTT	GGGCTTATCT	GTGGTCTTGC	TGGGGATGGT	ACTTTTCTTG	360
GCACCAACAA	TCTTGAATCA	TATTGGGTTA	GAAGCAGCAG	TAGCGGCAGT	AGCGGTTCGC	420
TATCTTTGGT	TTTTATCTAT	CGGGATTATC	CCCTTGTTGC	TCTTTAGCGT	CATTCGTTCC	480
TTGCTGGATT	CGCTGGGCTT	GACCAAACCTG	TCCATGTACC	TCATGCTTTT	GTTACTCCCT	540
CTCAATAGCG	GATTTAACTA	TCTCTTGATT	TACGGTGCCCT	TTGGTGTTC	AGAACTGGGA	600
GGGGCTGGTG	CTGGTTTAGG	AACATCCTTG	GCCTACTGGG	TCTTGCTTGG	GATTTCTGTT	660
CTGGTTTTAT	TTAAACAGGA	GAAGCTCAAA	GCCTTACACC	TTGAGAAACG	AATTCACCTT	720
AATATGGATA	AAATTAAGGA	AGGAGTTCGT	TTAGGTCTGC	CTATTGGGGG	AACTGTCTTC	780
GCGGAAGTGG	CTGTCTTTTC	AGTGGTTGGC	TTGATTATGG	CTAAGTTTTC	GTCTTGATT	840
ATAGCTAGTC	ACCAGTCAGC	TATGAACTTT	TCAAGTCTTA	TGTACGCCTT	TCCTATGAGT	900
ATCTCATCGG	CTATGGCTAT	TGTCGTTTCC	TATGAAGTGG	GAGCCAAGCG	ATTTGATGAT	960
GCGAAAACCT	ATATTGGTCT	AGGAAGATGG	ACTGCCCTCA	TTTTTGCGGC	CTTCACCTTA	1020
ACCTTCCTTT	ACATTTTATG	GGGAAATGTG	GCCAGTCTTT	ATGGTAACGA	CCCAAAATTT	1080
ATCGATTTGA	CAGCGCGTTT	TTTAACTTAT	AGTCTTTTCT	TCCAGTTAGC	AGATACCTTT	1140
GCGGCGCCGC	TTCAGGGAAT	TTTGCGGGGG	TATAAGGATA	CAGTTATTCC	TTTTTACCTT	1200
GGTTTGCTTG	GTTATTGGGG	CGTAGCAATC	CCTGTGGCTA	CGCTATTTGA	TTCCCTAACA	1260
GATTTTGGAG	CTTATTCTTA	CTGGATCGGC	TTGATTATTA	GTTTGATTGT	GAGCGGGGCG	1320
CTCTACCGTT	GCGGTTTAAC	TGTGATTATG	AAGAGATTTG	AATCTTTAGC	AAAATCCAAA	1380
CGCTAA						1386

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

AAGTACCAGA	AAACGAGACG	GTCAGCCAAC	GCGTCTGTGA	AGATGGTCCT	GTTTTCCGCA	60
CAGGAACAGT	TGTATTATAA	GGAGAAAATT	ATGACTACAA	ATCGATTACA	AGTTTCTCTA	120
CCTGGTTTGG	ATTTGAAAAA	TCCGATTATT	CCAGCATCAG	GCTGTTTTGG	CTTTGGACAA	180
AAGTATGCCA	AGTACTATGA	TTTAGACCTT	TTAGGTTCTA	TTATGATCAA	GGCGACAACC	240
CTTGAACCAC	GTTTTGGGAA	TCCAACCTCA	AGAGTGGCAG	AGACGCCTGC	TGGTATGCTC	300
AATGCAATTG	GCTTGCAAAA	TCCTGGTTTA	GAGGTTGTTT	TGGCTGAAAA	GCTACCTTGG	360
CTGGAAAGAG	AATATCCAAA	TCTTCCTATT	ATTGCCAATG	TAGCTGGTTT	TTCAAAACAA	420
GAGTATGCAG	CTGTTTCTCA	TGGGATTTCC	AAGGCAACTA	ATGTAAAAGC	TATCGAGCTC	480
AATATTTCTT	GTCCCAATGT	TGACCACTGT	AATCATGGAC	TTTTGATTGG	TCAAGATCCA	540
GATTTGGCTT	ATGATGTGGT	GAAAGCAGCT	GTGGAAGCCT	CAGAAGTGCC	AGTTTATGTC	600
AAATTAACCC	CGAGTGTGAC	CGATATCGTT	ACTGTCGCAA	AAGCTGCAGA	AGATGCGGGA	660

GCAAGTGGCT	TGACCATGAT	CAATACTCTG	GTTGGAATGC	GCTTTGACCT	CAAAACCAGA	720
AAACCAATCT	TGGCCAATGG	AACAGGTGGA	ATGTCAGGTC	CAGCAGTCTT	TCCAGTAGCC	780
CTCAAACCTCA	TCCGCCAAGT	AGCCCAAACA	ACAGACCTGC	CTATCATTTGG	AATGGGGGGA	840
GTGGATTTCGA	CTGAAGCTGC	CCTAGAAAATG	TATCTGGCTG	GGGCATCTGC	TATCGGAGTT	900
GGAACAGCTA	ACTTTACCAA	TCCTTATGCC	TGCCCTGACA	TCATCGAAAA	TTTACCAAAA	960
GTCATGGATA	AATACGGTAT	TAGCAGTCTG	GAAGAACTCC	GTCAGGAAGT	AAAAGAGTCT	1020
CTGAGGTAA						1029

(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

TTTNCCAGA	AAAGTGTGGA	TACGGCATCA	CGAAATCCGC	TTATTGGCCT	GGACAATGCA	60
ATATGGCATA	ATTCAAGTAC	CTTAAATATT	CCGACTAATA	TTGATTTGAC	CTCTATTCCCT	120
CCATACACAC	CAGAGATGAA	CCCATTGAAC	AAGTGTGGAA	AGAGATTCGT	AAACGTGGAT	180
TTAAGAATAA	AGCCTTTCGA	ACTTTGGAAG	ATATCATGA			219

(2) INFORMATION FOR SEQ ID NO:1122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

TGGTTACAGA	AGCTAGAAAA	GAAGAATGTA	ATGAACGAAA	TCAAATGTTT	CAACTGTGGG	60
GGAGTCTNTA	CAGTAAATGA	AAGCCAGTAT	TCTGAACTTT	TGTCCCAAGT	GAGAACGGCA	120
GAGTTTGATA	AGGAACTACA	CGATAGGATG	AGGCAGGAAC	TGGCCTTGGC	TGAGCAAAAAG	180
GCTATGAATG	AGCAACAGAC	TAAACTGGCT	CAGAAGGATC	AAGAAATTGC	GCAATTGCAG	240
AGTCAAATCC	AAAACTTTGA	TACAGAAAAA	GAATTGGCCA	AGAAAAGAAGT	TGAACAGACA	300
AGCCATCAGG	CCTTATTGGC	TAAGGACAAG	GAAGTACAGG	CCTTGGAAAA	CCAGTTGGCG	360
ACCTTGCGTT	TGGAGCATGA	AAATCAATTG	CAAAAGACCC	TTTCTGACCT	AGAAAAAGAA	420
CGCAATCAGG	TCAAAAATCA	GCTCCTACTG	CAAGAAAAGG	AAAATGAGTT	GTCCTTGGCT	480
TCTGTTAAGC	AAAACTACGA	AGCCCAGCTC	AAAGCAGCCA	GTGAACAAGT	CGAGTTTTAT	540
AAGAAATTTA	AGGCTCAACA	ATCTACAAAA	GCGATTGGGG	AAAGCCTAGA	ACAGTATGCA	600
GAGAGTGAGT	TTAACAAGGT	TCGTAGTTTC	GCCTTTCCAA	ATGCTTACTT	TGAGAAGGAT	660
AACAAGGTCT	CTTCGCGTGG	GTCTAAAGGG	GACTTTATCT	TCCGTGAGTG	TGATGAAAAT	720
GGAGTTGAAA	TCATTTCTAT	CATGTTTGAG	ATGAAAAACG	AAGCGGACGG	AACAGAGAAG	780
AAGCACAAGA	ATGCAGATTT	TTACAAGGAA	TTGGACAAGG	ACCGTCGGGA	GAAGAACTGT	840
GAGTATGCCG	TTTTGGTGAC	CATGCTTGAG	GCTGATAATG	ACTACTTTAA	CACAGGGATT	900
GTTGACGTCA	GTCACGAGTA	TGAAAAAATG	TATGTTGTTC	GTCCTCAATT	CTTTATCCAA	960
TTGATTGGTC	TCTTACGTAA	TGCGGCGCTA	AATTCCTTAA	AATACAAGCA	GGAGTTGGCC	1020
TTGGTTCGCG	AGCAAAATAT	TGACATTACG	CATTTTGAGG	AAGACTTGGA	TGCCTTTAAG	1080
CTAGCTTTTG	CTAAGAACTA	TAATTCAGCT	TCGACTAACT	TTGGAAAAGC	TATTGATGAA	1140
ATCGACAAGG	CCATCAAACG	CATGGAAGAG	GTTAAGAAAT	TCCTGACTAC	ATCTGAAAAC	1200
CAACTCCGTC	TAGCTAACAA	CAAATTGGAA	GATGTCTCTG	TTAAAAAATT	GACCCGGAAA	1260
AATCCAACAA	TGAAAGCGAA	GTTCGAAGCA	CTGAAGGGGG	AGTAG		1305

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

AAAAATAAGA	AGATAGTTGC	AATAAATAAC	GGAATTAATG	TATCAAATAG	CGATTTAGAT	60
GTAGTAGGTG	TTCAAGACTT	TAAAAAAGAA	TTTGTATATC	CAAATAACAA	AAAAATCATT	120
TGTTATGTTG	GAAGGTTGGA	TCCAGAAAAA	AGGCCGGATA	GATTCCCTGA	ATTTGCAGAA	180
AAATTATTTT	TAGTCAGAGA	AGATGTGATT	TTTATTATGG	CTGGAAATGG	TAGTATGTGG	240
GCTGCTTTGA	AAGAAAAAAT	TTGCCATTTG	AAATGTAGAG	ATAATTTFCAG	GTTACTTGGT	300
GAAATCTATC	CAGCTACTAT	AGTTTACCAA	ATATCGGATT	TATTGTATAT	TCCTTATGAT	360
ACAGAAGGAA	TACCTATGTG	TGTTTTAGAG	TCAATGTCAC	AAGGAACTCC	GGTTTTAGCT	420
AGTAATGTTG	GCGGGTTAAG	TGAAATTATT	GAACATAGGG	TTGATGGATT	TTTATTTGAG	480
AAGGAAGATG	TTGAGGGAGT	GTGTGCTTGT	GCTAATTTTT	TACTCAATGA	TTCTGAGTAT	540

TTGAAATATA TAGGTGAGAA TAGTAAATCA AAAATAAGAA AACATTTTTC TGTGCAAAAA	600
ATGTTTGTAG AAACCATGAG AGTATATGAT GAATTATTAG AGAAGAGTAG TCATGGATAG	660

(2) INFORMATION FOR SEQ ID NO:1124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

ATGAATAAGA AAAAAATGAT TTTAACAAGT CTAGCCAGCG TCGCTATCTT AGGGGCTGGT	60
TTTGTTACGT CTCAGCCTAC TGTGTAAGA GCAGAAGAAT CTCCCGTAGC CAGTCAGTCT	120
AAAGCTGAGA AAGACTATGA TGCAGCAGTG AAAAATGCTA CAGCTGCAA AAAAGCAGCA	180
GAAGATGCTC AAAGAGCTTT AGATGAAGCA AAAGCTGCGC AGAAAAAATA TGACGAGGAT	240
CAAAAGAAAA CTGAGGAGAA AGCGAAAGAA GTAAAAAAG CTTCGGAAGA GAACAAGCTG	300
CAAATCTGA	309

(2) INFORMATION FOR SEQ ID NO:1125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...6372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

AGAGGTAAGA AAATGGACGC TTAACTAGA CGACAATTTG ACAGAGCCAT GTTGCCAAG	60
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GAAAGGACGC	TGGCTATTTCG	TGTTGGTGAA	TATGCTTCAC	GGGATATCAA	AGAGGCTAGT	120
TTTGAGTATG	GCTACATCAA	GGGCGATACT	TATAAGCCTG	GTGGAACCTG	CGCTGGTAGC	180
GGTAAAAATTA	CCTTTACCAG	TATCATTACC	ACGTTCAATA	AGCTGGATAC	CCTGCACCCT	240
GAGATTGGTC	TACTGGTTGG	GGATACCTAC	CAGTGGGTCA	AGATGGGGGA	ATACTTCATC	300
AACGATATTG	AGATTGACCG	AAACCGCAAC	ACAACCACAC	TTGAACTTAT	GGACGGTATG	360
TTTAAGCTCA	ATCGTGAGTA	CGTGACGGAT	TTGCATTTCC	CAGCTGAAGT	ACGAGAGGTT	420
ATTTCAGGAAA	TCTGCCTGAA	AACAGGCATT	GAGTTAGCGA	ATGACTATTT	CGGAATCAGC	480
GCTATGCGTT	ACCATATCGA	GCAAGTTCCT	GAAGGTAAGA	AACTTTCGTT	CAGGGATATG	540
CTGAGCGCTA	TGACTCAGAT	GATTGGGATG	TCTTGCTTCT	TCAACCGAGA	AGGAAAGATG	600
GAAATCCGTG	ATTTGACCGA	GTCCAACATC	ACGATTAACG	CTGACAGTTA	CTTCTTGCA	660
GGATTGACCA	AGAGTGAAAT	CGAGTATCAG	ATAGCTGGTA	TCACTTGATA	GACGGATAAG	720
AAGTCTCTGA	CGGTCGGTAT	GACAACAGGT	CGGTCTTTGG	AACTTGATAA	TGTCCTTCATA	780
ACCCAGAGCG	CTTTAAATGA	CTTGTATTAC	AAACTGAAAA	ACCTAACTTA	CTATCCGTAT	840
AATCTCAACT	ACCAAGGACA	TTTGTACTTT	GAGGTTGGGC	AGTGGGTAAC	CATTTCAGACC	900
AACAAGAAAAG	AGACTTTTAA	AGTTCCTGTC	TTAAGTCAGA	GCTTTATCTT	TAAAGGTGGT	960
CTGAGAGGTC	GTATCAGTGC	AGATAGTAAG	GCTGGAAACG	ATACCCAGTA	TTCTTACGAG	1020
GGTACGATTA	CCAAGCAGAT	TAAGCAACAA	GATGGCTTTG	AAGCGAAAAT	CCAAGCGCAG	1080
ATTGAAGCAG	CAGATAAAGA	TTTTGACCAA	AAGGTCGACA	AAATCAAAAA	AGACTTTAAC	1140
GATCAAGTAG	AACTGGCCAA	AGCCAGAGCT	GAAGAAGTCA	AGAGAGAACT	GTCTGACACT	1200
ATCAATCAGC	GCTTTAATAG	CTTTGACAACT	GGGCCATTGA	AAGAAGCTAA	GCGCAAGGCT	1260
GAGGAAGCTT	TGCGAAATGC	TGGCGCAAGT	AGTTCTCTTG	CTCAGGAATC	CAAGCGGATT	1320
GGGCTGGATT	CTGTTGCTAG	ACTTGAAGCG	TTTAAGTTCG	AGACTACGAG	CGCACAAAACG	1380
GCTCTGTTCGG	GTGACTTTGGA	TGTTCTAAAA	CGAACTATCG	CAAACGATAT	TCGACCGAAG	1440
CAAGCACAGG	CTGAAGCTGA	GATTGCCAAG	CAAGTTGAAG	CACCTTAGCCG	GACTAAAAAT	1500
GAAGTGGATG	GCGCAAGTAC	CCTGCTTGCA	CAGGAAGCTA	AGCGGATTGA	GCTGGATTCT	1560
GTTGCTAGAC	TTGAAGCGTT	TAAGTCGCAG	ACTACGAGCG	CACAAACGGC	TCTGTCAGGT	1620
GACTTGGATG	TTCTAAAACG	AACTATCGCA	AACGATATTC	GACCGAAGCA	AGCACAGGCT	1680
GAAGCTGAGA	TTGCCAAGCA	AGTTGAAGCA	CTTAGCCGGA	CTAAAAATGA	ACTGGCTGGC	1740
GTGAAGTCAG	CGCAAGCGAC	GTATGAGGAG	ACGACGACTC	GTAGACTGTC	AGAACTGACC	1800
AACTTGGCCA	ATGGTAAAGC	CAGCAAGTCA	GAACCTCACGC	AAACAGCTGA	GGAGCTGGCT	1860
AGTCGGATTG	CGAGTGTGCA	GGCAGGTAGT	TCACGGAATT	ACTTCAGAAA	TTACAGTTCA	1920
AGAACGTTCA	CAACAGGAGG	TCAAGCGGTA	TACGACTATC	GAACATTTCAT	AGTTCCCTGAT	1980
TTCTGGAAGA	ACAGTGACAG	GTTCAAGCGT	GATTATGTTT	GCATATCTTT	TGATGTGACT	2040
TTCCCTGTCTG	CCCTAGTAAA	TGACATGCCT	GCTATGGTGC	ATTTTAGTGC	TCATCCATGG	2100
TATGCCCTACA	GAAACTTAAAT	TTTTAAAGGT	GGAACGTGTC	AACGCCAACA	TTTTGAGTTT	2160
ACGATTGACT	TGCTAGTTTC	TTCTGAGACC	TATCAGACTA	ATAATGTGTT	CATTCGTTTT	2220
GGCACTAATT	ATGGATTTCC	TGCTGGTCTG	CAGGTCGTCA	TTGAGAACGC	TATGTTATCG	2280
GTTGGTAATT	ATTTTCCAGC	CTATCAACCA	GCGTACGAAG	ACCAAGACGA	ACGTGTCTCA	2340
GCGGTCGAAT	CCAACTTTAA	ACAGCGTGCT	GATTCACTTG	ACGCTGGTGT	AAGCCGTCTG	2400
ACTGAAGGCC	TTAGAACCAA	AGTGGATATC	AGCTCACTCA	ATGTGACTGC	TGAAAAATATC	2460
CGGCAATCTG	TGAAGAGTCT	TGAGACAGAC	ACGCAAGAACA	AACTAAATCA	GAAGTTGAGT	2520
CAGGCTGAAT	TTGAGGTGCG	AGCTGGCTCT	ATCCGTCAGG	AAATCCTGAA	CGCAACCAAA	2580
GATAAAGCCA	GCAAGTCAGA	ACTCACGCAG	ACAGCTGAGG	AGCTAGCTAG	TAAGATAGCG	2640
AGTGTGCAC	TAGGGCGCAG	AAATCTGCTG	AAAGGCACAA	AAGAGCTTGC	GAGATACAAG	2700
CCGGTTAGTG	AATATAATGG	TTTTAAAGTT	ATCAGAACAG	TCGCAGGAGC	AACTAGATAT	2760
CAGGATAGCT	ATGTGGAAAG	AACCGTTATA	CCAACGGCTG	GGACAGAGTA	TATAGCTATC	2820
TTTTATGCAC	GAGCCAGTGA	AAATGACTAT	CCTGTGCGCT	GTCAATTTT	CAATCCTAAC	2880
ACGGTTGTAT	CATCAGAAAA	CAGCAGCGGA	TATAAGTCAA	GGTCGTCAGA	TGGCTTGTCT	2940
ATTATCCGTC	TCTCGACAGA	CTGGCAGTTG	TGCTGGGTTA	AATGGACCCA	AACCGCAACA	3000
GATCAAGCCA	AGACGGTCAT	CATTGGCCGC	CATGGCCCTC	AAGTAGGCGG	TAAAGAGGGG	3060
GTATGGGTTG	AAATCTGCGC	CCCTGCCATT	TTTGAGGGAA	ATCTTGACAG	TGACTGGTCA	3120
CCAGCATACG	AAGACCAAGA	CGAACGTGTC	TCAGTAGTCG	AATCCAACCT	TAAGCAGCGT	3180
GCTGATTAC	TTGACGCTGG	TGTAAGCCGT	CTGACTGAAG	GCCTTAGAAC	CAAAGCCGAT	3240
ATCAGCTCAC	TCAATGTGAC	TGCTGAAAAT	ATCCGGCAAT	CTGTGAAGAG	TCTTGAGACA	3300
GACACGCAGA	ACAAACTAAA	TCAGAAGTTG	AGTCAGGCTG	AATTTGAGGT	GCGAGCTGGC	3360
TCTATCCGTC	AGGAAATCCT	GAACGCAACC	AAGGATAAAG	CAGATAAGAC	TCTTGTCGTC	3420
ACTGAAGCTG	GGAAATTGCG	AGAAGAATTT	TCAAAAATGA	AGGTGGGAGG	CCGGAATCTA	3480

TGGATAAAAT	CCAAGACGGT	TGGAGCTGTA	ATTGAAAAAT	TACCTGAAAA	CCACGTCACA	3540
GGTCAAAAAG	AATGCTATAG	GCTAGAGAAC	AACTCTACTT	TAACGTTCAA	CCTTGAACCA	3600
GATTTTCAGCT	CAAGGTTGTA	CCAAAAAGTT	ACTTTTAGCG	CTTGGATCAA	GTACGAAAAAT	3660
GTAGTCCAAG	GTCGAAATTT	TTGGAATGTA	TTTAATTGCT	TCAAACATTA	TCTTTTTAGA	3720
AAAAATAGTG	AGACCGGAGT	ACAGAGTGGT	CCAGATTATG	CTACGCTTGG	TATGTATAAA	3780
GGTTCGGCAG	ATTGGAAAAA	TATTACATTG	ACTTATGACT	ACTCTGAAAA	AACAAATTTT	3840
GATCAATTGA	AGACATCATG	GCGATTCAAT	CCTGAAGGTG	CTACAAGCGG	TACAGCTTGG	3900
GTAACAGGAA	TCAAGGTTGA	AATCGGTAGT	GTGGCGACGG	ACTGGAATCC	TGCGCCTGAG	3960
GACGCTGATG	GTCTCATCAC	TGAGGCTAAG	GCTACCTTTG	AGCGGACAGC	TCAGGGCTTG	4020
CGAACCGACT	TATCAGCTAT	TCAGGAATAT	GTAAATAAAG	ACGGTCAGCG	ACAGGAAGCC	4080
CTACAGCGCT	ATACTCGTGA	GGAGAGCGCG	AGACAAGCGA	CAGCAGTCCG	TGAGCTGGTC	4140
AATCGTGATT	TCGTTGGTAA	GGCTACTTAT	CAAGAAGATG	TTAAGGGTAT	CAATCAGAGG	4200
ATTGAAGCTG	TTAAAACTAG	TGCGAATAAA	GACATCGCTA	GTCAAATCGC	TAGCTATCGT	4260
CAATCTGTAG	ATGGTAAGTT	CACGGATATT	TCAAGTCAGA	TAAC TACTTA	TAAGCAAGAT	4320
GTGGGCGGTC	AAATCAGTGG	TCTATCAAAT	AGACTTACAA	GCAGTGAGCA	AGGAACCACT	4380
ACTCAGATTT	CAAATCTTTC	AAATCGGATA	AACAGTAATA	AACAAGGCAC	AGATAATCAG	4440
ATTTCAAATT	TAAAGACTCA	GGTCGCTACA	AACAAGGATA	ATGCTGAACG	ACAAATGGGT	4500
AGAATATCTG	ATCAGGTTTC	TGCAAACAAA	GCGAATGCTG	ATAGTCAATT	TGCGAATGTG	4560
ACCAATCAAC	TAGCGCGAAA	AGTAGAGACT	ACTGACTTCC	AGCGTGTTAA	GGAAACCAGT	4620
AAACTTTACG	AGCGGATTTT	GGGCAATACT	GAAAATGGAA	TTGCGGATAA	GGTTGCTCGC	4680
ATGGCTCTGA	CTAATCAACT	GTTTCAGGTT	GAGGTTGGGA	AATATAGTGT	AAGCGGCCCT	4740
AACCTCATTA	AGAATAGTGA	TTTTAAAAAT	GCTACGAATG	AATGGGGCTC	AACTCAAAAT	4800
TTAGGAAGAT	TGGTTAAGCA	TAGCTTTTAT	CACAACGGGC	AGAAAGACCT	TATGCGTTTA	4860
AGTAATGCAA	CTAAAAACGA	AAACTTTTTG	TATAGTCACC	GTTTTAATCT	TGAACGAAAT	4920
ACTGACTATG	TACTGAATTT	TAGAGGATTT	AACAACAGTG	CTCTCGCAAG	CTATGATGTT	4980
TATATTTTGG	GACGAAGAGC	AGGCGAGAGC	GATGGATTCA	CAATCGTTAA	GAAAGTTGTT	5040
AGCAGCAAGA	AAC TATCTAC	CTCTAGATGC	GAAGATGTCT	CAGTAACTTT	TAATTCGGGA	5100
GAAATGGATA	ATGCTTACAT	TCGTTTTGAT	AACAATGGCT	CATCATCAGG	AACAGCTGAT	5160
TTGTATATTA	CAGAAGTTGA	CTTG TACAAA	GGTTATAAAC	CTAGAACATG	GCAACCACAT	5220
CCAGAAGATG	CAGTCGCAGA	TGCGAATAAG	AAGCTTGAAG	CAACGCAAAC	AAAAATGACT	5280
CAACTAGCTG	GCTCATGGGT	AGTTGAAAAC	ATCAACTCGG	CTGGAGATAT	CATCTCTGGA	5340
ATCAATCTTG	GCGCCAATGG	ACATAACCGC	TTAGTTGGGA	AATTGACCCA	CATCACTGGA	5400
GAGACCCTGA	TTGACAGAGC	AGTCATCAAG	TC TGCCATGG	TTGATAAGCT	CAAAACGGCC	5460
AATTTTGAAG	CTGGTTCGGT	CACGACTACG	ATATTAGAAG	CTGAAGCGGT	AACTGCTGAG	5520
AAGTTGAAAG	TTGACAATGC	GCTTATTTAA	AAATTAACTG	CAACTGATGC	TTTTATTGAC	5580
CAACTGATAT	CTAAACGTAT	CTTCTCTACT	AAGGTTGAGT	CCGTCATTTT	TAGCTCAACC	5640
TTCCTAGAAG	CCTATCAAGG	CCGAATCGGT	GGATTCAAC	TTGGTCAATT	TGACCAGGGT	5700
GGCGGTCGCT	GGATTT CAGG	TGTCAATCAG	TTCTCTGTTG	GTATGGGGAA	TGGTGCCGGG	5760
TATGGAGTCC	GGACAGCCTT	CTGGGCGAAC	TGGGGAAATA	ATTGGAAC TA	TGCCGGACCT	5820
AAAGCATGGA	ACGTCAATAC	TGATGGGAAA	ATGTACTGTA	GGAATGAAGT	CGGTTTTTAT	5880
GATCAAGTGG	ATTTTTTCGAA	TTCATCGAGA	GCAAAC TTCT	ATGGGAATAC	TACTTTTTCT	5940
CGTTCTCCTG	TGTTTTTCAA	TGGTATCGAA	CTTGGAAGTA	AAGATGTGCT	TGGTGATGGT	6000
TGGAATCCCA	AAGGCGGAAG	GAATGCGGTT	GT TGGTGGA	ATCAGGTCGG	TAGCGGTAGC	6060
TTGAAGTATT	GGATGGAACA	AAAATCAGAT	AGACGCTTAA	AAGAGAACAT	CACAGATACA	6120
GCTGTGAAAAG	CCTTGACAA	AATCAACAGA	TTAAGAATGG	TTGCATTTGA	TTTCATCGAA	6180
AATAAGAAAC	ATGAGGAGAT	TGGTCTAATA	GCTCAAGAGG	CTGAAACCAT	CGTTCCAAAA	6240
ATTGTCTCAC	GAGATCCTGA	GAATCCAGAT	GGCTATCTGC	ATATCGACTA	TACCGCTTTA	6300
GTTCTTACT	TAATCAAGGC	TATTCAAGAA	TTAAATCAAA	AAATAGAAAA	AATGGAGAAA	6360
ACAATAGCAT	GA					6372

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

AAAGGCAAGA	AGATGTCAAC	TTTAGATAAA	AATCTTTTGC	TAGAAATGTT	CCGTAAGATG	60
GAAGAAATCC	GTCGCATGGA	CTTAAAAATT	GCACAATTAG	TAAAGAAAGG	GAAAGTGCCA	120
GGAATGACGC	ACTTTTCTGT	TGGTGAAGAG	GCAGCTAACG	TGGGGGCTAT	GTTAGCTCTC	180
AATCCAGATG	ATCTGATTAC	CTCAAACCAC	CGTGGACACG	GGCAAGCTAT	TGCTAAAGGG	240
ATTGACCTCA	ACGGAATGAT	GGCTGAAATC	CTTGGTAAAT	ACACTGGAAC	CTGTAAAGGG	300
AAAGGTGGAT	CTATGCATAT	CGCTGACCTT	GATGCTGGGA	ACCTTGGTGC	CAATGGTATC	360
GTAGGTGGTG	GTATGGGGAT	CGCTGTCGGT	GCAGCCCTCA	GTCAGCAAAT	GCAAAAATACC	420
GGTAAAATCG	TTGTTTGCTT	CTTTGGAGAT	GGTGCGACCA	ATGAAGGTGT	TTTCCACGAA	480
GCAGTGAACA	TGGCTTCTAT	CTGGAACCTG	CCAGTCATTT	TCTATTGCAT	TAACAACGGT	540
TACGGTATCT	CTGCGGATAT	CAAGAAAATG	ACCAATATAG	AACATATCCA	TCAACGTAGC	600
GCCGCTTATG	GAATTCCTGG	AATGTTTCATC	GAAGACGGTA	ACAATGTCAT	CGATGTCTAT	660
GAAGGATTTT	AGAAAGCTGT	AGACCATGTT	CGCAGTGGCA	ATGGTCCAGT	CTTGATTGAA	720
AGTGTAACCT	ATCGCTGGCT	TGGTCACTCA	TCATCTGACC	CTGGTAAATA	TCGTACGCGT	780
GAAGAAGTGG	AATTGTGGAA	ACAAAAAGAT	CCAATCGAAA	ACCTCCGCAA	TTACCTTATT	840
GAAAATAACA	TTGCAAGTGC	CGAAGAAATT	GAAGAAATCC	AAGCGCAAGT	AAAGGAAGCA	900
GTAGAAGCTT	CTGTTAAATT	TGCAGAGGAA	AGCCCATTCC	CATCGCTTGA	ATCAGCCTTT	960
GAAGATATTT	ACGCAGACTA	A				981

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 951 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

ATGGGCAAGA	AAAGATGGGC	AAGAAATGGA	TCTGAGTCAA	ACGATGCTTC	TTATGCTCAA	60
GTAGTGAGTC	TTTATGATGA	TACAAGTATC	TCTGTTAGTA	ATAATGAGAC	GGACAAAGTG	120
TTGACTGGAT	CCCTCTATAC	TGAAACAAAT	GAACAGGGAT	TAACGATTCC	AAGCAGTTTA	180
CTAAAAAAT	GGAATGAACA	GACAGGAAAA	AATTTGACAA	CTAATGATCT	TATTGGCAAA	240
TCAGTCTCAG	CCAGCATTGT	AGAAAGTGCT	GCCGAAACTA	GTAAGATTGC	TCAATTTCAA	300
ACGAAGATTG	TACGTGTAAT	CAATGATGAA	GATGACATGG	AGGACAGCAA	CAGTTTCATG	360
CTGTCTCATC	AAATGGAAAC	GATTTTGAAA	GAGGCTGGAT	TTACGAAAGC	TGTATCTTAT	420
TTTATCTTGG	AACTCAAAGA	TCCATCACAG	ACAAAAGTAG	TAACAGAAGA	ATTACAGAAA	480
AATAAGAAGT	ATACTGTGCT	TTCTCAACAG	AGAGTTCTTG	ATATTGTGAT	TACCTTTATT	540
CGTGTTATTC	AGGGATTATT	GATTGTGCTT	TCATCACAAAG	CTATTGTGGT	AGCAGCGGTT	600
ATGATTGGTA	TCATTATTTA	CATCAATATC	ATGCAACGTT	CCAAGGAAAT	AGGTGTCATG	660
AAAGCAGTTG	GTTATCAGAA	TCGTGGTGTC	AAAGGAATTT	TTATTTACGA	GGCTATCTGG	720
ATTGTAGGCA	TCGCCTTGCT	GCTGGCATT	TTGGTTGCAC	AAGGGGTGGG	AAGTTTGGCG	780
AATGCGATTG	TAAGTCACCT	TTACCCATCC	ATCACTAAGG	TTTTTTGAATT	AAATCTTTTA	840
TCTGTTTTAG	GAACTCTAGT	TTTCGCTCTA	TTACTTGGTT	ATGTCTCAGC	CTACTTCCCC	900
GCGCGTAAGA	TTAGTAAAAT	GGATCCTGTA	GAATCGTTAC	GCTATGAATA	A	951

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

CCTCTAAAGA	AAACAACTGG	AACTTGCCAT	TTGCAGATAT	CGCATCTATC	TGGCGTGATG	60
GCTGTATCAT	CCCGTCCTCG	TTTCTTGCAA	AAGATTACAG	ATGCCTACAA	CCGCGATGCA	120
GATCTTGCCC	ACCTTCTTTT	GGACGAGTAC	TTCTTGGATG	TTACTGCTAA	GTATCAACAA	180
GCAGTGCGTG	ATATCGTAGC	TCTTGCGGTT	CAAGCTGGTG	TGCCAGTGCC	AACTTTCTCA	240
GCAGCTATTA	CTTACTTTGA	TAGCTACCGT	TCAGCTGACC	TTCCGGCTAA	CTTGATCCAA	300
GCACAACGTG	ACTACTTTGG	TGCTCACACT	TACCAACGTA	AAGACAAAGA	AGGAACCTTC	360
CACTACTCTT	GGTATGACGA	AAAATAA				387

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1515
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

AAACTAAAGA	AAAGGGAAGA	TATGATTACA	GGCGAATTAA	AAAATAAAAT	CGATCAGCTG	60
TGGGAAATTC	TTTGACACAGA	AGGAAACGCA	AATCCTTTAA	CAAATATTGA	ACAGTTGACT	120
TATCTCTTAT	TTATGAAAAGA	TTTGGATAGT	GTCGAGCTTG	GACGTGAAAG	TGATGCTGAA	180
TTTCTAGGGA	TTCTTATGA	GGGAGTTTTT	CCAAAAGATA	AACCTGAATA	CCGTTGGTCA	240
ACTTTTAAAA	ATATAGGAGA	TGCTCAGGAA	GTTTATCGTT	TAATGACTCA	GGAGATTTTT	300
CCGTTTATTA	AAAATCTCAA	GGGGGATACA	GATGATACAG	CCTTTTCACG	ATATATGCGA	360
GAAGCTATTT	TTCAAAATAA	TAAACCTGCT	ACGCTTCAAA	AGGCAATTTT	TATCTTAGAT	420
GTTTTTCCAA	CTAGGGGATT	AGATGTAGAT	TTTGATAATG	ACAAACAAAG	TATTACTGAT	480
ATCGGAGATA	TCTATGAATA	TCTGTTATCA	AAATTGTCTGA	CCGCAGGTAA	AAAATGGACAG	540
TTCCGTACAC	CTCGTCACAT	CATCGATATG	ATGGTTGAGT	TGATGCAACC	GACTATCAAA	600
GATATCATCT	CAGATCCCCG	TATGGGTTCT	GCTGGCTTCT	TAGTATCTGC	TAGCCGTTAC	660
TTAAAGCGTA	AGAAAGATGA	ATGGGAAACC	AATACAGATA	ATATCAATCA	TTTTCATAAT	720
CAGATGTTTC	ATGGAAATGA	TACGGATACG	ACTATGTTGA	GACTTGGGGC	GATGAACATG	780
ATGCTACATG	GAGTAGAAAA	TCCACAAATC	AGTTACCTTG	ACTCGCTGTC	TCAAGATAAT	840
GAAGAAGCTG	ATAAATATAC	TTTGGTTTTA	GCAAATCCTC	CTTTTAAGGG	CTCACTTGAC	900
TACAAATCAA	CCTCTAATGA	CCTTCTTGCA	ACCGTAAAAA	CCAAAAAAAC	AGAAATTACTC	960
TTTCTTTCTC	TTTTCTTGCG	AACTTTAAAA	CCAGGTGGAC	GAGCAGCAGT	TATCGTACCT	1020
GATGGTGTCC	TTTTTGGTTC	GTCTAAAGCT	CATAAAGGAA	TTCGTCAGGA	AATTGTAGAG	1080
AATCATAAGC	TTGATGCTGT	AATCTCAATG	CCTAGTGGTG	TGTTCAAGCC	TTATGCTGGA	1140
GTTTCAACTG	CCATTCTCAT	CTTTACAAAA	ACTGGTAAATG	GTGGTACTGA	CAAAGTCTGG	1200
TTTTACGATA	TGAAAGCGGA	TGGTTTAAGT	TTGGATGATA	AGCGACAACC	GATTAGAGAC	1260
AATGATATTC	CAGATATTAT	CGAACGCTTT	CATCATCTTG	AAAAAGAAGC	AGAACGTCAG	1320
AGAACGGATC	AATCTTTCTT	TGTTCCAGTT	GCTGAGATAA	AGGAAAATGA	TTATGATTTG	1380
TCTATCAATA	AATATAAAGA	GATTGAGTAT	GAAAAAGTTG	AGTATGAACC	AACAGAAGTC	1440
ATATTAAAGA	AAATCAATGA	TTTAGAAAAA	GAAATTCAAG	CTGGCTTGGC	TGAATTGGAA	1500
AAATTACTCA	AGTAG					1515

(2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

TTGCTAAAGA	AAACTGTCTGA	AAAAGCCGTT	GCAGACAACG	TTAAAGACAG	TATCGATGTT	60
CCAGCAGCCT	ACCTAGAAAA	AGCCAAGGGT	GAAGGTCCAT	TCACAGCAGG	TGTCAACCAT	120
GTGATTCCAT	ACGAACTCTT	CGCAGGTGAT	GGCATGTTGA	CTCGTCTCTT	GCTCAAGGCA	180
TCTGACAAGG	CACCATGGTC	AGATAACGGC	GACGCTAAAA	ACCCAGCCCT	ATCTCCACTA	240
GGTGA AACG	TGAAGACCAA	AGGTCAATAC	TTCTATCAAG	TAGCCTTGGA	CGGAAATGTA	300
GCTGGCAAAG	AAAAACAAGC	GCTCATTGAC	CAGTTCGGAG	CAAACGGTAC	TCAAAC TTAC	360
AGCGCTACAG	TCAATGTCTA	TGGTAACAAA	GACGGTAAAC	CAGACTTGGA	CAACATCGTA	420
GCAACTAAAA	AAGTCACTAT	TAACATAAAC	GGTTTAAATTT	CTAAAGAAAAC	AGTTCAAAAA	480
GCCGTTGCAG	ACAACGTTAA	GGACAGTATC	GATGTTCCAG	CAGCCTACTT	AGAAAAAGCC	540
AAGGGTGAAG	GTCCATTAC	AGCAGGTGTC	AACCATGTGA	TTCCATACGA	ACTCTTCGCA	600
GGTGATGGTA	TGTTGACTCG	TCTCTTGCTC	AAGGCATCTG	ACAAGGCACC	ATGGTCAGAT	660
AACGGTGACG	CTAAAAACCC	AGCTCTATCT	CCACTAGGTG	AAAACGTGAA	GACCAAAGGT	720
CAATACTTCT	ATCAAGTAGC	CTTGACGGA	AATGTAGCTG	GCAAAGAAAA	ACAAGCGCTC	780
ATTGACCAGT	TCCGAGCAAA	CGGTACTCAA	ACTTACAGCG	CTACAGTCAA	TGCTATGGT	840
AACAAAGACG	GTAACCCAGA	TTTGGACAAC	ATCGTAGCAA	CTAAAAAAGT	CAC TATTAAC	900
ATAAACGGTT	TAATTTCTAA	AGAAACAGTT	CAAAAAGCCG	TTGCAGACAA	CGTTAAGGAC	960
AGTATCGATG	TTCCAGCAGC	CTACCTAGAA	AAGGCCAAGG	GTGAAGGTCC	ATTCACAGCA	1020
GGTGTC AACC	ATGTGATTCC	ATACGAACTC	TTCGCAGGTG	ATGGTATGTT	GACTCGTCTC	1080
TTGCTCAAGG	CATCTGACAA	GGCACCATGG	TCAGATAACG	GCGACGCTAA	AAACCCAGCC	1140
CTATCTCCAC	TAGGTGAAAA	CGTGAAGACC	AAAGGTCAAT	ACTTCTATCA	AGTAGCCTTG	1200
GACGGAAATG	TAGCTGGCAA	AGAAAAACAA	GCGCTCATTG	ACCAGTTCCG	AGCAAACGGT	1260
ACTCAAAC TT	ACAGCGCTAC	AGTCAATGTC	TATGGTAACA	AAGACGGTAA	ACCAGACTTG	1320
GACAACATCG	TAGCAACTAA	AAAAGTCACT	ATTAACATAA	ACGGTTTAAAT	TTCTAAAGAA	1380
ACAGTTCAAA	AAGCCGTTGC	AGACAACGTT	AAAGACAGTA	TTGATGTTCC	AGCAGCCTAC	1440
CTAGAAAAAG	CCAAGGGTGA	AGGTCCATTC	ACAGCAGGTG	TCAACCATGT	GATTCCATAC	1500
GAACTCTTCG	CAGGTGATGG	CATGTTGACT	CGTCTCTTGC	TCAAGGCATC	TGACAAGGCA	1560
CCATGGTCAG	ATAACGGCGA	CGCTAAAAAC	CCAGCCCTAT	CTCCACTAGG	TGAAAAACGTG	1620
AAGACCAAAG	GTCAATACTT	CTATCAATTA	GCCTTGGACG	GAAATGTAGC	TGGCAAAGAA	1680
AAACAAGCGC	TCATTGACCA	GTTCCGAGCA	AATGGTACTC	AAACTTACAG	CGCTACAGTC	1740
AATGTCTATG	GTAACAAAGA	CGGTAAACCA	GACTTGGACA	ACATCGTAGC	AACTAAAAAA	1800
GTCATATTA	AGATAAATGT	TAAAGAAACA	TCAGACACAG	CAAATGGTTC	ATTATCACCT	1860
TCTAACTCTG	GTTCTGGCGT	GACTCCGATG	AATCACAATC	ATGCTACAGG	TACTACAGAT	1920
AGCATGCCTG	CTGACACCAT	GACAAGTTCT	ACCAACACGA	TGGCAGGTGA	AAACATGGCT	1980
GCTTCTGCTA	ACAAGATGTC	TGATACGATG	ATGTCAGAGG	ATAAAGCTAT	GCTACCAAAT	2040
ACTGGTGAGA	CTCAAACATC	AATGGCAAGT	ATTGGTTTCC	TTGGGCTTGC	GCTTG CAGGT	2100
TTACTCGGTG	GTCTAGGTTT	GAAAAACAAA	AAAGAAGAAA	ACTAA		2145

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

AGTTCAAAGA	ATACTTCAAC	AAGTAATGAT	GAGAAGACAG	TAGCAACATC	CAATAGTTCA	60
AAAGAAACAA	TCACTTTCGA	TACACCGGTT	GTAACAGACG	ATGCGATTGA	ATCAATACGC	120
ACTTATGCAG	ATTATATAGA	TCTTTATAAA	AATATTTTTG	ATGATTATTT	TACTAAAGCT	180
GAGGAAGGTT	TCAAAGGCAC	AGCTATGGAA	AATAATGACT	CGTTTACTAA	ACTAAAAGAG	240
TCAACTCAAA	AATTATTTCGA	TGCGCAGAAA	AAAAGGTTAA	ATAATGAAGA	TAGAATAGAA	300
ACAACCAAAA	ACAATGTGAT	TGCCAAACAT	TGTCAAACAG	TCCTTTCCTT	TTTGGTTTTG	360
ACTAGCTTTT	TTGTGAAAAA	TTGTGTAAAA	TAG			393

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

ACACAAAAGA	AAAGTTTTTG	GTATAATAAG	AGTATGTACA	CAAAAAATGA	AGAAGAGTTG	60
CAAGCCTTAG	GGGAGCGTTT	GGGCCATCTA	TTAGCAAAGA	ATGATGTTTT	AATCTTAACT	120
GGAGAACTGG	GTGCAGGTAA	AACGACCTTT	ACTAAAGGAC	TTGCAAAAGG	ATTACAGATT	180
TCTCAAATGA	TTAAAAGTCC	CACCTATACT	ATCGTGAGAG	AGTATGAAGG	TCGACTTCCA	240
CTTTATCACC	TAGATGTTTA	TCGTATTGAA	GGAGATGCTG	ATTCTATCGA	CTTGGATGAG	300
TTTATCTTTG	GTGGCGGCGT	GACTGTTATT	GAGTGGGGAA	ATCTCTTAGG	AGATGCCTTG	360
CCAGATGCTT	ATTTAGAAAT	GGAAATTCTA	AAAGAAGCAG	ATGGACGCCG	TTTAAATTTT	420
CAGGCAAAGG	GTTTGCGTGC	TGAGAAATTG	TTAGAGGAGC	TTCAATATGG	AGTATGA	477

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

AATAAAAAGA	ATTGCTGTGA	TATCAATAGA	TTTGGGGGAT	TTTTTAATAT	GGTACTGGAT	60
AAGGCAAGTT	GTGATTTGCT	TCAATATTTG	ATGGATCAAG	AAACGTCCAA	AACGATTATG	120
GCGATTTTCA	AAGATTTGAA	AGAGTCAAGA	AGGAAAATTT	ATTATCACAT	TGACAAAATC	180
AATGCTGCTC	TGGTTGACGA	GGCGCTTCAC	ATCATTAGTA	TTCCACGAAT	TGGTATTCAC	240
TTAACGGAAG	AGCAGAGAGA	TGCTTGTTGT	AAACTATTAT	CGGAAGTAGA	TTCGTACGAT	300
TATATCATGA	GTGCGCATGA	ACGTATGATG	ATAATGTTAC	TATGGATAGG	TATTTCTAAA	360
GAACGTATTA	CGATTGAAAA	ATTGATAGAG	TTAACAGAGG	TATCTAGGAA	TACTGTTCTC	420
AATGATTTGA	ATAGCATTCT	TTATCAACTA	ACTTTGGAAC	AATATCAGGT	GACCTTGCAA	480
GTGAGCAAGT	CACAGGGATA	CCACCTTCAT	GCCCACCTC	TTAATAAAAT	TCAGTATCTT	540
CAATCGCTTC	TATATCATAT	TTTTATGGAA	GAAAATGCCA	CTTTTGATC	TATTTTAGAA	600
GATAAGATGA	AAGAGAGGTT	AGATGATGAG	TGTTTGCTTT	CTGTTGAAAT	GAACCAATTT	660
TTTAAGGAAC	AGGTTCCTTT	AGTTGAACAA	GATTTAGGGA	AGAAAATAAA	CCATCATGAA	720
ATAACTTTTA	TGTTGCAGGT	TCTACCTTAT	TTGCTGTTAA	GCTGTCATAA	TGTTGAACAG	780
TATCAAGAAA	GACATCAGGA	TATAGAGAAA	GAATTTTCTT	TGATAAGAAA	AAGAATAGAG	840
TATCAGGTGT	CTAAGAAATT	AGGAGAACGG	TTGTTTCAAA	AGTTTGAAAT	TTCTTTGTCA	900
GGACTTGAAAG	TTTCTCTTGT	AGCTGTTCTC	CTCCTCTCCT	ATCGTAAAGA	TTTGGATATT	960
CATGCAGAAA	GTGATGATTT	TCGTCAATTA	AACTTGCTT	TAGAAGAATT	TATCTGGTAT	1020
TTTGAATCAC	AAATCCGAAT	GGAGATTGAG	AACAAGGATG	ATTTGTTACG	AAATTTGATG	1080
ATCCACTGTA	AAGCCTTGTT	ATTTAGAAAAG	ACTTACGGTA	TTTTTTCTAA	AAATCCTCTA	1140
ACAAAACAAA	TTCGATCCAA	GTATGGAGAA	TTATTTTATG	TCACTAGAAA	ATCTGCGGAA	1200
ATTTTAGAAG	GAGCATGGTT	TATTCGGCTA	ACAGACGATG	ATATTGCCTA	TTTGACGATT	1260
CATATTGGAG	GATTTTAAAA	GTATACACCA	TCGTCTCAAA	AAAATATGAA	AAAAGTTTAT	1320
CTCGTTTGTG	ATGAAGGTGT	TGCGGTTTCG	AGACTTTTGC	TGAAACAATG	CAAACTTTAT	1380
TTTCCAAATG	AGCAAAATGA	CACGTATTTT	ACAACAGAAC	AATTTAAGAG	TGTGGAAGAT	1440
ATTGCACAAG	TTGATGTAGT	GATTACTACT	AATGATGATT	TGGATAGCAG	ATTTCCGATT	1500
TTAAGGGTTA	ATCCTATCCT	TGAAGCAGAA	GATATTTTGA	AAATGCTAGA	CTATCTTAAA	1560
CACAATATAT	TTCGTAATAA	GAGCAAAAGT	TTCAAGTAAA	ATCTTTCTAG	TCTTATTTCTG	1620
TCTTATATTG	TAGACAGCAA	GTTGGCTAGT	AAGTTCCAAG	AAGAGGTTCA	AACACTTATA	1680
AATCAAGAAA	TAGTAGTTCA	AGCTTTTTTTG	GAAGATATTT	GA		1722

(2) INFORMATION FOR SEQ ID NO:1134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

AGTAAAAAGA	ATTTCACTGA	TAGCTTGCGA	TACTATCCTT	ATAGAAGCCT	AAAAGAAAGG	60
AACAGAAAAA	TGGAAGAATG	GAAAGAAAGA	TTTAAAAAAG	AATACTACGA	ATTGAAAGAA	120
CGATTCCAGA	AGTTAGATAT	GATGATTGGG	AAATACGAAA	AAGGGCAACT	AGAGTTTGAA	180
TCTAAATGTC	CGATTGATTC	GTTAAAAAGG	CAGCGTTCAA	CCATGTGGAA	TTATTTAAGA	240
ATTCTAGAAC	AACGTGCAAA	AATTGAAGAA	ATTAACTAT	AA		282

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

TTACGAAAGA	AAGAGGAAAAG	AAAAATTATG	CGCGCTAAGA	AATTAGATAA	ACTTGCAACA	60
GCTGTCCCTCT	ATACGATTGC	TAGCATCAT	GTGACAATCT	TGGCTTCCTT	GATTCTCTAT	120
ATCTTGTTTC	GGGGCTTGCC	CCATATCTCT	TGGTCTTTCT	TGACTGGAAG	GTCTTCTGCT	180
TTTCAAGCAG	GTGGTGGGAT	TGGCATTCAG	CTTTACAATT	CCTTTTTCCT	ATTGGTCATT	240
ACCTTGATTA	TTTCTGTACC	TCTTTCTATG	GGAGCTGGGA	TTTACTTGGC	TGAATATGCT	300
AAAAAAGGTC	CTGTTACCAA	CTTTGTGCGG	ACTTGTATTG	AAATCTTGTC	CTCTTTACCA	360
TCAGTGGTGG	TGGGTCTCTT	TGGTACTTG	ATCTTTGTAG	TCCAGTTTGA	GTATGGATTT	420
TCAATCATTT	CAGGTGCCTT	GGCCTTGACA	GTCTTTAACT	TGCCTCAGAT	GACGCGTAAT	480
GTAGAGGATA	GTTTGAAACA	CGTTCACCAT	ACCCAACGTG	AGGCTGGTCT	GGCTCTGGG	540
ATTTCTCGCT	GGGAGACAGT	GGTTCATGTT	GTTATTCCAG	AAGCGCTTCC	AGGTATTGTA	600
ACGGGTGTCG	TCTTGGCATC	TGGTCGTATC	TTTGGCGAAG	CTGCAGCTCT	GATCTATACA	660
GCAGGGCAAT	CGGCGCCAGC	TCTTGACTGG	TCTAACTGGA	ATATCCTCAG	TGTGACTAGC	720
CCCATCTCTA	TCTTCCGTCA	AGCAGAAACC	TTGGCTGTCC	ATATCTGGAA	AGTCAATAGT	780
GAAGGCACTA	TTCCAGATGG	AACCATTGTA	TCAGCAGGTT	CTGCCGCTGT	GCTCCTGATC	840
TTTATCCTGA	TTTTTAACTT	TGGAGCTCGT	AAGTTCGGAA	GCTATCTACA	CAAGAAATTA	900

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

GTTTTGAAGA AAAACTTTTCG TGTA AAAAGA GAGAAAGATT TTAAGGCGAT TTTCAAGGAG	60
GGGACAAAGTT TTGCTAATCG CAAATTTGTG ATCTACCAAT TAGAAAACCA GAAAAACCAT	120
TTTCGAGTAG GTCTATCAGT TAGCAAAAAA CTGGGGAATG CCGTCACTAG AAATCAAATT	180
AAGCGACGGA TTCGGCATAT TATCCAGAAT GCAAAAGGGA GTCTGGTAGA AGATGTCGAC	240
TTTGTGTGTC TTGCTCGAAA AGGAGTCGAA GCCTTGGGAT ACGCAGAGAT GGAGAAAAAT	300
CTACTCCACG TATTAAAAAT ATCAAAGATT TACCAGGAAG GAAATGGGAG TGAAAAAGAA	360
ACTAAAGTTG ACTAG	375

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

CTGTTGAAGA AGAGATTGAT TTGTCAGATA TTGAAATTTT GTAAGAGGGT AACGATGTCA	60
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AGAATTGAAT	TTTCACCATC	TTTGATGACC	ATGGATTG	ACAAATTCAA	AGAGCAGATT	120
ACTTTTTTGA	ATGATAAAGT	AGCATCTTAT	CATATCGATA	TTATGGATGG	CCATTTTGTT	180
CCCAATATTA	CCTTGTCTCC	TTGGTTCATT	CAAGAAGTTC	AAAAAATTAG	TGACACACCT	240
TTATCAGTTC	ATCTGATGGT	CACAGACCCA	ACCTTTTGGG	TAGATCAAGT	TCTCGATTTA	300
CAATGTGAGT	ATATTTGTAT	TCATGCTGAA	GTTCTGAATG	GTCTTGCTTT	TCGTTTGATT	360
GATAAAATTC	ATGATGCAGG	TCTAAAGGCT	GGTGTGTGCC	TTAATCCTGA	AACACCTGTT	420
TCTACAACTC	TTCCCTACAT	TGATTTACTT	GACAAAAGTAA	CTATTATGAC	TGTAGATCCA	480
GGTTTTGCAG	GACAACGCTT	TTTGGAGTCT	ACCTTGTATA	AAATCCAAGA	ACTCCGTCAG	540
CTTAGAGTTC	AGAATGGTTA	TCACTACATC	ATTGAGATGG	ATGGTTCCTC	GAGTCGTAAG	600
ACTTTCAAAC	AAATTGATGT	GGCAGGACCA	GATATTTATG	TTATAGGTCG	CAGTGGATTA	660
TTTGGTTTGG	ATGACGATAT	TGCCAAAGCC	TGGGATATCT	GTTCTAGAGA	TTACGAAGAA	720
ATGACCGGAA	AAACAATGCC	AATCAAATAA				750

(2) INFORMATION FOR SEQ ID NO:1138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...465
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

ACCATGAAGA	AAATGAAGTA	TTACGAAGAA	ACAAGCGCTT	TGCTACATGA	GTTTTCTGAG	60
GAGAATCAAA	AGTATTTTGA	GGAGTTGTGG	GAAAGTTTTA	ATCTTGCTGG	ATTTCTCTAT	120
GATGAAGACT	ATCTCAGAGA	GCAGATCTAT	TTGATGATGC	TAGATTTCTC	AGAAGCAGAA	180
CGAGATGGCA	TGAGTGACGA	GGATTATCTA	GGTAAGAATC	CTAAAAAAT	AATGAAAGAG	240
ATTCTCAAGG	GAGCACCTCG	CAGTTCTATC	AAAGAGTCCC	TTTGGACGCC	AATTCTTGTC	300
CTGGTGGTAT	TACGTTATTA	TCAACTACTA	AGTGATTTTT	CTAAAGGTCC	TCTCTTAACA	360
GTCAATTTGC	TCACATTTTT	AGGGCAACTT	CTTATTTTTT	TGATTGGATT	TGGACTTGTG	420
GCCACAATTT	TACGAAGAAG	TTTAGTCAAG	ATTCTCCTAA	AATGA		465

(2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GAGATGAAGA	AAACAAGCTC	TAAACTCTTT	GTAGTGCCCT	ACATGCTTTG	GATTGCCCTC	60
TTTGTATTGG	CACCCCTGGT	CTTGATTTTC	GGACAATCCT	TTTTCAACAT	TGAAGGCCAG	120
TTTAGTTTAG	AAAAATTATA	ATCTTACTTT	GCGTCACAAC	ACTTGACCTA	CCTCATAAAT	180
GAGTTTCAAC	TCAGTGCTTT	ATGCAGGGAT	TGTGACCTTT	GTGACCTGTC	TTATCAGCTA	240
TCCAACAGCC	CTCTTTTGA	CCCGTCTCAA	GCACGCGTCA	ACTCTGGCTC	ATGCTGA	297

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1407 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

AGGATGAAGA	ATCAGGAGTA	TTGGGCGAAG	AGGAAAGCCA	ATCTGATTTA	CCAGCAGATG	60
GACAAGGCCG	AAAAGCAGGC	AGACCAGTTC	GATAAGGTCT	ATCAGGAAGC	TAAGACTTAC	120
TTGGATAAGG	AAATCAATAA	GATTTTCGAT	AAATTCCAAC	GTGATTATGG	TCTAAGTCAG	180
GTAGAAGCTA	GACAAGTCTT	GAAGAACATG	AAAGACAAGA	AAAATCTGAA	TGAACTTCGT	240
AAAGTACTTG	AAGCGAGACC	GAATGACCCG	AACATCCAAA	GATTACTAGC	TGACTTAGAC	300
AGCCCAGCTT	ATTCTTTCCG	CATGAAGCGC	CTAGAGCGTT	TGAGCGACGA	TTTAGATCGT	360
ATGCGTGAAT	CTATCTATCA	TTCGGAGAAG	ACAGGCTCAG	ATGCCTTTTA	TAGCGACCTG	420
ATGAAGGATA	GTTACTACAA	GGCTACCTTT	GACCTACAAC	AGCAGACAGG	ACTAGCATAT	480
GGCTTTTCTG	GGCTTCCTGA	GAACGAGATT	AAACATCTAC	AGTCTTTTAG	TTGGGTAGGA	540
GATGGAAGTA	CGTACTCAAC	AGACATCTGG	AAGAATACAG	GAAACTTAC	TTCCAGCATA	600
AAAGATGAAC	TCCTCATTAG	CCTCATGACA	GGCAGAGATA	CACGAGAAAC	TGCACAAGCA	660
ATTGCTGAGA	GGTTCAATGT	AGGTCAGAAC	GATGCAAGGC	GTTTGGTTTCG	AACAGAATCC	720
GCCTTTTTTC	ATAACCAGAT	GGAGCTACTC	AGCTATGAAG	AAGCAGACAT	AGAAAAGTAT	780
ATCTTTGTGG	CCGTCTTAGA	CAAGCGTACA	TCACGCATTT	GTCAGGAGCA	TGACAAATCAG	840
GTCTATGATA	GGGATAAGGC	TGTCCCTGGT	GTCAATTGTC	CGCCTATGCA	CCCTTGGTGT	900
AGGTCTACTA	CTGTCGGATA	CGATGAGGAC	GCAGACTACA	GCAAGTTGAA	GCGCAGAGCA	960
AGGAATCCAG	AGACAGGTAA	AGTTGAGTAC	GTGCCTGCCG	ATATGACTTA	TAAAGAGTGG	1020

TATAGCAAGT	ATGTGGATGG	TAATAGAGAG	TCTATAAAAC	GTAAAGCGTT	TGATAAAACT	1080
ATTAAAGATG	GTATAATAGT	AAGTGTATCA	GGGACTACAA	TTGGACACAC	TCCGCCTGGC	1140
AAAATAGGTT	TGCCTAATAG	TGTAGTTCAG	CATAATGCTA	CAAACGGAGA	TGTCCTTGGT	1200
AGAACTTACT	ATGATGCTAG	AGGTTTTTAAA	ACGAAAAGATG	TTCATTTTAC	AAACCATAAA	1260
CAACCGGCAC	GTCATCCTTA	TGGAAAAATC	GGAGAACATG	CTCATGATTT	TGTATTTGAT	1320
GATGAAGGTA	AGTTCGTTAG	TAGGAGTACT	AGGGAATTAA	CAGACGATGA	AAGAAAGGAG	1380
AATCAAGATA	TATTATGGCG	ATATTAG				1407

(2) INFORMATION FOR SEQ ID NO:1141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

AATCAGAAGA	AGTTGGAAAG	GATTCCCTCTA	TCTATTCTCA	CTTTTTATAT	CCCAAAAGTT	60
CCCTCTTACT	CTATTAAAGA	AAAACAAAGC	AAGTGGTTAC	AATCCCGCTA	TAAATCTATC	120
AAAACAGACA	AAGCTATTCT	TTCGTCTTCT	CCCATCCAGA	CTATACTGTC	GGTTGTGGAA	180
TCTCACCACA	TCAGCTTGCG	CTCGCGGACT	TCTTTAAAGA	GAAGGAAATA	G	231

(2) INFORMATION FOR SEQ ID NO:1142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 894 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

AGGGAGAAGA	AGATGCAGAA	TAAACAAGAA	CAATGGACTG	TATTGAAGCG	CTTGATGTCC	60
TATCTCAAGC	CTTATGGACT	CCTTACCTTT	TTGGCACTCA	GTTTTCTCCT	AGCGACGACG	120
GTCATTAAAA	GTGTCAATTCC	CCTTGTGGCT	TCCCACTTTA	TCGACCAGTA	TCTCAGCAAT	180
CTTAACCAAC	TAGCCGTGAC	CGTTTTGCTG	GTCTACTATG	GTCTCTACAT	CCTACAAACT	240
GTAGTTCAGT	ATGTCGGCAA	TCTTCTCTTT	GCGCGCGTGT	CTTACAGTAT	TGTTAGGGAT	300
ATTCGTCGGG	ATGCCCTTGC	CAATATGGAG	AAACTGGGCA	TGTCTTACTT	TGACAAGACG	360
CCAGCAGGTT	CTATCGTTTC	TCGTTTGACC	AACGATACCG	AGACGATTAG	TGATATGTTT	420
TCTGGGATTT	TATCCAGCTT	TATCTCAGCA	GTTTTTATCT	TTCTGACAAC	CCTTTATACC	480
ATGTTGGTGC	TGGATTTTCG	TTTGACAGCA	TTAGTCTTGC	TCTTTCTCCC	CTTGATTTTC	540
CTTTTGGTCA	ATCTCTATCG	AAAAAAGTCA	GTGAAAATCA	TCGAGAAAAC	CAGAAGTCTC	600
TTGTCAGATA	TCAATAGTAA	GCTGGCAGAG	AATATCGAGG	GAATCAGGAT	TATTTCAGGCT	660
TTTAATCAAG	AGAAGCGCCT	GCAGGCAGAA	TTTGATGAAA	TCAACCAAGA	GCACCTTGCC	720
TATGCCAACC	GTTCTGTAGC	CTTGGATGCC	CTCTTTTGA	GACCTGCCAT	GAGTTTGTTG	780
AAACTTCTAG	GTTATGCTGT	CTTGATGACC	TATTTTGGCT	ATCGTGGTCT	TTCTATCGGG	840
ATAACGGCCG	GGACCATGTA	TGCTTTTATC	CAGTACATCA	ACCGCCCTCT	TTGA	894

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

ATATTTGAGA	AGACCTTACG	TCCTTCTTCC	ACTGCGACGA	TAATAGTCGC	AAAGTTATCA	60
TCTGCAAGAA	TCATATCAGA	AGCCCCCTTA	GAAACCTCTG	TACCAGTGAT	TCCCATACCG	120
ATACCGATGT	CTGCTGTTTT	CAGAGCTGGG	GCATCATTGA	CACCGTCACC	TGTCATGGCA	180
ACGACCTTAC	CTTGTTTTTG	CCAAGCCTTG	ACGATACGAA	CCTTGTGCTC	TGGAGACACA	240
CGGGCATAA						249

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

TTTGGAGAGA	AAGGATTCAT	TTTGAAATCA	ATAGGCTTTA	TTGAAAAGCT	GAAGGGGTTG	60
TCTAGTAAAG	AGCTGATTTT	ATTGGGAATT	ATCCTGAGTA	TCTTTTACC	CTTTTATCTT	120
TTTGTAGTTG	TACTCTGTTT	ATATATTATC	AGTTTGATTT	TTACAGGAGA	CATGAAAAGT	180
ATTCTTCAGA	AAATGGGGGA	GCATCCGATG	CTGCTTCTTT	TTCTTAGCTA	TAGTACTGTT	240
ATATCCATTC	TTGCACAAAA	TTGGATGGGT	CTTGTGGCTT	CAGTAGGAAT	GTTTCTATTT	300
ACTATTTTCT	TTTTGCACTA	TCAGTCGATT	TTATCCCAT	AATTCTTTCG	ATTGATTTTG	360
CAGTTCGTCT	TGTTTGCTAG	TGTCTTGTC	GCTGTTTTTG	CCAGTTTAGA	ACATTTCCAA	420
ATTGTGAAGA	AATTTAACTA	TGCTTTTCTT	TCACCCAATA	TGCAGGTGTG	GCATCAGAAC	480
CGGGCAGAAG	TGACCTTCTT	TAATCCTAAT	TATTATGGAA	TTATTTGTTG	TTTCTGTATT	540
ATGATTGCTT	TCTATCTGTT	TACAACGACC	AAGTTGAATT	GGTTGAAAGT	ATTCTGTGTG	600
ATTGCAGGCT	TTGTTAATCT	CTTTGGTTTG	AACTTTACTC	AAAAATCGAAC	TGCCTTTCCCT	660
GCTATTATCG	CTGGAGCAAT	TATCTATCTC	TTTACGACTA	TTAAAAACTG	GAAGGCCTTT	720
TGGCTTAGTA	TTGGGGTCTT	CGCGATTGGT	TTGAGTTTCC	TCTTTTCTAG	TGATTTGGGA	780
GTTCGAATGG	GTACTTTAGA	CTCTTCTATG	GAAGAACGCA	TTTCTATCTG	GGATGCTGGG	840
ATGGCCTTGT	TTAAGCAAAA	TCCTTTTGG	GGTGAAGGGC	CATTGACCTA	TATGCACTCT	900
TATCCTCGGA	TACATGCTCC	TTATCATGAA	CATGCCAC	GTCTTTATAT	TGATACGATT	960
CTGAGTTACG	GAATTGTGGG	TACCATTTTA	TTAGTTTGT	CTTCTGTTGC	TCCTGTTCCG	1020
TTGATGATGG	ATATGAGTCA	GGAGTCGGGG	AAACGTCCGA	TTATCGGCCT	TTATCTATCT	1080
TTCCTTACAG	TGGTTGCTGT	GCACGGAATT	TTTGACTTGG	CTCTCTTCTG	GATTCAGTCA	1140
GGCTTTATTT	TCTTGCTAGT	TATGTGCAGT	ATTCCATTGG	AGCATCGAAT	GTTGGTATCG	1200
GACATGACGG	ATTAA					1215

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

AATTTGGAGA	AAATTTTTAT	GGAACCAGAT	ATTTTCATCA	TCACAAAAC	CTTATCAGAC	60
CCTTCTCGGA	TGCACATTTT	AGATATTCTA	ATGGATGGAA	AAGCTCACAC	GGTTAACGAA	120
ATTGCCAGCT	TTACCAAAAT	CAAGCAACAT	ACTGTCAGCT	ATCACCTCAA	ATTACTTACC	180
GAAGCGCAGG	TAACCACTCT	ACAAACCTAT	GGACGTTTTT	ATTATTATTC	TTTAAAAAGT	240
GCTGCCATTG	CAGAAATGCT	GGAATTTCTC	AGCTTCTACT	CTCCTCAGCG	TGATGTCAAA	300
AGTTATAAAC	AACACATTCA	CAAAAAGGAA	TAAAGGTTCG	CTCGCACCTG	CTATGACCAT	360
ATTGCTGGTG	AGCTTGGCAT	TTCCATTACC	AATTATCTCT	TGCAAGAAAA	TCTCCTCAGC	420
GAATCAGAAA	AAGACTTCCA	ACTCACTGAA	GCTGGGAAGT	CTTATTTCCA	AAGAAAATTA	480
CACATTGATA	CGGATGAATT	GAAAAAGAAA	AAACGGAAAT	TTTGGCCCTAA	ATGTTTGGAT	540
TGGAGCGAAC	GTAAAAATCA	TGTCGGCGGA	GCTCTCGGCA	ATGCTCTTTT	AGAATTTTTC	600
AGTGA AAAAC	AATTGGTCAT	CCCTGCACAA	ACGCCACGTT	CACTTACCAT	TACAGAGAAG	660
GGCAAAGAAT	TCCTCGAAAA	GGAATGGGGG	ATTTAA			696

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

TATAAGGAGA	AATATATGTA	TCTTATTGAA	ATTTTAAAT	CTATCTTCTT	CGGGATTGTT	60
GAAGGAATTA	CGGAATGGTT	GCCGATTTCC	AGTACAGGTC	ATTTGATTTT	AGCAGAGGAG	120
TTTATCCAAT	ACCAAAATCA	AAATGAAGCC	TTTATGTCCA	TGTTTAATGT	CGTGATTCAG	180
CTTGGTGCTA	TTTtagcagt	TATGGTGATT	TATTTTAACA	AGCTCAATCC	TTTTAAACCG	240
ACTAAGGACA	AACAGGAAGT	TCGTAAGACT	TGGAGACTAT	GGTTGAAGGT	CTTGATTGCT	300
ACTTTACCTT	TACTTGGTGT	CTTTAAATTT	GATGATTGGT	TTGATACCCA	CTTCATAAC	360
ATGGTTTCAG	TTGCTCTCAT	GTTGATTATC	TACGGGGTTG	CCTTCATCTA	TTTGGAAAAG	420
CGCAATAAAG	CGCGTGCTAT	CGAGCCAAGT	GTAACAGAGT	TGGACAAGCT	TCCTTATACG	480
ACCGCTTTCT	ATATCGGACT	CTTCCAAGTT	CTTGCTCTTT	TACCAGGGAC	TAGCCGTTCA	540
GGTGCAACGA	TTGTCGGTGG	TTTGT TAAAT	GGAACCAGTC	GTTCA GTTGT	GACAGAATTT	600
ACCTTCTATC	TTGGGATTCC	CGTTATGTTT	GGAGCTAGTG	CCTTAAAGAT	TTTCAAATTT	660
GTGAAAGCCG	GAGAACTCTT	GAGCTTTGGG	CAATTGTTTT	TGCTCTTGGT	CGCGATGGGA	720
GTAGCTTTTG	CGGTCAGCAT	GGTGGCTATT	CGCTTCTTGA	CCAGCTATGT	GAAAAACAC	780
GACTTCACCC	TTTTTG GTAA	ATACCGTATC	GTGCTTGGTA	GTGTTTTGCT	ACTTTACAGT	840
TTTGTCCGTT	TATTTGTATA	A				861

(2) INFORMATION FOR SEQ ID NO:1147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 906 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...906
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

TATAAGGAGA	AAAAGATGAC	AAAGAAACAA	CTTCACTTGG	TGATTGTGAC	AGGGATGAGT	60
GGCGCAGGGA	AAACTGTAGC	CATTCAGTCC	TTGCAGGATC	TAGGTTATTT	CACCATTGAT	120
AATATGCCGC	CAGCTCTCTT	GCCTAAGTTT	TTGCAGCTGG	TTGAAATTAA	GGAAGACAAT	180
CCTAAGTTGG	CCTTGGTAGT	GGATATGCGT	AGCCGTTCTT	TCTTTTCAGA	GATTCAAGCT	240
GTTTTGGATG	AGTTGGAAAA	TCAAGATGGT	TTGGATTTCA	AAATCCTCTT	TTTGGATGCG	300
GCTGATAAGG	AATTGGTTCG	TCGTTACAAG	GAAACCAGAC	GGAGTCACCC	ACTAGCAGCA	360
GACGATCGTA	TTTTAGATGG	AATCAAGTTG	GAACGTGAAC	TCTTGGCACC	TTTGAAAAAT	420
ATGAGCCAAA	ATGTGGTGGA	TACGACTGAA	CTCACTCCAC	GTGAGCTGCG	CAAAACCCTT	480
GCAGAGCAGT	TTTCAGACCA	AGAACAAGCC	CAGTCTTTCC	GTATCGAAGT	CATGTCTTTC	540
GGATTTAAGT	ATGGAATCCC	GATTGATGCG	GACTTGGTCT	TTGATGTCCG	TTTCTTGCCA	600
AATCCCTATT	ATTTACCAGA	ACTGAGAAAC	CAAACGGGTG	TGGATGAACC	TGTTTATGAT	660
TATGTCATGA	ACCATCCTGA	GTCAGAAGAC	TTTTATCAAC	ATTTATTGGC	CTTGATTGAG	720
CCGATTCTGC	CAAGTTACCA	AAAGGAAGGT	AAGTCCGTTT	TGACCATTGC	CATGGGATGT	780
ACGGGTGGAC	AACACCGTAG	TGTGGCATTT	GCTAAACGCT	TGGTGCAGGA	CTTATCCAAG	840
AATTGGTCTG	TTAATGAAGG	GCATCGCGAC	AAAGACCGCA	GAAAGGAAAC	GGTAAACCGT	900
TCATGA						906

(2) INFORMATION FOR SEQ ID NO:1148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

AACAAGGAGA	AAGCTATGCC	AGTAAATGAA	TATGGTCAGA	TGATTGGTGA	GTCAATGGAA	60
GGTTATACAC	CCGGTGCAC	GCCTTCTATT	GATTTCTTAG	AAGGGCGTTA	TGCTAGGATA	120
GAGGCTCTCT	CGGTAGAAAA	ACATGCGGAG	GATTTGCTAG	CTGTTTATGG	CCCGGATACT	180
CCTCGGGAGA	TGTGGACCTA	TCTTTTTCAG	GAGCCAGTAG	CAGATATGGG	GGAGCTGGTT	240
AGCCTTTTAA	ATCAGATGTT	GGCTCGTAAG	GACCGTTTTT	ACTATGCAAT	CATAGACAAG	300
GCGACTGGTA	AGGCTTTTGG	AACTTTTTCT	CTCATGCGCA	TTGACCAGAA	TAACCGAGTA	360
ATAGAAATCG	GAGCAGTCAC	TTTTTCTCCA	GAGCTAAGGG	GTACACGGAT	AGGAACTGAG	420
GCTCAGTATC	TCCTAGCTCG	CTATATTTTT	GAGGAGCTAA	ACTATCGTCG	CTACGAGTGG	480
AAATGCGATG	CCTTAAATCT	GCCATCCAGA	CGAGTTGCGG	AGCGTTTGGG	ATTTGTCTAT	540
GAAGGAACCT	TCCGCCAGGC	GGTGGTTTAT	AAGGGGCGTA	CGAGAGATAC	GGATTGGTTG	600
TCTATGATTG	ATATGGACTG	GCCTCAAGTC	AAAGATCGTT	TGGAAACATG	GCTGCGTCCT	660
GAAAAATTTG	ATAAAAATGG	ACAGCAGTAC	AAGAGCTTGA	GAGAACTTTA	A	711

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

ACAAAGGAGA	AAAAAATCAT	GTTTGAACAT	TATTCAGTAG	CTGATTTGTT	TGCAAATCTT	60
TATAAAAAGC	GAAAAGCAAA	TATTTTAGCT	CTCATCGCTT	TATTTGCTCT	CATTGCTGTA	120
CCATTTACAA	TTAAAGCAGT	TAGGAATAAA	AACACTGTCA	AAGATACAAC	AAGTTATTCA	180
ACTTATCTTA	TCTATAAAAT	CACTCCTCCA	AAAGAGTCGG	CCAAAACGAT	TTTGAATCAT	240
CAAATTGGTG	GTTATAGTGA	TTTTTATGGG	AAATTGATTG	ATGGTAATTT	GAATGGAGCT	300
TATCTTTTCA	ATGATGTAGA	ACCCAGTGAG	TTGAAAAAAA	TTGCCAGTGA	ATTAGACACG	360
ACAGAAACAA	CCTTGAAAAA	TTCAACGAAT	GACTATTGGT	GGAAAAAATT	GACCGTCTAC	420
TATATGATTG	ACGATGCAGG	GGTTGGTGTG	AAAATTTTGA	CATCAAGTAA	AGATGCCAAT	480
GACTTGTTAG	AGAAAAAAAT	TGATGGGTTG	ATTGAGAAAT	TTAAACATGC	TTATGCAAAT	540
GTGAAAAATT	AAAAACTGGA	AACCATCAAC	TCTAAAGAAT	TGAACGCAAA	TGGTGAAACA	600
GCGCTTGGCT	TAAATGTGAA	AAATCTGATT	CTTCGTTTAG	TTGTTATTGG	AGTGGTTTGT	660
GTGATTTTGG	TTGTGATGGG	AAATGTGTTA	GTTTATCTCT	TTAATCCAAC	AATCAATAGA	720
GTAGGTGATT	TTTCTCAGTA	TCAAATTGAT	TTTGTAACAG	AGATTACAAC	AATTGCTAAC	780
CTAGCAGATG	TTTTGTCTATA	CAAAAATACT	GGACAGGAAT	TGACCATCGT	TAGCTCAAAT	840
AAAGCTATCC	TAGATAAAAT	GAAACAGAGT	CAAGAAGCTT	TAAAAGGAAT	GCATTTTGTG	900
GATTTACAGG	ATGTATCATC	TCTTTTGGAA	AGAGATACAG	TCCTTCTTGT	TGAAGAGTAC	960
GGAGTGACTC	GTTATAAGAA	ATTTGAGCAA	AGTCTTCAAA	TTCTCAGAAA	CTTAAATCGT	1020

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

AAAAAGGAGA AGAATAGAAA CATGAGAAAG CACCAACTAC AAGTTCACAA ATTGACCATT	60
TTATCTATGA TGATTGCCCT TGATGTAGTC CTTACACCTA TCTTTCGGAT TGAGGGAATG	120
GCACCGATGT CCAGTGTAGT CAATATTCTA GCGGGAATCA TGATGGGACC TGTTTATGCC	180
TTGGCTATGG CTACAGTGAC AGCCTTTATC CGTATGACGA CTCAAGGGAT TCCGCCTTTA	240
GCTCTCACAG GAGCGACTTT TGGAGCCCTT CTAGCAGGTC TCTTTTATAA GTACGGTCGA	300
AAATTTTACT TTTCTGCCTT GGGAGAAATT GTGGGAACAG GTATTATTGG TTCTATTGTT	360
TCCTATCCTG TTTATGGTGCT CTTTACAGGA TCGGCTGCTA AGCTTAGTTG GTTTATCTAC	420
ACGCCTCGAT TTTTCGGAGC AACCTTGATT GGTACAGCGA TTTCCCTTTAT TGCATTTTCGA	480
TTTTTAATCA AGCAGGAATT CTTTAAAAAA GTGCAAGGAT ATTTCTTTGC TGAAAGGATA	540
GAATGA	546

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

AAAAAGGAGA	ATGAAGTGGT	AGTACAGTTA	TTAGAAAATT	GGCTCCTAAA	GGAACAAGAA	60
AAAATTCAAA	CCAAATATCG	TCACCTAAAT	CACATTTCTG	TTGTAGAACC	AAACATTCTT	120
TTTATTGGGG	ATTCCATTGT	CGAGTATTAT	CCTCTACAGG	AGCTATTTGG	GACTTCAAAG	180
ACGATTGTCA	ATCGAGGAAT	TCGTGGCTAT	CAGACAGGAC	TGTTACTAGA	GAACCTTGAT	240
GCTCATCTAT	ATGGTGGAGC	AGTAGATAAA	ATTTTTCTTC	TGATTGGGAC	AAATGATATC	300
GGAAAGGATG	TTCCGTGTAA	TGAGGTTCTC	AATAATCTCG	AAGCTATCAT	TCAATCCGTT	360
GCTCGCGATT	ATCCATTGAC	AGAGATTAAA	TTGCTTTCCA	TTTTGCCTGT	CAATGAGGGA	420
GAGAAGTACC	AGCAGGCAGT	CTATATCCGC	TCGAATGAAA	AAATTCAGAA	TTGGAATCAA	480
GCCTATCAAG	AGCTTGCATC	TGCCATATATG	CAGGTGGAAT	TTGTGCCAGT	ATTTGATTGT	540
TTGACAGACC	AAGCAGGCCA	ACTCAAAAAA	GAATATACAA	CTGATGGACT	GCACCTCAGT	600
ATTGCTGGTT	ATCAGGCTTT	GTCAAAATCC	TTGAAAGACT	ATCTTTACTA	A	651

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

GAAAAGGAGA	AATGTATGGG	GTGGTGGCGC	GAAACCATTG	ATATCGTAAA	AGAAAATGAT	60
CCAGCGGCC	GCACCACTTT	GGAGGTTTTG	CTGACTTATC	CAGGTGTCAA	GGCCTTGGCG	120
GCCCACCGT	TCTCGCATTT	TCTCTGGAAG	TACGACTTCA	AACTCTTAGC	TCGTATGCAC	180
AGTCAGTTTT	GGCGCTTTTG	GACTCAGATT	GAGATTCATC	CAGGAGCCCA	GATTGATTCA	240
GGTGTCTTTA	TTGACCATGG	TTCTGGTCTG	GTGATTGGAG	AGACAGCGAT	TGTTGAAAAA	300
GGCGTTCTTC	TCTATCACGG	AGTGACTCTC	GGGGGAACAG	GGAAAGACTG	TGGCAAACGC	360
CATCCGACTG	TACGAAAGGG	AGCCCTCATA	TCAGCCCATG	CCCAAGTTAT	CGGGCCTGTG	420
GAAATTGGTG	AAAATGCCAA	GGTCGGTGCT	GCAGCAGTTG	TCGTAGCAGA	TGTACCTAGT	480
GATGTGACGG	TTGTCGGTAT	TCCGGCCAAG	ATTGTCCGTC	TTCATGGTAA	GAAAGATGAG	540
CCTGTTATTC	ACGAAGTCGA	AGAAAAACGG	GAGTATTATG	TCAATAAACT	CGAGCAGGCT	600
AAAGATGCCA	GTCACAGATC	GTCTGGTTTTG	TAG			633

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...798
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

ATACATTGGA	AGACCTCGAT	GGCAACGATT	AAAGAAATCA	AAGAACTCCT	TGTGACAGTC	60
AAGGAGTTAG	AAAGCCCTAT	TTTTTTAGAT	CTTGAAAAGG	ATAATCGCTC	AGGAGTTCAA	120
AAAGAAATCA	GCAAGCGTAA	AAGAGCCATT	CAAGCTGAAT	TAGATGAAAA	TTTGCGCTTG	180
GAATCCATGC	TTTCTTATGA	AAAAGAACTT	TATAAGCAAG	GATTGACCTT	AATTGCAGGT	240
ATTGATGAGG	TTGGTCGTGG	TCCTCTTGCT	GGTCCTGTAG	TCGCTGCGGC	CGTTATTTTA	300
CCTAAAAATT	GTAAGATTAA	AGGTCTCAAC	GACAGCAAGA	AAATTCCTAA	AAAGAAACAT	360
CTGGAGATTT	TCCAAGCCGT	TCAAGACCAA	GCCTTGTCGA	TTGGAATTGG	TATCATAGAT	420
AATCAGGTCA	TCGACCAAGT	CAATATCTAT	GAAGCAACCA	AACTAGCCAT	GCAAGAAGCA	480
ATCTCCAGC	TCAGCCCTCA	ACCAGAGCAT	CTTTTGATTG	ATGCCATGAA	ACTGGACTTG	540
CCCATTTCAC	AAACCTCCAT	TATCAAAGGA	GATGCCAACT	CCCTCTCTAT	CGCAGCAGCA	600
TCTATAGTAG	CCAAGGTAAC	ACGTGATGAA	TTGATGAAAG	AATACGATCA	GCAGTTCCCT	660
GGCTATGATT	TCGCTACTAA	TGCAGGATAT	GGCACAGCTA	AACATCTGGA	AGGCCTCACA	720
AAACTAGGAG	TTACCCCAAT	TCATCGAACC	AGCTTTGAAC	CCGTTAAATC	ACTGGTTTTA	780
GGTAAAAAAG	AAAGTTAA					798

(2) INFORMATION FOR SEQ ID NO:1154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...391
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

CTTNGTTGGA	ATNTCNTTGG	TGAGGCTGGA	CCNCGGTGGT	GCGTTGGTGG	GTCGGGGTGG	60
CTTGGTTTTT	TCTCCCTGTG	GGGGGCNNGG	GGTCGCGGGG	CGGGGGCCCG	GGGGTCCCGT	120
GCGGGGCGGG	GGTGGCTCGT	CGCCTTGCTG	TCTGTGCTGG	GCTGCGTGCC	GCGCTCTGGG	180
TTGTGGCGGG	TGGGCGNNGG	CCGGGGCGGG	GGGGGGTGCG	TGTGTGGTGG	CCNGCTGCNC	240

CGTTTGGTTG CCGCGGATCT GGGGAGGCTG CGGCCGGCTG CGCTGGGGGG TGCGGCGGGT	300
CGCGCCCCCTC GCGCCAGAGT GGGGACGGGG GAGGTGGGGA GGAGTACAGG ACTAGAGGAT	360
GGCGTGCTTA TGTGTCCGG CGCCCCGCC C	391

(2) INFORMATION FOR SEQ ID NO:1155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...360
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

GGAAGATGGA ACCAGCGTCA CAGTTCGAGC TTAAGAAAGG AAAAGGAAAT GATAGAGGCA	60
CAGGGTTTCT TAGTGGATAA GCAAACAAGA TGCATTTCATT ACCATAGCAA GCTGGATATT	120
ATTGCTTTAC AATGCTATGA TTGTAAAAAG TATTATGCTT GTTATCGGTG TCATGATTCA	180
TTAGAAAATC ACCCTTTTGA GCCGTATCCC TTATCTTTGA TACAGGATAA GCCTATTTTA	240
TGTGGTGTTC GTCTAAACT ACTAACATAT AAGCAATATA AAGAAAGTTT AAGTTGCCCC	300
TTTTGTTCCT CTCGCTTTAA TCCAGGTTGC CAAAATCATA AGGAACGCTA TTTTAAATAG	360

(2) INFORMATION FOR SEQ ID NO:1156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

TCCGTGTGGA	AATTTTCATCA	GACTCACACC	CATTCTACAC	TGGACGTCAA	AAGTTCACTC	60
AAGCAGATGG	ACGCGTGGAT	CGTTTCAACA	AAAAATACGG	TCTCAAATAA	TGATAAGAGA	120
ACAGTTTCGG	CTGTTCTTTT	TTGTTTCTTG	AAATCAACTG	CTGTTTTCAT	GTTCCAAACT	180
CATCTGTAG						189

(2) INFORMATION FOR SEQ ID NO:1157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...747
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

TTTAGACGGA	ACATTTTATAA	GGGGAAAGAC	CGAATCCCTG	CTGGAGAGAC	TTTGTTCAT	60
GAATTGCAAA	AGCGGGACAT	TCCTATTCTG	TTTGTNACCA	ACAATACAAC	CCGCACTCCA	120
GAGAGTGTTA	AGGAGATGTT	GGCTCAGAAT	TTTAATATCG	ATACGCCCNT	ATCGACTGTC	180
TACACAGCGA	CTTTGGCAAC	CATCGACTAT	ATGAATGATT	TGGGGCTTGA	AAAGACCGTC	240
TATGTCGTCG	GAGAAGCAGG	ACTCAAGGAA	GCCATCAAGG	CGGCTGGTTA	TGTGGAAGAC	300
AAGGAAAAAC	CTGCCTACGT	GGTAGTTGGT	CTGGATTGGC	AAGTCGACTA	TGAAAAATTT	360
GCCACAGCAA	CTCTTGCTAT	TCAAAAGGGT	GCCCATTTTA	TCGGAACCAA	TCCTGACCTC	420
AACATCCCGA	CGGAACGCGG	TCTTTTGCCA	GGTGCTGGCT	CACTGATTAC	GCTGCTTGAA	480
GTAGCGACAC	GAGTGAAGCC	GGTTTATATC	GGAAAACCAA	ATGCCATCAT	TATGGACAAG	540
GCGGTTGAGC	ACTTAGGTTT	GGAACGTGAA	GAGTTAATCA	TGGTTGGGGA	CAATTATTTG	600
ACTGATATTC	GGGCTGGGAT	TGACAATGGC	ATTCCAACGC	TCTTGGTGAC	GACAGGTTTT	660
ACTAAGGCAG	AAGAAGTAGC	TGGCCTGCCA	ATCGCACCGA	CACATGTGGT	TTCTAGCATT	720
GCGGAGTGGG	ATTTTGATGA	AAACTAA				747

(2) INFORMATION FOR SEQ ID NO:1158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

CAAAC TAGGA AACTAGCTGC GGGCTGCTCT AAACACTGTT TTAAGGTTGT AGATGGA	60
ACT GACGAAGTCA GCTCAAAACA CTGTTTTGAG GTTGTGGATA GAACTGACGA AGTCAGTAA	120
CTACCTACG GCAAGGCGAC GTTGACGTGG TTTGAAGAGA TTTTCGAAGA GTATAAGTCT	180
CTACATAATA AAACGCATAT TACCAAGGTT GTGTAA	216

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

GGAAGTAGGA AAAGTATGTA TCCAGATGAT AGTTTGACAT TGCACACGGA CTTGTACCAG	60
ATCAACATGA TGCAGGTTTA CTTTGACCAA GGGATTACACA ATAAGAAGGC GGTCTTTGAG	120
GTGTATTTCC GCCAACAGCC TTTTAAGAAC GGCTATGCGG TTTTGCAGG TTTGGAAAGA	180
ATTGTGAAT ATCTTGAAGA CTTGCGTTTT TCAGATAGTG ATATAGCCTA TTTGGAGTCG	240
CTTGGTTATC ATGGGGCGTT CTTGGATTAC CTTGCAATT TCAAGTTGGA GTTGACCGTT	300
CGTTCTGCCC AAGAAGGGGA TTTGGTTTTT GCTAATGAAC CGATTGTGCA GGTGGAAGGA	360
CCTCTAGCCC AATGTCAGTT GGTCGAAACG GCTCTTTTGA ACATCGTCAA CTACCAGACC	420
TTGGTGGCGA CGAAGGCAGC TCGTATTCGT TCGGTTATCG AAGATGAACC CTTGATGGAG	480
TTTGGGACAC GTCGGGCTCA AGAAACGGAT GCGGCCATCT GGGGAACACG CGCAGCGGTG	540
ATTGGTGGCG CCAATGGAAC CAGCAACGTG CGTGCGGGTA AGCTCTTTGA CATTCCTGTT	600
TTGGGAACCC ATGCCCATGC CTTGGTACAG GTTTATGGCA ATGACTATGA GGCTTTCAAG	660
GCTTACGCTG CGACCCACAA AAATTGTGTC TTTCTTGTGG ATACCTATGA TACCCTTCGC	720
ATCGGTGTAC CAGCTGCCAT TCAGGTGGCG CGTGAGCTGG GTGATCAGAT TAACTTTATG	780
GGTGTGCGGA TTGACTCTGG GGATATTGCC TACATTCTA AGAAAGTCCG TCAGCAACTG	840
GACGAGGCTG GATTTACAGA GGCTAAGATT TATGCTTCTA ATGATTTGGA CGAAAATACT	900
ATCCTCAATC TCAAGATGCA AAAGGCCAAG ATTGATGTCT GGGGTGTGGG TACCACAGCT	960
GATTACAGCC TATGA	975

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

AATGGTAGGA	AGAATTGGAG	AGTAGAGATG	CCGAAAGAAG	TGAATTTAAC	AGGCGAAGAA	60
GTTGTCGCTT	TAACCAAAGA	ATATTTAACG	GAAGAGGATG	TTCATTTTGT	CCATAAGGCC	120
TTGGTCTATG	CTGTTGAATG	CCACAGTGGT	CAATATCGCA	AATCAGGCGA	GCCTTATATC	180
ATTCACCCTA	TCCAAGTGGC	AGGTATTTTA	GCTAAGCTAA	AGCTGGATGC	TGTAACAGTA	240
GCTTGTGGAT	TCTTGCATGA	TGTGGTGGAA	GATACAGATG	CGACCTTGGG	CGATTTGGAA	300
AGAGAGTTTG	GTCCTGATGT	GCGGGTGATT	GTTGACGGAG	TTACCAAGCT	TGGCAAGGTC	360
GAGTACAAAT	CGATCGAGGA	GCAATTAGCG	GAAAATCATC	GCAAGATGCT	CATGGCCATG	420
TCTGAGGACA	TCCGCGTTAT	TTTGGTCAAA	CTGTCTGACC	GCTTGCACAA	TATGCGGACC	480
CTGAAACATC	TTCGAAAAGA	CAAGCAGGAG	CGTATTTCCA	AAGAAACCAT	GGAAATCTAT	540
GCCCCACTTG	CCCATCGTTT	GGGGATTTCC	AGTGTCAAAT	GGGAATTAGA	AGACTTGTCT	600
TTCCGTTATC	TCAATCCAAC	GGAGTTTTAC	AAGATTACCC	ATATGATGAA	GGAAAAGCGC	660
AGGGAGCGTG	AGGCCTTGGT	GGATGAGGTA	GTCACAAAAT	TAGAGGAGTA	TACGACAGAA	720
CGTCACTTGA	AAGGGAAGAT	TTATGGTCGT	CCCAAGCATA	TTTACTCAAT	TTTCCGCAAA	780
ATGCAGGACA	AGAGAAAACG	GTTTGAGGAA	ATCTATGATC	TGATTGCTAT	TCGTTGTATT	840
TTAGATACCC	AAAGTGATGT	TTATGCCATG	CTTGGTTACG	TGCATGAATT	TTGGAAACCG	900
ATGCCAGGTC	GCTTCAAAGA	CTATATTGCC	AACCGCAAGG	CCAATGGTTA	TCAGTCTATC	960
CATACGACTG	TTTATGGACC	AAAAGGGCCG	ATTGAATTCC	AGATTCGAAC	CAAGGAAATG	1020
CACGAGGTGG	CTGAGTACGG	GGTTGCGGCT	CACTGGGCTT	ATAAGAAAGG	TATAAAGGGG	1080
CAAGTTAACA	GCAAGGAATC	AGCTATTGGA	ATGAATCTGA	TCAAGGAGAT	GATGGAGCTC	1140
CAAGACCAGG	CTGATGATGC	TAAGGAATTT	GTGGACTCTG	TTAAGGAAAA	CTATCTGGCT	1200
GAGGAGATTT	ACGTTTTTAC	CCCAGATGGA	GCTGTCCGTT	CCCTTCCCAA	AGATTCAGGA	1260
CCGATTGATT	TTGCCCTACG	AATCCATACC	AAGGTCGGTG	AAAAAGCAAC	TGGTGCCAAG	1320
GTCAATGGCC	GCATGGTTCC	ACTGACAACC	AAGTTAAAGA	CAGGGGATCA	GGTTGAAATT	1380
ATCGCCAACC	CGAACTCCTT	TGGACCTAGC	CGTGACTGGC	TCAATATGGT	CAAGACTAGC	1440
AAGGCGCGCA	ATAAGATTCT	CCAGTTCTTT	AAAAACCAAG	ATAAGGAATT	GTCTGTCAAC	1500
AAGGGTCGTG	AGATGCTGAT	GGCTCAGTTC	CAAGAAAATG	GCTATGTGGC	AAATAAATTT	1560
ATGGACAAGC	GCCACATGGA	TCAAGTTCTG	CAAAAGACCA	GTTACAAGAC	AGAAGACTCC	1620
CTCTTTGCGG	CCATTGGTTT	TGGGGAAATC	GGTGCGATTA	CCGTCTTTAA	CCGTCTGACT	1680
GAAAAGGAAC	GCCGTGAGGA	AGAGCGTGCC	AAGGCCAAGG	CTGAGGCAGA	GGAGCTTGTC	1740
AAAGGTGGCG	AGGTCAAGGT	TGAAAATAAA	GAAACTCTCA	AGGTCAAGCA	TGAGGGGGGA	1800
GTGGTTATTG	AAGGTGCTTC	TGGTCTCCTA	GTGCGGATTG	CTAAGTGTTG	TAACCCCGTG	1860
CCTGGTGACG	ATATTGTTGG	CTACATTACC	AAGGGTCGTG	GTGTGGCTAT	TCACCGTGTG	1920
GACTGTATGA	ACCTGCGTGC	CCAAGAAAAC	TACGAGCAAC	GTCTCCTTGA	TGTGGAATGG	1980
GAAGACCAGT	ACTCTAGCTC	AAATAAGGAG	TATCTGGCCC	ATATCGATAT	CTACGGTCTC	2040
AACCGTACAG	GACTGTTGAA	CGATGTACTG	CAAGTTCTTT	CAAATACAAC	CAAGAATATT	2100
TCAACGGTCA	ATGCCCAACC	AACCAAGGAT	ATGAAGTTTG	CTAATATCCA	TGTGTCCTTC	2160
GGTATTGCCA	ACCTCTCTAC	ACTGACCACG	GTTGTCTGATA	AAATTAAGAG	TGTGCCAGAA	2220

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

ATTTACAGGA AATTAGGCTG GAGAACCAGC CTTTTTCTAA AGATAAGGAG AAATATGAAC	60
AAAAAAACAA GACAGACACT AATCGGACTG CTAGTGTTAT TGCTTTTGTC TACAGGGAGC	120
TATTATATCA AGCAGATGCC GTCGGCACCT AATAGTCCCA AAACCAATCT TAGTCAGAAA	180
AAACAAGCGT CTGAAGCTCC TAGTCAAGCA TTGGCAGAGA GTGTCTTAAC AGACGCAGTC	240
AAGAGTCAAA TAAAGGGGAG TCTGGAGTGG AATGGCTCAG GTGCTTTTAT CGTCAATGGT	300
AATAAAACAA ATCTAGATGC CAAGGTTTCA AGTAAGCCCT ACGCTGACAA TAAAACAAAG	360
ACAGTGGGCA AGGAAACTGT TCCAACCGTA GCTAATGCCC TCTTGTCTAA GGCCACTCGT	420
CAGTACAAGA ATCGTAAAGA AACTGGGAAT GGTTCAACTT CTTGGACTCC TCCAGGTTGG	480
CATCAGGTCA AGAATCTAA GGGCTCTTAT ACCCATGCAG TCGATAGAGT CATTGGGCAG	540
TCTTCACCAC GAGTAGTAGA CGGT	564

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

TTTTGCAGGA	AGTCTAATAA	AGAAACTAGC	AAGGTCATGC	CTTACTTTTAT	TGGTGGACAT	60
CCAGGATTTA	ATTGTCCTCT	ACTTGATGAT	GGAGTCTATG	AAGATTATTA	TCTAGAGTCT	120
GAGAAAGAAG	AGACTTGCTC	TGTTCCACGT	CCTTTCCAG	AAACAGGTAT	GTTGGATTTT	180
CAAGATAGAA	GTCCATGGCT	AGAGGGACAA	AAAGAAATAG	ATCTTAGTTA	TGATCTTTTC	240
AGCACAGATG	CAGTGACTTT	GGATGAATTG	CAATCTCGAA	CAATTGCCCT	TCGTTCTCTT	300
AAACATGATA	AGGGATTGAA	AGTGCATTTT	GCAGAATTTC	CAAACCTCAT	CATCTGGTCA	360
ACTTTGAACA	AGGGACCTTT	CATTACCTTT	GAACCATGGT	CTGGCTTGTC	AACATTCCTT	420
GAAGAAGGAG	ATCATTTAGA	AGATAAGAAG	AATGTTTGTC	TCTTAGAAGC	CAATCAGGTT	480
GAAGAATTAG	GGTTTGAGAT	AGAAGTTTTA	TAA			513

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GCTAGCAGGA	ACTCCTATGG	ACAAGATTGT	ACGCACACTG	GAAGCGAATG	GCTACGAAGT	60
GATTGGATTA	GACTAATGAC	AGATGAACGG	ATTCATGTCC	TACGGGATAT	TTTGTTAGAA	120
TTGCACAATG	GCGCCTCTCC	TGAGTCGGTT	CAAGATCGCT	TTGATGCGAC	CTTTACGGGC	180
GTGTCAGCCA	TCGAGATTTC	CCTTATGGAG	CACGAGCTGA	TGAACTCGGA	TTCGGGCGTC	240
ACTTTTGAAG	ATGTTATGGA	ACTCTGTGAT	GTCCATGCCA	ATCTTTTTTAA	AAATGCTATC	300
AAAGGTGTGC	AAGTTTCAGA	TACTGAGCAT	CCAGGTCACC	CAGTTCGTGT	CTTCAAAGAA	360
GAAAACTGG	CTCTCCGTGC	GGCCTTGATT	CGCATTCGTA	GATTGTTAGA	TACCTATGAG	420
TCTATGGAAG	ACGAGGAAAT	GCTGGCGGAG	ATGCGTAAAG	GTTTGGTGCG	TCAGATGGGA	480
CTTGTGGGTC	AATTTGACAT	CCATTACCAA	CGTAAGGAAG	AACTCTTCTT	TCCTATCATG	540
GAGCGCTATG	GACACGATTC	ACCTCCCAAA	GTTATGTGGG	GAGTGGATGA	TCAGATTAGG	600
GAACTCTTTC	AAACAGCTCT	AACGACAGCC	AAGTCACTAC	CAGAAGTGTC	AATTAGCAGT	660
GTAAAGGAAG	CTTTTGAAGC	TTTTGCGACA	GAGTTTGAAA	GTATGATTTT	CAAGGAAGAG	720
TCCATCCTGC	TCATGATTCT	CCTTGAGTCT	TTTACTCAGG	ATGACTGGCT	TCAGATTGCG	780
GAGGAGAGTG	ATGCCTATGG	CTATGCCATC	ATCCGTCCGT	CAGAGAAATG	GGTGCCAGAA	840
CGACAGATCT	TTATTGAGGA	AAAGATTGCA	GAGGAGCCTG	TACAGCTAGA	TACGGCAGAA	900
GGTCAAGTTC	AACAAGTCAT	AGATACGCCA	GAAGGCCATT	TTACCATTAC	CTTTACCCCT	960
AAGGAAAAGG	AAGCTGTGCT	GGACCGCCAT	AGTCAACAGG	CTTTTGGTAA	TGGCTATCTT	1020
TCAGTCGAGC	AGGCCAATCT	CATCCTCAAT	CATCTCCCTA	TGGAGATTAC	CTTTGTCAAT	1080
AAAGAAGATA	TTTTCCAGTA	TTACAATGAC	AATACGCCAG	CTGATGAGAT	GATTTTCAAA	1140
CGGACGCCGT	CCCAAGTCGG	GCGCAATGTC	GAAGTCTGTC	ATCCGCCTAA	GTATTTGGAC	1200
AAGGTCAAGG	CTATCATGAA	GGGACTTCGT	GAGGGGACCA	AGGACAAGTA	TGAAATGTGG	1260
TTCAAGTCTG	AGTCGCGAGG	AAAGTTTGTC	CACATCACCT	ATGCTGCAGT	ACACGATGAA	1320

AACGGAGAAT TCCAAGGTGT ACTGGAATAC GTTCAGGATA TCCAGCCCCTA CCGTGAGATT	1380
GATACGGACT ATTTCCGTGG ATTAGAATAA	1410

(2) INFORMATION FOR SEQ ID NO:1164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

AGGACAAGGA ATGTGGCTTT CTACGGACTG ACCTCGGTCT CAAACTGGTC TCTGAGCTCT	60
AACATAAGCA CACGCTTGAT TGAAGTATTT CTAATTCATC ATTTACACTA TACAAGTGAC	120
CAGATTCACG AGGAAGCTGA CGTCTTGGAT AACACTGTCT CTGACCTGTT CGTGGAAAGA	180
CTAGATAAAC TGCTAGGTTT CCCTAAAACC TGCCCCACG GAGGAACTAT TCCTGCCAAG	240
GGAGAACTAC TCGTTGAAAT CAATAACCTC CCACTAGCTG ATATCAAGGA AGCTGGCGCC	300
TACCGCCTGA CTCGGGTGCA CGATAGTTTT GACATTCTCC ATTATCTGGA CAAGCACTCA	360
CTTCACATCT GTGACCAGCT CCAAGTCAAG CAGTTTGATG GCTTCAGCAA TACCTCCACT	420
ATCCTCAGTA ACGACGAGGA TTTACNAGTG AATATGGACA TTGCAAAACA ACTCTATGTC	480
GAGAAAATCA ACTAA	495

(2) INFORMATION FOR SEQ ID NO:1165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

GATGAAAGGA	ACTTTAGAAA	TCTTATGATG	AACATGCAAA	ACATGATGCG	TCAAGCACAA	60
AAACTTCAAA	AACAAATGGA	ACAAAGCCAA	GCTGAACTTG	CTGCTATGCA	ATTTGTTGGC	120
AAATCTGCTC	AAGATCTTGT	CCAAGCGACC	TTAAGTGGCG	ATAAGAAAAGT	TGTCAGCATT	180
GATTTCAATC	CAGCTGTCGT	TGACCCAGAG	GACCTTGAGA	CTCTTTCTGA	TATGACCGTT	240
CAAGCCATCA	ACTCTGCTCT	TGAACAAATC	GATGAAACTA	CCAAGAAAAA	ACTGGGTGCT	300
TTCGCTGGGA	AATTACCTTT	CTAA				324

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

ATAGAAAGGA	ACTATATGAT	TTACAAAGTT	TTTTATCAAG	AAACAAAAGA	ACGTAGCCCA	60
CGCCGTGAAA	CAACACGCGC	GCTTTACCTA	GACATCGATA	CCAGCTCAGA	ACTTGAGGGC	120
CGTATCACTG	CTCGCCAACT	TGTCGAAGAA	AATCGCCCAG	AGTACAATAT	CGAATATATC	180
GAACTCTTGT	CTGACAAATT	GCTCGATTAC	GAAAAAGAAA	CTGGCGCCTT	CGAAATTACG	240
GAGTTCTAA						249

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

AAAAGAAGGA	ATTTATACCA	ATTGAAAAAA	CCAATTATCG	AATTCAAAAA	CGTCTCTAAA	60
GTTTTTTGAAG	ACAGCAACAC	CAAGGTTCTC	AAAGACATCA	ACTTTGAGTT	GGAAGAAGGG	120
AAATTCTACA	CCCTTCTAGG	TGCATCTGGT	TCGGGGAAAT	CAACTATCCT	AAACATTATT	180
GCAGGTTTAC	TGGATGCGAC	GACAGGAGAT	ATCATGCTAG	ACGGTGTTCT	TATCAATGAT	240
ATTCCAACCA	ACAAGCGCGA	CGTACATACC	GTCTTCCAAT	CCTATGCCTT	GTTCCACAT	300
ATGAATGTGT	TTGAAAATGT	TGCCTTTCCA	CTTCGCTTGC	GTAAAAATTGA	TAAGAAAGAA	360
ATCGAGCAGC	GTGTAGCGGA	AGTTCTCAAG	ATGGTTCAGT	TGGAAGGTTA	TGAAAAACGT	420
TCCATCCGCA	AACTTTCTGG	AGGACAACGT	CAGCGTGTGG	CCATCGCCCG	TGCTATCATC	480
AACCAACCCC	GTGTGGTCTT	GTTGGACGAG	CCTTTATCAG	CGCTGGACTT	GAAATTGAGA	540
ACAGACATGC	AGTACGAATT	GCGTGAATTA	CAACAACGAT	TGGGCATTAC	CTTTGTCTTT	600
GTCATCACG	ATCAGGAAGA	AGCTCTTGCC	ATGAGTGAAT	GGATTTTCGT	TATGAATGAT	660
GGCGAGATTG	TCCAGTCTGG	AACCCCTGTG	GACATCTACG	ATGAGCCAAT	CAACCACTTT	720
GTTGCCACCT	TTATCGGGGA	GTCAAACATC	TTGCCAGGTA	GCATGATTGA	GGACTACTTG	780
GTCGAATTTA	ACGGCAAACG	CTTTGAAGCG	GTTGATGGTG	GGATGAAGCC	AAATGAACCT	840
GTTGAGGTCG	TTATTTCGTCC	AGAGGACTTG	CGCATTACCC	TTCTGAAGA	AGGCAAGCTC	900
CAAGTTAAGG	TCGATACCCA	GCTCTTCCGT	GGGGTGCATT	ATGAAATTAT	CGCCTATGAC	960
GAACTTGGA	ATGAATGGAT	GATCCACTCA	ACCCGTAAGG	CCATCGTGGG	TGAGGAAATC	1020
GGTCTGGACT	TTGAACCAGA	AGACATCCAC	ATCATGCGTC	TCAATGAAAC	CGAAGAAGAG	1080
TTCGATGCTC	GTATTGAGGA	GTACGTAGAA	ATCGAAGAGC	AAGAAGCAGG	TTTGATCAAT	1140
GCACACTCGA	GGAGTTAA					1158

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

AGGGTGAGGA	AGTCAAGAGT	GAACAATAGT	CAACAGATGT	TACAGGCTTT	GGAGGAGCAA	60
GATTTAACTA	AGGCTGAGCA	TTATTTTCGCC	AAAGCTTTAG	AAAATGATTC	AAGTGATCTT	120
CTGTATGAAT	TGGCAACTTA	TCTTGAAGGG	ATTGGTTTCT	ATCCTCAGGC	CAAGGAAATT	180
TACCTGAAAA	TTGTAGAGGA	TTTTCCAGAG	GTTCATCTTA	ATCTAGCTGC	AATTGCTAGC	240
GAGGATGGTC	AAATAGAAGA	AGCCTTTACC	TATCTTGAGG	AAATCCAAGC	TGACAGTGAC	300
TGGTATGTCT	CGTCTTTGGC	TCTGAAGGCA	GACCTTTACC	AGCTGGAAGG	TTTGACAGAT	360
GTGGCACGTG	AGAAATTATT	GGAGGCCCTG	ACCTACTCAG	AGGATTCTCT	CTTGATATTG	420
GGTTTGGCAG	AGTTGGATAG	TGAGTTGGAA	AATTACCAAG	CGGCTATTCA	AGCCTATGCC	480
CAGTTAGATA	ATCGCTCGAT	TTATGAGCAA	ACGGGCATTT	CCACCTATCA	ACGAATTGGC	540

TTTGCCTATG	CTCAGTTAGG	GAAATTTGAA	ACGGCTACTG	AGTTTTTTAGA	AAAAGCCCTG	600
GAGTTAGAA	ACGATGACTT	AACAGCTTTT	GAGTTGGCCA	GTCTTTATTT	TGATCAAGAA	660
GAATATCAAA	AAGCCACCCT	CTACTTTAAG	CAGCTTGATA	CCATTTCTCC	TGACTTTGAA	720
GGCTATGAGT	ATGGGTACAG	TCAGGCTTTA	CATAAGGAAC	ATCAAGTTCA	AGAAGCCCTG	780
CGTATCGCTA	AGCAAGGATT	AGAGAAAAAT	CCCTTTGAAA	CTCGCCTCTT	GCTAGCTGCT	840
TCACAATTTT	CTTATGAATT	GCATGATGCT	AGTGGTGAG	AAAATTATCT	CCTTACTGCA	900
AAAGAAGACG	CTGAGGATAC	AGAAGAAATC	TTGCTTCGTT	TAGCCACTAT	TTATCTGGAG	960
CAGGAGCGTT	ATGAGGATAT	TCTAGAATTG	CAGAGT			996

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

AAAAAGAGGA	ACTCAATGCT	ACATTATACA	AAAGAAGACT	TGCTCGAATT	GGGTGCAGAA	60
ATCACTACGC	GTGAAATCTA	CCAACAACCT	GATGTATGGA	GAGAAGCTTT	TGAATTTTAT	120
CAAGCAAAAC	GTGAAGAAAT	TGCAGCCTTC	CTACAAGAAA	TCGCTGATAA	ACATGACTAT	180
ATTAAGGTTA	TCTTGACAGG	TGCTGGGACT	TCTGCTTATG	TGGGAGACAC	CTTGCTACCT	240
TACTTTAAGG	AAGTCTATGA	CGAACGCAAA	TGGAATTTCA	ATGCTATTGC	GACAACAGAT	300
ATCGTTGCCA	ATCCAGCAAC	CTATTTGAAA	AAAGATGTGG	CAACTGTCCT	TGTGTCTTTT	360
GCTCGTAGTG	GGAAGCTGCC	TGAAAGTGTG	GCGACTGTTG	ATTTGGCCAA	ATCCTTGGTG	420
GATGAGCTTT	ATCAAGTGAC	GATTACTTGT	GCAGCAGATG	GTAAATTGGC	TCTTCAAGCT	480
CACGGTGATG	ATCCGTAATCT	CTTGCTCTTG	CAACCAGCTG	TCTCTAATGA	TGCTGGATTT	540
GCCATGACTT	CTAGCTTTAC	GTCTATGATG	TTGACAATCT	TCTTGGTCTT	TGATCCTACA	600
GAATTTGCTG	TTAAGTCTGA	ACGTTTTGAA	GTTGTATCTA	GTCTTGCCCG	TAAAGTTTTA	660
GACAAGGCAG	AAGATGTCAA	AGAGCTCGTT	GATTTAGACT	TTAACCGTGT	CATCTATCTA	720
GGCGCTGGTC	CTTTCTTTGG	ACTTGCTCAT	GAAGCTCAGC	TCAAGATTTT	GGAATTAAC	780
GCTGGTCAAG	TTGCGACCAT	GTATGAAAGC	CCAGTTGGCT	TCCGTCACGG	TCCAAAATCT	840
CTTATCAACG	AAAATACAGT	TGTTTTGGTC	TTTGGTACAA	GGACAGACTA	CACTCGTAAG	900
TACGACTTGG	ACTTGGTTCG	TGAAGTTGCT	GGTGACCAGA	TTGCTCGTCG	TGTTGTGCTT	960
TTGAGTGATC	AAGCTTTTGG	TCTTGAAAAT	GTCAAAGAAG	TGGCCCTTGG	TTGTGGCGGT	1020
GTCTTGAAATG	ATATTTACCG	TGTCTTCCCT	TACATCGTTT	ATGCCCAACT	CTTTGCCCTA	1080
TTGACTTCAC	TCAAGGTAGA	AAATAAACCA	GATACACCGT	CTCCTACAGG	TACAGTAAAC	1140
CGTGATAGTAC	AAGGTGTCAT	AATTCACGAA	TATCAAAAGT	AA		1182

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

TTTTGGAGGA AGATTTTGTC TCTATTATTT ATTATTTTAA ATTTATTTAT TTTGTATAAG	60
ATCTATTCTT TGAGGCGGGA AAAATCGAAA TACTTGATTT ATACGGCCTA TATCATATTT	120
GGGGTAAATG TAGTATATGG TATTCAATGG TTATTAAAAG AACTGATTTC AACTATTTCC	180
CCTTAA	186

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1005 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

ATAAGGAGGA ATCTGGTAAT GGTAGTATTT ACAGGTTCAA CTGTTGAAGA AGCAATCCAG	60
AAAGGATTGA AAGAATTAGA TATTCCAAGA ATGAAGGCTC ATATCAAAGT CATTTCTAGG	120
GAGAAAAAAG GCTTTCCTTG TCTATTTGGT AAAAAACCAG CCCAAGTGGA TATTGAAGCG	180
ATTAGTGAAA CACTGTTGT CAAAGCAAAT CAACAGGTAG TAAAAGGCGT TCCGAAAAAA	240
ATCAATGATT TGAACGAGCC TGTGAAGACG GTTAGTGAAG AAACCGTTGA CCTTGGTCAT	300
GTGGTTAATG CTATTAAAAA AATAGAGGAA GAAGGTCAAG GTATTTCTGA TGAAGTCAAG	360
GCTGAAATCT TAAAACATGA AAGACATGCC AGCACTATCT TAGAAGAAAC TGGTCACATT	420
GAGATTTTAA ATGAACTTCA AATCGAGGAA GCGATGAGGG AAGAAGCAGG CGCTGATGAC	480
CTTGAAACTG AGCAAGATCA AACTGAAAAT CAAGACTTGA AAGAGATGGG CTTGAAGGTC	540
GAGCAAAGTT ATGATATTGC CCAGGTGGCT ACGGATGTGA CTGCCTATGT TCAAGCGATT	600

GTGGATGACA	TGGATGTTGA	AGCTACACTT	TCAAATGATT	ATAACCGTCG	TAGCATCAAT	660
CTACAAATTG	ACACCAACGA	ACCAGGTCGT	ATTATCGGCT	ACCATGGTAA	AGTCTTGAAG	720
GCCTTGCAAC	TGTTGGCTCA	AAATTATCTT	TACAACCGCT	ATTCCAAAAC	CTTCTACGTT	780
ACAAATCAATG	TCAATGATTA	TGTCGAACAC	CGTGCAGAAG	TCTTGACAGAC	CTATGCGCAA	840
AAATTGGCGA	ATCGTGTTTT	GGAAGAAGGT	CGCAGTCATA	AAACAGATCC	AATGTCAAAT	900
AGCGAACGCA	AGATTATCCA	TCGTATTATT	TCACGTATGG	ATGGCGTGAC	TAGTTACTCT	960
GAAGGTGATG	AGCCAAATCG	CTATGTTGTT	GTAAGATACAG	AATAA		1005

(2) INFORMATION FOR SEQ ID NO:1172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...870
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

ACAAGGAGGA	ATCTGATGCT	TGGAGCAATT	ATTGGAGATA	TTGTCGGTTC	TGTTTACGAA	60
TGGAACAATA	TCAAAACAAA	GGACTTTCCCT	TTATTTTCGGA	AGGACTGCTT	TTTTACAGAT	120
GACACGGTTA	TGACCTGTGC	TGTTGCAGAA	GCAATTATGA	ATGGTGGACA	AAAAAGACGAT	180
TTCATTGACG	CGATGAAGAA	ATATGGCAGA	ATGTATCCGA	ATGCTGATTA	CGGTGCTCGG	240
TTTAATGCAT	GGCTAAACAG	CGATAACCGT	GAGCCTTATA	ATAGCTTTGG	GAATGGATCA	300
GCTATGCGTA	TTTCTCCATG	TGCTTGATC	ATGGACTGTG	GTTTTTATGC	GAAAACTGGT	360
ATGTGGCCAT	CATCTAGAGG	ACTTACGAGT	CTTTCTGCAG	AGGTAACTCA	TAATCATCCA	420
GAAGGTGTCA	AAGGCGCTAT	GGCTACAGCT	GATGCTATCT	TTCTATGTCG	TTTTTACTTT	480
GGTGGTTATT	GTAGAGAGTA	CGAGCAATCA	ATTAACGACA	ATCCTACAGA	GTGTAAAAGA	540
CGAATTAAGG	ATTATATAGA	AAAAGAATAC	GATTACAATC	TATCTCAAAC	TTTAGATGAA	600
ATCCGTCCTA	ACTATCGTTT	TAACGAAACA	TGTCAGGAAA	CTGTCCCTCA	AGCCATTATC	660
GCCTTTCTTG	AAAGTAGAGA	CTTCGAAGAT	GCGATAAGAA	ATGCCATCTC	ACTTGGTGGC	720
GACAGTGATA	CTCTCGCAGC	AATCACTTGT	AGCATAGCAG	AGGCAGCTTA	CGGTATTCCCT	780
GATTGGATCA	AGGATAAGGC	CTATTCTTAC	TTGGATGAAC	CCTTAAAGGA	TGTAGTTAGG	840
CGATGGGAAA	ATAGAATAAA	AGCGTATTAA				870

(2) INFORMATION FOR SEQ ID NO:1173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

GAAAGGAGGA	AAACTAAGAT	GCAGAATCTG	AAATTTGCCT	TTTCATCTAT	CATGGCTCAC	60
AAGATGCGTT	CTTTGCTTAC	TATGATTGGG	ATTATTATCG	GTGTTTCATC	AGTTGTTGTG	120
ATTATGGCTT	TGGGTGATTC	CCTATCTCGT	CAAGTCAATA	AAGATATGAC	TAAATCTCAG	180
AAAAATATTA	GCGTCTTTTT	CTCTCCTAAA	AAAAGTAAAG	ATGGGTCTTT	TACTCAGAAA	240
CAATCAGCTT	TTACGGTTTC	TGGAAAGGAA	GAGGAAGTTC	CTGTTGAACC	GCCAAAACCG	300
CAAGAATCCT	GGGTCCAAGA	GGCAGCTAAA	CTGAAGGGAG	TGGATAGTTA	CTATGTAACC	360
AATTCAACGA	ATGCCATCTT	GACCTATCAA	GATAAAAAGG	TTGAGAATGC	TAATTTGACA	420
GGTGGAAACA	GAAC TTACAT	GGACGCTGTT	AAGAATGAAA	TTATTGCAGG	TCGTAGTCTG	480
AGAGAGCAAG	ATTTCAAAGA	GTTTGCAAGT	GTCAATTTTG	TAGATGAGGA	ATTGTCCATT	540
AGTTTATTTG	AATCTCCTCA	AGAGGCTATT	AACAAGGTTG	TAGAAGTCAA	TGGATTTAGT	600
TACCGGGTCA	TTGGGGTTTA	TACTAGTCCG	GAGGCTAAAA	GGTCAAAAAT	ATATGGGTTT	660
GGTGGCTTGC	CTATTACTAC	CAATATCTCC	CTTGCTGCGA	ATTTTAATGT	AGATGAAATA	720
GCTAATATTG	TCTTTTCGAGT	GAATGATACC	AGTTTAACCC	CAACTCTGGG	TCCAGAACTG	780
GCACGAAAAA	TGACAGAGCT	TGCAGGCTTA	CAACAGGGAG	AATACCAGGT	GGCAGATGAG	840
TCCGTTGTAT	TTGCAGAAAT	TCAACAATCG	TTTAGTTTTA	TGACGACGAT	TATTAGTTCC	900
ATCGCAGGGA	TTTCTCTCTT	TGTTGGAGGA	ACTGGTGTCA	TGAACATCAT	GCTGGTTTTG	960
GTGACAGAGC	GCACTAGTGA	GATTGGTCTT	CGTAAGGCTT	TGGGTGCACA	ACGTGCCAAT	1020
ATTTTAAATC	AGTTTTTTGAT	TGAATCCATG	ATTTTGACCT	TGTTAGGTGG	CTTAATTGGC	1080
TTGACAAATG	CAAGTGGTTT	AAC TGCCTTA	GCAGGTTTGT	TACTGCAAGG	TTTAATAGAA	1140
GGTATAGAAG	TTGGAGTATC	AATCCCAGTT	GCCCTATTTA	GTCTTGCAAGT	TTCCGGCTAGT	1200
GTTGGTATGA	TTTTTGGAGT	CTTGCCAGCC	AACAAGGCAT	CGAAACTTGA	TCCAATTGAA	1260
GCCCTTCGTT	ATGAATGA					1278

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

TTCCTTGGGA	ACGGTAACCA	ATGTCTTTGT	TCCAGGTTTCG	GTTGTCAAGG	CGGCGACCAT	60
CAGCTCAGGT	TGGGAAAATG	GAGTCTTGTC	AGGAAACCAG	ACCTTGACAG	ACCAGTCCAT	120
TGCTTTCCAA	GGTTCAGCTC	CCATCAATTC	TTGGTATACT	CAGGCTTACG	GTTTCATTCCC	180
TATCACAGCG	GTCCAAGCTC	TGGAGTATTC	ATCAAATACC	TATATGGTCC	AAACAGCCTT	240
AGGTCTTATG	GGGCAAACCT	ATCAACCCAA	TATGTTTGTC	GGCACCAGCA	ATCTAGAGTC	300
TGCTATGGAG	AAACTGCGTT	CAACCTTTGG	CGAATATGGC	TTGGGTACTG	CGACAGGAAT	360
TGA						363

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

TTATCAGGGA	ATACTACAGC	TCTCAGTCAA	TCTTTGTCGG	TGACACCGAA	TAATGGTGTT	60
TCTGCAGCAG	ATGATGGTTA	TGTCTTTAAC	CCTAATGATA	TTGTCAGAGA	TACAGGTGAT	120
GCTTATATAG	TAAGACACGG	GGATCACTAT	CATTATATTC	CTAAGTCATC	TCTTAACAAT	180
CCCCCATCAC	ACTCTAACAC	GGAAGAGGCA	GGAAGTTCTT	CTAGTTCTGT	ATTAAGTAAT	240
CCGTCACTAC	ATGTCCACCA	TGAGGAAGAA	GATGGTCATG	GTTTGTGATG	CAATCGAATT	300
ATAAGTGAAG	ATTGAGAAGG	TTTGTGATT	CCTCATGGCG	ACCACAATCA	CTACATCAAG	360
GTTCAAACCT	AGGGATATGA	AGCGGCTTTG	AAAAACAAGA	TTCCATCCCT	GCAATCCAAC	420
TATCAACCTG	GAACCTTTGA	TGAGAAGGCA	GTCTTGGCAA	AAGTAGATCA	ACTTCTAGCT	480
GATAGCAGAA	GCATCTACAA	AGACAGATTG	AGTTAG			516

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

```
AGAAAGGGGA AATCAGTCAC AATGGCAAAC GTAACATTAT TTGACCAAAC TGGTAAAGAA      60
GCTGGCCAAG TTGTTCTTAG CGATGCAGTA TTTGGTATCG AACCAAATGA ATCAGTTGTG      120
TTTGATGTAA TCATCAGCCA ACGCGCAAGC CTTCGTCAAG GAACACACGC TGTTAAAAAC      180
CGCTCTGCAG TATCAGGTGG TGGACGCAAA CCATGGCGTC AAAAAGGAAC TGGACGTGCT      240
CGTCAAGGTT CTATCCGCTC ACCACAATGG CGTGGTGGTG GTGTTGTCTT CGGACCAACT      300
CCACGTTCAT ACGGCTACAA ACTTCCACAA AAAGTTCGTC GCCTAGCTCT TAAATCAGTT      360
TACTCTGAAA AAGTTGCTGA AAACAAATTC GTAGCTGTAG ACGCTCTTTC ATTTACAGCT      420
CCAAAACTG CTGAATTTGC AAAAGTTCTT GCAGCATTGA GCATCGATTC TAAAGTTCTT      480
GTTATCCTTG AAGAAAGAAA TGAATTCGCA GCTCTTTCAG CTCGTAACCT TCCAAACGTG      540
AAAATGCAA CTGCTACAAC TGCAAGTTTT CCTGACATCG CAAATAGCGA CAAACTTCTT      600
GTCACACAAG CAGCTATCTC TAAATCGAA GAAGTACTTG CATAA                        645
```

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

```
ATGAAGGGGA AAGAGTATGA AAACAGAACT GTTTCCTTTG CTATTAGTTC AAAAGGAGAA      60
AAAATGAAAAG TAGAAAATAT TTCGTATAGG GTGGATCATC GTATATTGTT TGATAATATT      120
TCTTTTGATA CTTCGAGTTC AGGCGTGACA TTAATTACTG GTAAAAATGG TACAGGAAAG      180
TCAACTTTAC TATAG                        195
```

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

ATTACCAACC TACTCATCTT CTCACCAGAG GCGGGTATTA ACTTTGATCA TAAAATCGGA	60
TACTCCCTCT ATCCAGAAAA TATGCTCAGA ATGATTGTCT CTAAACAATA CCTGCTCTTT	120
TACCTCATTC ATGAAAAAGA AGTCCATACC CTGAGAATTA TCAACTCACG CACCGACTAC	180
CTAAACCAAC TCGACCACCT CTTTCGTACA TGTAGGAAAC TATTTTCCTC ACAAATAATC	240
TCATTATAA	249

(2) INFORMATION FOR SEQ ID NO:1179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...288
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

GAGCCAAACC TAAAAACTAG CTTAATACTC TTCGAAAATC TCTTCAAACC ACGTCAGCGT	60
CGCCTTACCG TATATATGTT ACTGACTTCG TCAGTTCTAT CTGCCACCTC AAAACGGTGT	120
TTTGAGCTGA CTTCGTCAGT TTCATCTACA ACCTCAAAAC CATGTTTTGA GCTGACTTCG	180
TCAGTTTCAT CCACAACCTC AAAACAGTGT TTTGAGCAAC CTGCGGTTAG CTTCTAGTT	240
TGCTCTTTGA TTTTCATTGA GTATAAGTTT TCCTTAGAGA AAGCTTAA	288

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

CTCCAAAACC TTATCAACGA TTTGCTCCAC AGAAGAAGCA TTGATAGCTC CATGTCCGTT	60
GATACAGTAA GGCGTCCCCA CACGTGCGTA GAGGAGACGC AGATAGTCAT TGATTTCAGT	120
CGTCGTTCCC ACCGTCGAGC GAGGATTTTT ACTAGTCGTT TTCTGGTCGA TGGAAATAGC	180
TGGGCTGAGA CCATCAATGG CATCTACATC TGGTTTTTCC ATATTTCCCA AGAACTGACG	240
AGCGTAGGCG GACAAACTCT CTACATAGCG ACGTTGTCCC TCCGCATAGA GAGTATCAAA	300
AGCCAGACTG GACTTCCCTG A	321

(2) INFORMATION FOR SEQ ID NO:1181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

TTCGTTTTTG AACTAGTTGC TTTCGTTGAC GAAGATGTCT CCGATGAACT GCTTGTACTT	60
GAATTTGATG TGCTTGAAC TGGTGCTACT GGTTTTGTAG TCACCTTCAT TATTGTATCA	120
AACGGAGTGA TAACTGCCGG TAAGACAACA CCATTGCGGT CGATTGCCTG CAAAGGTACT	180
GAACCACTGT AA	192

(2) INFORMATION FOR SEQ ID NO:1182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

ATTGGTTTTG	AGGAGTTAGA	AATGAAAGTA	TTAGTGACAG	GTTTTGAGCC	CTTTGGAGGG	60
GAAAAGGGCA	ATCCAGCTTT	GGAGGCCATT	AAAGGTTTAC	CAGCTGAAAT	CCATGGTGCT	120
GAGGTCCGTT	GGCTAGAGGT	GCCGACAGTT	TTTCACAAAT	CTGCTCAAGT	ATTGGAAGAA	180
GAGATGAATC	GTTATCAACC	TGACTTTGTC	CTTTGTATTG	GGCAAGCTGG	TGGAAGAACT	240
AGTTTGACAC	CTGAACGAGT	GACCATTAAT	CAAGACGATG	CATGCATTTC	TGATAACGAA	300
GATAATCAAC	CGATTGACCG	TCCCATTTCGC	CCAGATGGTG	CTTCGGCCTA	CTTTAGTAGT	360
TTGCCGATTA	AAGCGATGGT	TCAAGCTATA	AAAAAAGAGG	GCTTACCGGC	CTCTGTTTCC	420
AATACGGCAG	GGACTTTTGT	CTGCAGCCAT	TTGATGTATC	AGGCTCTCTA	TTTGGTAGAA	480
AAGAAATCTC	CATATGTTAA	GGCAGGTTTT	ATGCATATTC	CTTATATGAT	GGAACAGGTG	540
GTGAACAGAC	CGACTACTCC	AGCTATGAGT	TTAGTGGATA	TTCCGGCGAGG	GATAGAAAGCA	600
GCAATCGGCG	CTATAATAGA	ACATGGAGAT	CAGGAACTCA	AGTTGGTAGG	CGGAGAAACT	660
CATTGA						666

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

AATTCATTTG	AAAAGTATGT	CCAAGAGCAT	AAAATACTTC	TTAGTATTTT	TGATTTGGAT	60
GAGACAGTTA	CTGACTATTA	TGGAAAGCTA	GAGAGTTTCT	TGGAAGAAAA	TTCTTCTATA	120
GATGGAATTT	TTACAATCAA	CGATTTTACA	GCTTTGGATG	TGATTGAAAT	ACTAGAAAAA	180

AATGGTAAAC GTATTCCTCA TGATGTCCAA ATTATTGGAT ACGATGGAAT TAAAATGGCT	240
GGAGATAGAG ATTATCTACT TTCAACTATT GAACAACCAT TGGAAGAAAT GGCAAAAGAA	300
GCGGTTTCGTA TTTTGTGTTGA TATAATTGAT GGAAAGACTG TTAATTTGCA GACAATCCTA	360
CCAGTAAAT TTGTTGAAGG AAAAAACAACA AAAAATGAAA ATAAGTCTTG A	411

(2) INFORMATION FOR SEQ ID NO:1184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

ATAAAATTTG ATAAACGGAC TTTATCTTAT TACAGAGGAG AAGAAATGGA TCCGAAAAAA	60
ATTGCTCGTA TCAATGAGCT TGCTAAAAAG AAAAAACAG AAGGCTTAAC ACCAGAAGAA	120
AAAGTGAAC AAGCCAACT ACGTGAGGAG TACATCGAAG GTTATCGCCG CGCTGTTTCGT	180
CACCACATTG AAGGAATCAA AATTGTGGAC GAAGAAAGAA ACGATGTTAC ACCAGAAAAA	240
CTACGCCAAG TACAACGTGA AAAAGGATTA CATGGCCGTA GTCTTGATGA TCCAAATTCA	300
TAA	303

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1536
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

AGAAAATTTG	AAATAGAAAAG	TGGTGTCTTT	TTGGCAATTA	ACGCACAAGA	AATCAGCGCT	60
TTAATTAAGC	AACAAATTGA	AAATTTCAAA	CCCAATTTTG	ATGTGACTGA	AACAGGTGTT	120
GTAACCTATA	TCGGGGATGG	TATCGCGCGT	GCTCACGGCC	TTGAAAAATGC	CATGAGTGGA	180
GAGTTGTTGA	ATTTTGAAAA	CGGCTCTTAT	GGTATGGCTC	AAAACCTTGA	GTCAACAGAC	240
GTTGGTATTA	TCATCCTAGG	TGACTTTTACA	GATATCCGTG	AAGGCGATAC	AATCCGCCGT	300
ACAGGGAAAA	TCATGGAAAGT	CCCTGTAGGT	GAAAGTCTGA	TTGGTCGTGT	TGTGGATCCG	360
CTTGGTCGTC	CAGTTGACGG	TCTTGAGAGAA	ATCCACACTG	ATAAACTCG	TCCAGTTGAG	420
GCACCAGCTC	CTGGTGTTAT	GCAACGTAAG	TCTGTTTCAG	AACCATTGCA	AACTGGTTTG	480
AAAGCTATTG	ACGCCCTTGT	ACCGATTGGT	CGTGGTCAAC	GTGAGTTGAT	TATCGGTGAC	540
CGTCAGACAG	GGAAAAACAAC	CATTGCGATT	GATACAATCT	TGAACCAAAA	AGATCAAGAT	600
ATGATCTGTA	TCTACGTCGC	GATTGGACAA	AAAGAATCAA	CAGTTCGTAC	GCAAGTAGAA	660
ACACTTCGTC	AGTACGGTGC	CTTGGACTAC	ACAATCGTTG	TGACAGCCTC	TGCTTCACAA	720
CCATCTCCAT	TGCTCTTCCT	AGCTCCTTAT	GCTGGGGTTG	CTATGGCGGA	AGAAATTTATG	780
TATCAAGGTA	AGCATGTTTT	GATTGTATAT	GATGATCTAT	CAAAACAAGC	GGTAGCTTTAT	840
CGTGAACGTG	CGCTCTTGCT	TCGTGCTCCT	CCAGGTCGTG	AAGCCTTCCC	AGGGGATGTT	900
TTCTATCTCC	ACAGCCGTTT	GCTTGAGCGC	TCAGCTAAAG	TTTCTGATGA	ACTTGGTGGT	960
GGATCAATTA	CAGCCCTACC	ATTTATCGAG	ACACAAGCAG	GAGATATCTC	AGCCTATATC	1020
GCAACCAACG	TGATTTCTAT	CACTGATGGA	CAAACTTCC	TTGGCGATGG	CCTCTTCAAT	1080
GCAGGTATTC	GTCCAGCCAT	CGATGCGGGT	TCATCTGTAT	CTCGTGTAGG	TGGTTCTGCA	1140
CAAATCAAAG	CCATGAAGAA	GGTTGCTGGT	ACACTTCGTA	TCGACCTTGC	TTCATACCGT	1200
GAGTTGGAAG	CCTTTACTAA	GTTTGGTTCT	GACTTGACG	CAGCAACACA	GGCTAAGTTG	1260
AACCGTGGAC	GTCCGTACCGT	TGAGGTCTTG	AAACAACCTG	TTCACAAACC	ATTACCTGTT	1320
GAGAAACAAG	TAACCATTTCT	TTATGCTTTG	ACACATGGTT	TCTTGGATAC	TGTTCCAGTA	1380
GATGATATTG	TTCGTTTCGA	GGAAGAGTTC	CATGCCTTCT	TTGATGCTCA	ACATCCAGAG	1440
ATTTTGGAAA	CCATTTCGTGA	TACAAAAGAC	TTGCCAGAAG	AAGCAGTCTT	GGATGCTGCG	1500
ATTACAGAGT	TTCTCAATCA	ATCTAGCTTC	CAATAA			1536

(2) INFORMATION FOR SEQ ID NO:1186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

GTAAGATTTG	AAGATATTCT	AAGTTCTTTT	ATTCTTTTTC	CAACATCACA	TACATTTATC	60
ACATACATTT	ATCATATTCA	TACACCTCTC	ATAAAAAAGAA	TAGCACACTC	TTGTCATAAT	120
TTTTTAAATA	AAAAAATTAT	GACAAAACAA	GGAAGCAATT	TATTGATGCT	GCTTAAAAAT	180
CTAAAATTGA	TGAGTTCCTA	TCAAAAATCG	TATCTTCAAC	CTCAAAACAG	TACTTAA	237

(2) INFORMATION FOR SEQ ID NO:1187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 897 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...897
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

ATGAGGTTTG	AATTTATCGC	AGATGAACAT	GTCAAGGTTA	AGACCTTCTT	AAAAAAGCAC	60
GAGGTTTCTA	AGGGATTGCT	GGCCAAGATT	AAGTTTCGAG	GTGGAGCTAT	TCTGGTCAAT	120
AATCAACCGC	AAAATGCAAC	GTATCTATTG	GACGTTGGAG	ACTACGTTAC	CATTGACATT	180
CCCGCTGAGA	AAGGCTTTGA	AACCTTGGAG	GCTATTGAGC	TTCCATTAGA	TATTCTCTAT	240
GAGGATGACC	ACTTTCTAGT	CTTGAATAAA	CCCTATGGAG	TGGCTTCTAT	TCCTAGTGTC	300
AATCACTCTA	ATACCATTCG	CAATTTTATC	AAGGGTTACT	ATGTCAAGCA	AAATTATGAA	360
AATCAGCAGG	TTACATTGT	TACCAGACTA	GATAGGGACA	CTTCTGGCTT	GATGCTCTTT	420
GCCAAGCACG	GTTATGCCCA	TGCACGATTA	GACAAGCAGT	TGCAGAAGAA	ATCTATCGAG	480
AAACGCTACT	TTGCTTTGGT	TAAGGGAGAT	GGACATTTGG	AGCCAGAAGG	GGAAATTATT	540
GCTCCGATTG	CGCGTGATGA	AGATTCCATT	ATTACCAGAC	GAGTGGCTAA	AGGCGGAAAG	600
TATGCCCATA	CTTCATACAA	GATTGTAGCT	TCTTATGGAA	ATATTCACTT	GGTCTATATT	660
CACCTGCACA	CTGGTCGAAC	CCATCAAATC	CGAGTCCATT	TTTCTCATAT	CGGTTTTCTT	720
TTGCTGGGAG	ATGATTTGTA	TGGTGGTAGT	CTGGAAGATG	GTATTCAACG	TCAGGCTCTG	780
CATTGCCATT	ACCTATCCTT	TTATCATCCA	TTTTTAGAGC	AAGACTTGCA	GTTAGAAAGT	840
CCCTTGCCGG	ATGATTTTCA	TAACCTTATT	ACCCAGTTAT	CAACTAATAC	TCTATAA	897

(2) INFORMATION FOR SEQ ID NO:1188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

CTTTTCTTG	ATAAAGGAAG	AAATAGTGGA	GAGGAAGTTA	GAATGAAAAA	ATTCGACAAT	60
TATATTATTG	AGAAGCCTTG	CGATTCTAAT	TCAGATAAAC	TGCAAAAAAT	CTTAATAATT	120
GAAAATTTGG	TAGATGATAT	TTTGCAATTT	TCTCTCAGAA	TCAATAATAG	TGTAGGAGAG	180
ATTTTCCTCC	TACAACCGTT	TCAAAAGAAA	ACTATCTTTA	TTCCATGTTA	TTTTGAGGAA	240
GATATTGTGA	AAGTCAAAGA	TGATGATAAA	GTTGAGTGGA	ATTTGTTAGA	ATTTCAAAAA	300
TTTAGAGCAT	TTTTGGCTTA	G				321

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

AGAAGACTTG	ACAGACAAAG	GCTTCACCAA	CGAATTTGTG	AAATAATGAC	AGAAATTAGA	60
CTAGAGCACG	TCAGTTATGC	CTATGGTCAG	GAGAGGATTT	TAGAGGATAT	CAACCTACAG	120
GTGACTTCAG	GCGAAGTGGT	TTCCATCCTA	GGCCCAAGTG	GTGTTGGAAA	GACCACCCTC	180
TTTAATCTAA	TCGCTGGGAT	TTTAGAAGTT	CAGTCAGGGA	GAATTGTCCT	TGATGGTGAA	240
GAAAATCCCA	AGGGGCGCGT	GAGTTATATT	TTGCAAAAGG	ATCTGCTCTT	GGAGCACAAG	300
ACGGTGCTTG	GAAATATCAT	TCTGCCCTC	TTGATTCAAA	AGGTGGATAA	GGCAGAAGCT	360
ATTTCCCGAG	CGGATAAAAT	TCTTGCGACC	TTCCAGCTGA	CAGCTGTAAG	AGACAAGTAT	420
CCTCATGAAC	TTAGCGGTGG	GATGCGCCAG	CGTGTAGCCT	TACTCCGGAC	CTACCTTTTT	480
GGGCACAAGC	TCTTTCTCTT	AGATGAGGCC	TTTAGCGCCT	TGGATGAGAT	GACAAAGATG	540
GAACTCCACG	CTTGGTATCT	TGAGATTCAC	AAGCAGTTGC	AGCTAACAAC	CCTGATCATC	600
ACGCATAGTA	TTGAGGAGGC	CCTCAATCTC	AGCGACCGCA	TCTATATCTT	GAAAAATCGC	660
CCTGGGCAGA	TTGTTTCAGA	AATTAAACTA	GATTGGTCTG	AAGATGAGGA	CAAGGAAGTC	720
CAAAAGATTG	CCTACAAACG	TCAAATTTTG	GCGGAATTAG	GCTTAGATAA	G TAG	774

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

AGCATGCTTG	ATTGGAAACA	ATTTTTTCTA	GCCTATCTGC	GCTCCCGTAG	TCGTCTTTTT	60
ATCTATCTGC	TTTCTTTGGC	ATTTCTTGTC	TTACTCTTTC	AGTTTTTATT	TGCCAGTCTA	120
GGAATTTACT	TCCTCTACTT	TTTCTTCTTG	TGTTGCTTTG	TAACCATATT	ATTTTTCACT	180
TGGGACATAT	TGGTGGAAAC	GCAGGTCTAT	CGCCAGGAAC	TTCTCTATGG	AGAGAGGGAA	240
GCCAAGTCTC	CTTTGGAAAT	AGCTTTAGCA	GAAAAATTAG	AAGCGCGTGA	GATGGAACCTC	300
TATCAGCAGA	GGTCAAAAGC	AGAAAGAAAA	CTGACGGATT	TGCTGGATTA	CTATACCTTG	360
TGGGTCCATC	AGATAAAGAC	CCCCATTGCA	GCCAGTCAAC	TCCTAGTTGC	AGAAGTGGTC	420
GACCGCCAAC	TGAAGCAGCA	GCTAGAACAG	GAAATTTTCA	AAATCGACTC	CTATACCAAC	480
CTAGTTTTAC	AGTACCTGCG	TTTAGAAAAGT	TTCCATGATG	ATTTGCTCTT	AAAGCAGGTT	540
CAAATTGAGG	ACTTGGTCAA	GGAAATAATT	CGTAAATATG	CTCTTTTCTT	TATTCAAAAA	600
GGCTTAAATG	TCAATCTACA	TGACCTTGAT	AAAGAAATCG	TGACGGATAA	AAAGTGGCTG	660
CTAGTGGTTA	TTGAGCAAAT	CATCTCAAAC	AGTCTCAAGT	ACACCAAGGA	AGGTGGTCTG	720
GAGATTTATA	TGGATGACCA	AGAGCTTTGT	ATCAAAGATA	CGGGAATCGG	GATAAAAAAC	780
AGTGATGTCC	TCCGAGTATT	TGAACGTGGC	TTTTCAGGAT	ACAATGGCCG	TTTGACCCAG	840
CAGTCCTCTG	GACTTGGCCT	TTATCTATCT	AAGAAAATTT	CTGAAGAACT	GGGGCACCAG	900
ATTCGTATCG	AGTCTGAGGT	CGGAAAAGGA	ACGACAGTGC	GGATTCAAGT	TGCTCAAGTG	960
AACTTAGTCC	TTGAGTAA					978

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1068 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

GTGCTAATTG	ATCAGACAGA	GAGGAGTGAT	GAGATGGTTA	CAGAGCGTCA	GCAGGATATT	60
TTAAATCTGA	TTATTGACAT	CTTTACCAA	ACGCACGAAC	CTGTCGGATC	AAAAGCCTTG	120

CAAGAGTCTA	TTAACTCTAG	CAGTGCAACC	ATTCGTAATG	ACATGGCGGA	ACTAGAAAAA	180
CAAGGGTTGC	TTGAGAAGGC	TCATACTTCA	AGCGGTCGGA	TGCCAAGTGT	TGCTGGTTTT	240
CAGTACTATG	TGAAACACTC	ACTGGATTTT	GACCGGCTGG	CTGAAAATGA	GGTATATGAG	300
ATTGTCAAAG	CCTTTGATCA	GGAATTCTTC	AAATTGGAGG	ATATTCTGCA	AGAGGCTGCT	360
AACTTGCTAA	CAGACCTGAG	TGGCTGTACG	GTAAGTGGAC	TGGATGTTGA	GCCGAGCAGG	420
CAACGTTTGA	CAGCCTTTGA	TATCGTTGTT	TTGGGGCAAC	ATACAGCCTT	GGCGGTATTT	480
ACCTTAGACG	AGTCGCGAAC	GGTTACTAGT	CAGTTTCTGA	TTCCAAGGAA	CTTCTTGCAG	540
GAGGATTTGC	TGAAACTGAA	GAGCATCATT	CAGGAACGTT	TCCTCGGTCA	CACCGTTTTA	600
GATATTCACT	ACAAGATTCG	GACGGAGATT	CCGCAGATTA	TCCAGCGTTA	CTTTACAACA	660
ACGGATAATG	TCATCGATCT	CTTTGAACAC	ATCTTTAAGG	AAATGTTCAA	CGAAAACATT	720
GTGATGGCGG	GCAAGGTCAA	TCTCTTGAAT	TTTGCCAATC	TAGCAGCCTA	TCAGTTCTTT	780
GACCAACCGC	AAAAGGTGGC	CTTGGAGATT	CGTGAGGGGT	TGCGTGAGGA	TCAGATGCAA	840
AATGTTCTGT	TTGCAGACGG	TCAAGAGTCC	TGTTTAGCTG	ACCTAGCGGT	GATTAGTAGT	900
AAGTTCCTCA	TTCTTATCG	GGGAGTTGGA	ATTCTAGCCA	TTACCGGTCC	AGTTAATCTG	960
GATTACCAAC	AGCTAATCAA	TCAAGTCAAT	GTGGTCAACC	GTGTTTTGAC	CATGAAGTTG	1020
ACAGATTTTT	ACCGCTACCT	CAGCAGTAAT	CATTATGAAG	TACATTAA		1068

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

TTCTCAATTG	AGCAGTTTTT	TTTAAAAGGA	AAAATTGCTC	TCATCACCGG	CGCTTCTTAT	60
GGAATTGGAT	TTGCTATTGC	CAAATCCTAC	GCTGAAGCCG	GCGCTACTAT	TGTCTTTAAC	120
GATATCAATC	AAGATCTGGT	CAATAAAGGG	ATTGAAGCTT	ATCGTGAAGT	TGGCATCGAA	180
GCCCATGGAT	ATGTCTGTGA	CGTGACAGAC	GAGGACGGTA	TCCAAGCCAT	GGTCAAGCAA	240
ATCGAACAA	AGGTTGGTGT	CATTGACATC	CTCGTTAATA	ACGCTGGTAT	TATCCGCCGA	300
GTTCCAATGT	GCGAAATGAG	CGCCGCTGAT	TTCCGTAAGG	TCATCGATAT	TGACTTAAAC	360
GCACCATTTA	TCGTTTCAAA	GGCAGTTATT	CCTTCTATGA	TAAAGAAAGG	GCATGGAAAG	420
ATTATCAATA	TTTGTTTCGAT	GATGAGCGAA	CTGGGACGTG	AAACAGTTAG	CGCTTATGCT	480
GCTGCTAAAG	GGGGCTTGAA	AATGTTGACC	CGCAACATTG	CGTCTGAATA	CGGTGGAGCC	540
AATATCCAAT	GTAACGGAAT	TGGACCGGGT	TATATTGCCA	CTCCTCAAAC	AGCACCTCTT	600
CGTGAGTTGC	AAGAAGATGG	TTCTCGCCAC	CCATTTGACC	AGTTCATCAT	TGCAAAAAACA	660
CCTGCTGCAC	GTTGGGGAAA	TCCTGAAGAT	TTGATGGGCC	CTGCTGTCTT	TCTCGCTAGT	720
GATGCCAGCA	ATTTTGTCAA	TGGCCACATC	CTATATGTAG	ATGGCGGTAT	CTTAGCCTAC	780
ATCGGAAAAC	AACCTGAGTA	A				801

(2) INFORMATION FOR SEQ ID NO:1193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...608
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

AAGAAATTGA	AAAAAATGTT	CTTCCGGGGG	AAAAAATTGTA	TGAAATTGGT	TCCAAATATA	60
ACCAAATTTT	CCCCCGGCCA	GTGTTTTTTT	TTGTTTTTCAA	AAAAGAATTC	GGTGGGAACG	120
AAAATTTTAG	GAAAACAGGG	TTATCAAAAG	TTAAGGGGAA	ATTATTCCAA	CAGGATGTTG	180
TTAAAGGGGG	GAATAAACGT	TTTTATCGCC	CTACTTTTCG	CATGCACTTA	ACAAATAAAG	240
AAATTCCTGA	CAAGATTTTA	AGCTATTTCAG	AAGACTTGAA	ACACCACTAT	CAGATCTATC	300
AACTCTTACT	TTTTCACTTT	CAGAACAAAG	ACCCTGAGAA	ATTTTTTCGGA	CTCATTTGAGG	360
ACACTCTGAA	GCAGGTTTCAT	CCTATTTTTTC	AGACTGTCTT	TAAAACCTTT	CTAAAGAACA	420
AAGAAAAAAT	CGTCAACGCT	CTTCAATTAC	CTTATTCCAA	CGCAAAATTG	GAAGCGACCA	480
ATAATCTCAT	CAAACTTATC	AAACGAAACG	CCTTTGGATT	TCGGAACTTT	GAAAACCTTCA	540
AAAAAAGGAT	TTTTATCGCT	CTGAACATCA	AAAAAGAAAG	GACGAATTTT	GTCCTTTCTC	600
GAGCTTAG						608

(2) INFORMATION FOR SEQ ID NO:1194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

AAGAGGATTG ATATGTCTAT AGAGTTGCTG AAGAAATTAA CAGGCGAAGA AGATACTCAG	60
CTTCTCATGT TGCTCCAAAC GAGGGCTACA AATCTTATCT TGTCAGAGAC TAATCGCACA	120
TCTTTGACAC CTGCTTTAAG TCTTTTAATA CCTGAGGTTG CTATCGAACT CCACAACCGC	180
TCAGGAGCGG AAGGAGAGCA TTCTAGAACC GAGGGTGGTA TAGCAGTAGT CTACGGAGAA	240
AACGGCCTGT CTACGGATCT TCTACAGCGA ATACGCATGC ACAGGCTAGC AAGGGTGGCA	300

GGTCATGTTT TTGAAGCAGA GTAG	324
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(2) INFORMATION FOR SEQ ID NO:1195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

ACAACTGACC TTTTGATCAA CGAATCAATC GTGACAACTG AAGCTCGTGC TAAAGAAATC	60
CGTAAAACTG TTGAAAAAAT GATTACTCTA GGTAAACGTG GTGATTTGCA TGCACGTCGT	120
CAAGCAGCTG CTTTCGTACG TAATGAAATC GCATCTGAAA ACTATGATGA AGCAACTGAT	180
AAGTACACTT CTAATACAGC ACTTCAAAAA TTGTTCCTCAG AAATCGCACC TCGTTATGCT	240
GAACGTAACG GTGGATACAC TCGTATCCTT AAAACTGAAC CACGTCGTGG TGATGCAGCG	300
CCAATGGCGA TCATCGAATT AGTATAA	327

(2) INFORMATION FOR SEQ ID NO:1196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GTGGTGTCTG	ATTATCTTTG	TTGCCTATAT	GGTAGCAGGA	TTTATTTTCT	ACTTTATCAA	60
GCAAATCAAG	AGAAAGTCAT	CCTAATACTC	TTCGAAAATC	TCTTCAAACC	ACGTCAGTTT	120
CCATCTGCAA	CCTCAAAACA	CTGTTTTGAA	CAACCTGCGG	CTAGCTTCCT	AGTTTGCTCT	180
TTGATTTTCA	TTGAGTATAA	GATACAAGGG	ATTCAATTTT	GAATTTAA		228

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

CTATTCCCTG	ATCTAGTCTT	CCAGTATGAC	CCATGTAAAG	GAGCTTTCCC	TATGGACAAA	60
CCAGATATCG	CAACTATCAT	TGATTACAT	TTTGAAGAAA	TGACAGACCT	AGAGCAAGAA	120
ATCGCTCGCT	ATTTTTTGCA	AGCTGAAACG	ATTACAGATG	ATTTATCTTC	TCAACAAGTC	180
ACCCAAAAAT	TACATATTTT	TCAAGCTGCT	TTGACCCGCT	TTGCTAAAAA	GTGTGGCTTT	240
ACTGGCTACC	GAGAATTTAT	TTTCCAATAC	CAACATCAGG	CAGAAAAATCA	AGCCAACCAA	300
GTCTCCAAGC	ATAGTCCACT	GACCAAACGA	GTCCTCAGAA	GTTATAGCAA	TATGAGGGAA	360
CAAACACAAG	ACTTGATTGA	CGAAATCCAA	CTAGAGCGAA	TTGCCCAGCT	AATCGAAGAT	420
GCTGAGCGTA	TCTACTTCTT	TGGAACAGGG	AGTTCTGGCC	TCGTCGCCCC	TGAAATGAAA	480
TTACGTTTTA	TGCGACTAGG	TGTGGTCTGC	GAAGCTTTGA	CAGACCAAGA	CGGCTTTGCC	540
TGGACAACCA	GCATCATGGA	TGAAAATTGT	CTAGTACTGG	GTTTCTCACT	TTCAGGCTCA	600
ACTCCTTCTA	TTTTAGATAG	TCTATTAGAT	GCCAAGGAGA	TGGGGGCAAA	GACTGTACTC	660
TTTACAAGTG	TTCCCAATAA	AGATAGCCAG	ACCTATACAG	AGACTGTTCT	TGTAGCCACC	720
CACAGCCAAC	CCTCCTACAT	CCAACGAATA	TCCGCTCAAC	TTCTTATGCT	CTTCTTTATC	780
GATTTGATTT	ATGCCTACTT	TTTGGAAATC	AATCGCGAAA	GCAAGGAAAA	AATCTTTAAT	840
AGCTACTGGG	AAAATAAAAA	ACTCAACGGC	TATCGTAGAC	AAAAACGTGT	AAGAAAATCC	900
TAG						903

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

AGGCTTACTG	AGTCTGCTTC	ATGCTGTTCT	TTAGTTTTGA	TGTCGACAAC	GTTTACGTTG	60
ATTTCAACAA	TTTCCAAGTC	AGTCATTTTA	GCAACTTCTG	AAGATACGAT	TTCTCTGATT	120
TCTGAATATA	AAGCTGGAAC	ATTTTTTTTG	TACTCAACAA	TAACGTTTAA	GTCAACTGCA	180
ACTTGTGTTT	TACCAACTTC	TACGTTAACA	CCACTTGTTA	CGTCATCGCT	GTTAACGATT	240
TTTTCTTTAA	GATTTGAGAA	GAAACCACCA	TCGATTCCCA	AAAGACCTGA	AACGTTTTCT	300
AGTGAAAGAC	CAATGATTTT	TTGGATAACT	TTATCTTCGT	AA		342

(2) INFORMATION FOR SEQ ID NO:1199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 930 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

GAAAGGACTG	AAAACATCAT	GACTGAAAAA	CTTCAATTAA	CTAAATCAGA	TCGTAAAAAA	60
GTTTGGTGGC	GTTCAACCTT	CTTACAAGGG	TCTTGGAAC	TTGAACGGAT	GCAAACTTG	120
GGCTGGGCTT	ATACACTCAT	TCCAGCTATC	AAAAAACTCT	ATACTAAAAA	AGAAGATCAA	180
ATCGCTGCTC	TTGAGCGTCA	CCTTGAGTTC	TTCAACACTC	ATCCATACGT	AGCTGCTCCA	240
GTCATGGGGG	TTACTCTTGC	GCTTGAAGAA	GAACGTGCTA	ACGGTGTGGA	AATCGATGAC	300
GCTGCTATCC	AAGGGGTCAA	AATCGGTATG	ATGGGACCTC	TTGCTGGTAT	CGGTGACCCA	360
GTATTCTGGT	TTACAGTACG	CCCAATCCTT	GGATCTCTCG	GTGCTTCACT	TGCCCTTACT	420
GGCAATATCT	TGGGTCCACT	CCTCTTCTTT	GTTGCATGGA	ACTTGATTCT	TATGTCATTC	480
TTGTGGTATG	TTCAAGAGAT	TGGATACAAG	GCTGGATCAG	AAATCACTAA	AGATATGTCT	540
GGTGGTATCC	TTCAAGATAT	CACTAAAGGA	GCTTCTATCC	TTGGGATGTT	CATTCTTGCT	600
GTCCTTGTTT	AACGCTGGGT	AAATATTAAA	TTTGCTTTTC	ATGTTTCTAA	AGTTCAACTA	660
GATGAAAAGG	CTTATATCCA	TTGGGATAAA	TTGCCAGAAG	GGTCTAAAGG	TATCCAAGAA	720

GCATTTCGCAC	AAGTAGGACA	AGGATTGTCT	CAAACCTCCTG	AAAAAGTTAC	TACTTTCCAA	780
CAAAACTTGG	ATATGTTGAT	TCCTGGATTA	TCAGGACTAC	TCCTTACTTT	ACTTTGCATG	840
TACTTACTTA	AGAAAAAAGT	ATCTCCAATC	ACTATTATCC	TTGCCCTCTT	CGCAGTGGGT	900
ATTGTGGCAC	ATGTTCTTCA	CATCATGTAA				930

(2) INFORMATION FOR SEQ ID NO:1200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

TGGAGGACTG	AAATGAAAAA	TATAAATGGG	AAAAAGGTAA	CTATTTATGA	TATTGCACGT	60
TTATCAGGTT	TTTCTCCAAA	AACAGTTTCA	CGAGTTATTA	ATGGTGGAGT	AAATGTTAAA	120
GAAGAACTT	ATCAAGCGAT	TCAAAAAGTT	ATAGAGGAAT	TGTCGTATAT	TCCAAATGCG	180
TATGCAAAAA	ATTTAACTAA	AAAAGAAGCT	ATAAATATAT	TGATTTCTGT	AAAAAAAATC	240
GACTCTTTTC	CTTTAATTTG	GTTTCATACG	CTGTTAGATA	AAGTGTTACG	GACGTGTAAA	300
GAATTTGGTG	TTAATGCTAT	AGTTGAGTAC	TTTGAGAGAG	AGGATACAAT	TAGTAATTCA	360
ATTATATCAA	GCACAGGTAG	CCTAGTAGAT	GGTGTTATTG	TTTTTTATGA	AAGTGTAGAT	420
GATATCAGAA	TTCAGTATTT	AAAGAAGAAC	CATATGCCTT	TTCTTGTTTT	CGGTGAATCT	480
CAAACGTCTG	GAGTAGTCTA	TGTATCTAAT	AATAATTTTC	AAGCTACTTA	TGATATGATG	540
AAAGCTGTAA	CTGAAGAAAA	ATTTAAAAAT	ATGTGGTTGC	TTATGGGAGG	AGAATCCCAT	600
GTTAATAAGG	ATCGTGAAAG	AGGTGTGCGT	TCTTTTCTGA	ATGATAAAAA	TTACTTTTATG	660
GATTTAAAAG	TCATTTTATG	GCTTATCTAC	AATTGA			696

(2) INFORMATION FOR SEQ ID NO:1201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

ACTGAAGCTG	ATGAGGGTAT	GCAAGCTGCG	CGTGCAGCCC	TGCCAGCATG	GCGAGCTTTA	60
TCAGCAATTG	AACGTGCGGC	TTATTTCAT	AAAACAGCAG	CTATTTTAGA	ACGCGATAAG	120
GAAAAAATTG	GTACTATCCT	TGCCAAAGAA	ATAGCAAAAG	GGATTAAAGC	AGCAATTGGA	180
GAAGTAGTGC	GTACAGCAGA	CTTGATTTCG	TATGCTGCTG	AGGAAGGTCT	CCGTATCACT	240
GGACAAGCAA	TGGAAGGTGG	TGGTTTTGAG	GCAGCAAGTA	AAAACAAACT	GGCTGTTGTC	300
CGTCGTGAAC	CAGTTGGTAT	CGTGCTAGCG	ATTGCTCCTT	TTAATTATCC	AGTTAATTTA	360
TCTGCTTCTA	AAATTGCACC	TGCCTTGATT	GCAGGGAATG	TTGTCATGTT	TAAGCCACCA	420
ACACAAGGTT	CCATTTCTGG	ACTCTTGTTG	GC'TAAAGCAT	TTGAAGAAGC	AGGGATTCCG	480
GCAGGTGTTT	TCAACACCAT	TACAGGTCGT	GGTTCAGAAA	TTGGGGATTA	TATCATTGAG	540
CACAAAGAAG	TCAACTTCAT	CAACTTTACA	GGTTCAACTC	CTATTGGAGA	ACGTATTGGT	600
CGTTTAGCTG	GTATGCGTCC	TATCATGTTG	GAAC'TTGGTG	GGAAAGATGC	AGCTCTTGTA	660
CTAGAAGATG	CAGATTTGGA	ACATGCTGCC	AAGCAAATTG	TTGCGGGAGC	CTTTAGCTAC	720
TCAGGACAAC	GTTGCACGGC	CATTAAACGT	GTCATTGTTC	TCGAAAGTGT	AGCAGATAAA	780
TTAGCTACTT	TGCTTCAGGA	AGAAGTTTCT	AAATTAACAG	TTGGTGATCC	ATTTGACAAT	840
GCTGATATTA	CACCTGTTAT	TGACAATGCT	TCAGCCGACT	TCATTTGGGG	CTTGATTGAG	900
GATGCACAAG	AAAAAGAGGC	TCAGGCTCTT	ACACCAATCA	AACGTGAGGG	CAATCTCCTC	960
TGGCCAGTGC	TTTTTGACCA	AGTTACAAAA	GATATGAAAG	TGGCATGGGA	AGAGCCATTT	1020
GGTCCTGTTT	TACCAATCAT	TCGTGTGGCT	AGTGTAGAGG	AAGCTATTGC	CTTTGCCAAC	1080
GAATCTGAAT	TCGGCCTTCA	ATCATCAGTC	TTTACAAATG	ATTTCAAAAA	AGCCTTTGAA	1140
ATTGCTGAAA	AACTTGAAGT	AGGTACAGTC	CACATTAATA	ATAAAACCCA	GCGTGGTCCA	1200
GATAATTTCC	CATTCCTTGG	TGTCAAAGGT	TCTGGAGCTG	GAGTGCAAGG	AATTAAATAT	1260
AGCATTGAAG	CGATGACAAA	TGTCAAATCC	ATTGTTTTTG	ATGTGAAATA	A	1311

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GCTCAGGCTG	AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAT	CGTGTGGGAT	60
CGCTTTCACA	TTGTACAACA	TCTTAGCCGT	GCTATGAGTC	GTGTGCGTGT	CCAAATCATG	120
AATCAGTTTC	ATCGAAAAATC	CCATGAATAC	AAGGCTATCA	AGCGCTACTG	GAAGCTCATA	180

CAACAGGATA	GCCGTAAACT	GAGTGATAAG	CGATTTTATC	GTCCTACTTT	TCGTATGCAC	240
TTAACCAATA	AAGAGATTTT	AGACAAGCTT	TTGAGCTATT	CACAAGACTT	GAAACATCAC	300
TATCAGCTCT	ATCAACTCTT	GCTGTTTCAC	TTTCAGAATA	AGGAACCAGA	GAAATTTTTC	360
GGGCTTATTG	AGGACAATCT	AAAGCAGGTT	CATCCTCTTT	TTCAGACTGT	CTTTAAAACC	420
TTTCTAAAGG	ACAAAGAGAA	AATCGTCAAC	GCCCTTCAAC	TACACTATTC	TAATGCCAAA	480
CTGGAAGCGA	CCAATAATCT	CATCAAACCT	ATCAAGCGCA	ATGCCTTTGG	TTTTCGGAAC	540
TTTGAAAAC	TCAAAAAACG	GATTTTCATC	GCTCTGAACA	TCAAAAAAGA	AAGGACGAAA	600
TTTGTCCCTT	CTCGAGCTTA	G				621

(2) INFORMATION FOR SEQ ID NO:1203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GCTCAGGCTG	AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAT	CGTTCTTGAT	60
CGCTTTCACA	TTGTGCAACA	TCTTAGCCGT	GCTATGAGTC	GTGTGCGTGT	CCAAATCATG	120
AATCAGTTTC	ATCGAAAAATC	CCATGAATAC	AAGGCTATCA	AGCGCTACTG	GAAACTCATT	180
CAACAGGATA	GCCGTAAACT	GAGTGATAAA	CGTTTTTATC	GTCCTACTTT	TCGTATGCAC	240
TTAACCAATA	AAGAGATTTT	AGACAAGCTT	TTGAGCTATT	CACAAGACTT	GAAACACCAC	300
TATCAGCTCT	ATCAACTCTT	GCTGTTTCAC	TTTCAGAATA	AGGAACCGGA	GAAATTTTTC	360
GGACTCATTG	AGGACAATCT	AAAGCAGGTT	CATCCTCTTT	TTCAGACTGT	CTTTAAAACC	420
TTTCTAAAGG	ACAAAGAGAA	AATCGTCAAC	GCCCTTCAAC	TACACTATTC	TAACGCCAAA	480
TTGGAAGCGA	CCAATAATCT	CATCAAACCT	ATCAAACGCA	ATGCCTTTGG	TTTTCGGAAC	540
TTTGAAAAC	TCAAAAAACG	GATTTTCATC	GCCCTGAACA	TCAAAAAAGA	AAGGACGAAA	600
TTTGTCCCTT	CTCAAGCTTA	G				621

(2) INFORMATION FOR SEQ ID NO:1204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

GCTCAGGCTG	AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAT	CGTTCTTGAT	60
CGCTTTCACA	TTGTACAACA	TCTTAGCCGT	GCTATGAGTC	GTGTGCATGT	CCAAATCATG	120
AATCAGTTTC	ATCGAAAATC	CCATGAATAC	AAGGCTATCA	AGCGCTACTG	GAAACTCATT	180
CAACAGGATA	GCCGTAAACT	GAGTGATAAA	CGTTTTTATC	GCCCTACTTT	TCGTATGCAT	240
TTAACCAATA	AAGAGATTTT	AAACAAGCTT	TTGAGCTATT	CAGAAGACTT	GAAACACCAC	300
TATCAGCTCT	ATAATAAGGA	ACCAGAGAAA	TTTTTCGGAC	TTATTGAGGA	CAATCTTAAG	360
CAGGTTTCATC	CTATTTTTCA	GACTGTCTTT	AAAACTTTTC	TAAAGGACAA	AGAGAAAATC	420
GTCAACGCC	TTCAACTACC	CTATTCAAAC	GCCAAATTGG	AAGCGACCAA	TAATCTCATC	480
AAACTTATCA	AACGCAATGC	CTTTGGTTTT	CGAAACTTTG	AAACTTCAA	AAAACGGATT	540
TTTATCGCTC	TGAACATCAA	AAAAGAAAGG	ACGAAATTTG	TCCTTTCTCA	AGCTTAG	597

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

GCTCAGGCTG	AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAT	CGTTCTTGAT	60
CGCTTTCACA	TTGTACAACA	TCTTAGCCGT	GCTATGAGTC	GTGTGCGTGT	CCAAATCATG	120
AATCAGTTTC	ATCGAAAATC	CCATGAATAC	AAGGCTATCA	AGCGCTACTG	GAAACTCATT	180
CAACAGGATA	GCCGTAAACT	GAGTGATAAA	CGTTTTTATC	GTCTACTTTT	TCGTATGCAC	240
TTAACCAATA	AATAG					255

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

GCTCAGGCTG	AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAT	CGTTCTTGAT	60
CGCTTTCACA	TTGTGCAACA	TCTTAGCCGT	GCTATGAGTC	GTGTGCGTGT	TCAAATCATG	120
AATCAGTTTC	ATCGAAAATC	CCATGAATAC	AAGGCTATCA	AGCGCTACTG	GAAGCTCATA	180
CAACAGGATA	GCCGTAAACT	GAGTGATAAG	CGATTTTATC	GTCCTACTTT	TCGTATGCAT	240
TTAACCAATA	AAGAGATTTT	AAACAAGCTT	TTGAGTTATT	CACAAGACTT	GAAACACCAC	300
TATCAGCTCT	ATCAGCTCTT	GCTTTTTCAC	TTCCAGAATA	AGGAACCAGA	GAAATTTTTC	360
GAACTTATCG	AGGACAATCT	TAAGCAGGTT	CATCCTATTT	TTCAGACTGT	CTTTAAAACC	420
TTCTCAAAG	ATAAAGAAAA	GATTATCAAC	GCCCTTCAAC	TACACTATTC	TAATGCCAAA	480
CTGGAAGCGA	CCAATAATCT	CATCAAACTT	ATCAAGCGCA	ATGCCTTTGG	TTTTTCGAAAC	540
TTTGAAAACT	TCAAAAAACG	GATTTTATC	GCTTTGAACA	TCAAAAAAGA	AAGGACGAAA	600
TTTGTCTTTT	CTCGAGCTTA	G				621

(2) INFORMATION FOR SEQ ID NO:1207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1230
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

GTGTTGGGCTG	AGAAATTTTC	TCAACCTCAT	TTTTTAAAGT	GGACATATAG	AAAGGTCTTG	60
CAAGACTGTA	ACATGAAAAA	AGAATTTAAT	TTAATTGCAA	CTGTGGCAGC	AGGGCTTGAG	120
GCTGTCGTTG	GTCGTGAAGT	GCGAGAGATG	GGCTACGATT	GTCAGGTTGA	AAATGGACGT	180
GTTCGTTTTT	AAGGAGACGT	GAGAGCTATT	ATCGAAACCA	ACCTTTGGCT	TCGGGCAGCA	240
GATCGTATCA	AAATTATCGT	AGGAACGTTT	CCAGCTAAGA	CTTTTGAAGA	GCTATTTTCAG	300
GGAGTTTTTCG	CTTTGGATTG	GGAAAATTAT	TTACCACTTG	GAGCTCGGTT	CCCGATTTCA	360

AAAGCTAAAT	GTGTTAAGTC	CAAAC TTCAC	AATGAGCCCA	GTGTT CAGGC	TATTTCTAAG	420
AAAGCTGTTG	TCAAGAAAT	GCAGAAACAC	TATGCTCGCC	CAGAAGGGGT	TCCTCTGATG	480
GAGAAATGGCC	CAGAGTTTAA	GATTGAGGTC	TCTATTCTCA	AAGATGTGGC	AACTGTCATG	540
ATTGATACGA	CCGGGTCTAG	CCTCTTTAAA	CGTGGTTATC	GTACCGAAAA	AGGTGGCGCT	600
CCTATCAAGG	AAAATATGGC	AGCAGCCATT	TTACAAC TTT	CTAATTGGTA	TCCAGACAAG	660
ACTTTGATTG	ATCCGACCTG	TGGTTCGGGG	ACTTTCTGTA	TTGAGGCAGT	TATGATTGCT	720
AGAAAGATGG	CGCCAGGTCT	TCGTGCTCT	TTTGCATTTG	AGGAATGGAA	CTGGATCAGC	780
GATCGCTTGA	TTCAAGAAGT	GCGCACAGAA	GCGGCTAAAA	AAGTAGACCG	TGAGCTTGAG	840
CTGGATATCA	TGGGCTGTGA	TATTGATGCT	CGCATGGTGG	AAATTGCTAA	GGCCAATGCT	900
CAGGCAGCTG	GTGTTGCAGG	AGACATTACT	TTTAAGCAGA	TGCGCGTGCA	GGATTTACGT	960
TCCGATAAAA	TCAATGGAGT	AATCATTTCC	AATCCGCCTT	ATGGTGAACG	TTTGT CAGAT	1020
GATGCAGGGG	TGACCAAGCT	CTATGCTGAG	ATGGGGCAAG	TATTTGCACC	GCTGAAA ACT	1080
TGGAGCAAAT	TTATCCTGAC	TAGTGATGAA	GCTTTTGAAA	GCAAGTATGG	TAGCCAAGCA	1140
GATAAGAAGC	GTAAGTTATA	CAACGGAACC	TTGAAAGTGG	ATCTATATCA	ATATTTTGGT	1200
CAGCGTGTCA	AACGGCAAGA	GGTAAAATAG				1230

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

AGAGCTTATG	AAGTTTTTTTGA	CGAGAATAAC	TTAAATATTA	CTTTTTTTTGA	TACATTTTCT	60
GAAATTAAAA	ATAATATTGA	TTATTATATT	ATTGCGCTTC	CGACAGATTA	TGATGAGAAA	120
ATTGGTAGTT	TTAATACATA	TGAAATCGAA	CAAACGGTAT	CGAAGATTCT	GAGGGTAAAA	180
CCTAATGGAA	AGATTATTTT	AAAGTCAACA	GTTCCGATCG	GCTTTTCAAA	CAAATTAAAA	240
AGGCTGTTTG	ATACAAAAAA	TATCATTTTT	GTCCCTGAAT	TTTTGAGAGA	AGGTGTGTTCT	300
ATATATGATA	ATTTATATCC	AAGTCGCATA	GTTGTTGGAG	ATGAGACAGT	TGAAGGAAGA	360
AAAATGTCAG	AGTTGTTTCT	TTCGATTAGT	ACTCATAGTA	CTGCCAATAT	TAAAAATGTT	420
ATGTTAGTTT	CTCCTACTGA	AGCAGAAGCA	ATTAAGCTTT	TTTCTAACAC	ATTCTTAGCT	480
CTCCGTGTTG	CTTTTTTTTAA	TGAACTAGAT	TCTTTTGCTG	AGAGGAGAAG	TTTAAATGCT	540
GAAGTTGTAA	TAAAAGGTGT	TTGTTTAGAT	CCAAGAATTG	GAAATTTTTA	TAATAATCCT	600
TCTTTTGGAT	TTGGAGGATA	TTGTCCTCCC	AAAGATACTA	AACAATTAAA	AAAAGAATTT	660
ATAGAAATAA	ATGCCCCAGT	GATAGAAGCG	ATTGATATTT	CAAAACACAA	TAGAAAACAG	720
TTCATAGTTA	AACAAATATT	GGAACGAAAG	CCAAAGATAG	TAGGAATATA	TAAATTGGGG	780
ATGAAATATA	ATT CAGATAA	TTACAAAGAG	TCAGCTATTT	TAAGTATAAT	TAATGAAC TA	840
TTGATTGTCTG	GTATAAAAAAT	TTTAGTATAT	GAACCAAATT	TAAACGTTAG	TTATAGATAA	900

(2) INFORMATION FOR SEQ ID NO:1209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

CAAACATATG AAACACGTAC AGTTATCGTA GCAACTGGTT CTAAACACCG TCCTTTGGGA	60
GTACCTGGAG AAGAAGAACT GAACAGTCGT GGTGTTTCTT ACTGTGCTGT GTGTGATGGT	120
GCTTTCTTCC GTGACCAAGA TTTATTGGTA GTTGGTGGTG GAGATTCAGC TGTTGAAGAA	180
GCCCTCTTCT TGACTCGTTT TGCTAAGACT GTTACCATTG TTCACCGTCG TGACCAACTT	240
CGTGCCCAAA AGGTTTTACA AGATCGCGCC TTTGCGAATG AAAAAATCAG CTTTATCTGG	300
GATTCTGTAG TAAGGGAAAT CAAGGTGAA AACCGAGTAG AATCAGTCGT ATTTGAAAAT	360
GTGAAAACAG GTCAAGTGAC AGAACAAGTC TTCGGTGGTG TCTTTATCTA TGTTGGATTG	420
GACCTCTTA GCGATTTTGT TAAAGAATTG AATATCCAAG ATCAGGCAGG ATGGATTGTG	480
ACAGATAACC ACATGAAAAC TGCAGTCGAC GGTATCTTTG CAGTTGGAGA TGTTTCGCTTG	540
AAAGACCTTC GCCAAGTAAC AACAGCGGTT GGAGATGGAG CTATCGCTGG TCAAGAAGCC	600
TATAAATTCA TTACAGAACA TAGTTAA	627

(2) INFORMATION FOR SEQ ID NO:1210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

AAAGGAGACC TCATGACACT TCCAGTTAGA AAATCCCTGC ACGATGCAGT TTTACAGGCT	60
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TCGAAAGCGG	ATACTTGGGA	ACAAGCGACC	AAGGAATGGA	ATGAAGTTTC	CTTTATTTTT	120
AACGGTATCG	GCCGTAGCAA	TTGTGTCTGT	GGAAATGCCA	TCAAATACGC	TTATGAACTC	180
TTTAACGGTG	TCACAGGCCA	ACGCCTCTTT	CCAATTGGTA	GCGACTGTGT	TCGTCATTTT	240
CATCGATTGC	CCCTTGACCA	GCAATTGGAA	GAGGAAGAAA	AACTGCTCAG	AAAGGTTGAA	300
AATCTAACCA	GAAAAGCTCA	GAAAAAGGAA	AAAATCAAGG	TCAATAAAAAG	TGACTTTGAC	360
GAGCGACTTC	TAAAATGGCT	CTGGGAAAAA	GGTGTTTTCA	AACCCAATCG	TGGCAATCAA	420
TTTGCGCCTG	AGAGAGACTA	CCAGCTTTTC	CTAGAAGTCT	TTCAGGGAGG	AAGTTGGACC	480
AAGGCGGAAC	CAAAAGAAAA	GGCTCGGATG	GAAGAAGTCC	TTGAAAAGTG	TATCAAACCC	540
TTTTTACTTG	GGAAATCGGA	TGACCAACTC	TACCTTGTC	AGCTAGGCAA	GGAGAAAATT	600
GACTACGAAC	AAGAATCCC	GTATCCAGGC	AGAGAAAAGAA	CGCAAGAAGA	GGGATAA	657

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

TTACATCATG	AAAAAGTAGG	TTTTATTATG	AAAAATTATCC	TTGTTCGGAGG	GGGAAAAGTT	60
GGTTTTGCC	TCTGTCGCTC	CTTGGTTGCA	GAAAAGCATG	ATGTTTTGCT	GATTGAGCAA	120
GACGAAGCTG	TTCTCAATCA	TATTGTCAGT	CGCTTTGATA	TCATTGGTAT	CCTTGGTAAC	180
GGGGCCGATT	TTGCCATTCT	TGAGCAAGCC	AGCGTCCAAG	ATTGTGATAT	CTTTATCGCC	240
CTGACTGAGC	ACGATGAAGT	CAACATGATT	GCAGCAGTTC	TAGCCAAGAA	AATGGGAGCT	300
AAAGAAACTA	TCTGTCGGGT	GCGGAACCCCT	GAATATTCTA	ACTCTTATTT	CAAGGAAAAG	360
AATATTCTCG	GTTTTTCTCT	TATCGTTAAT	CCTGAGCTCT	TGGCTGCCCCG	CGCTATCGCG	420
AATATCATTG	ACTTCCCCAA	CGCCCTGTCT	GTCGAACGCT	TTGCTGGTGG	ACGCGTTAGC	480
CTCATGGAAT	TTGTCGTCAA	GTCCACCAGC	GGTCTTTGCC	AAATGCCCAT	TTCTGATTTT	540
CGTAAAAAAT	TTGGTAATGT	CATTGTCTGT	GCGATAGAGA	GGGAGCATCA	AATTATCATT	600
CCAAGCGGTG	ACATGACTGT	ACAGGATAAA	GATAGAATCT	TTGTCACTGG	TAACCGTGTC	660
GATATGATAC	TCTTCCATAA	TTATTTTAAA	TCACGCGCCG	TGAAGAGCCT	TCTCATCGTT	720
GGGGCAGGTA	GAATTGCCCTA	TTATCTACTT	GGTATTCTCA	AAGATAGTCG	TATCGATACA	780
AAAGTCATTG	AAATCAATCC	TGAAATCGCC	AGCTTCTTTA	GCGAGAAATT	CCCAAATCTC	840
TACATCGTTC	AAGGAGATGG	AACCGCAAAA	GATATCCTGC	TGGAAGAAAG	TGCTCAACAC	900
TATGATGCCG	TTGCGACTCT	AACAGGTGTC	GATGAGGAAA	ATCTGATTAC	ATCTATGTTC	960
CTTGACAGGG	TAGGTGTACA	GAAAAATATT	ACTAAGGTCA	ATCGTACCAG	TCTCCTCGAG	1020
ATTATCAATG	CGCCTGATTT	TTCAAGTATC	ATCACACCTA	AAAGCATCGC	TGTAGATACG	1080
ATTATGCACT	TTATTTCGTGG	TCGAGTTAAT	GCCCAGTATT	CAGACCTTCA	AGCCATGCAC	1140
CATCTAGCCA	ATGGCCAAAT	CGAAACCCTG	CAATTCCATA	TCAAGGAAGC	CAATAAAATG	1200
ACTGCCAAAC	CTCTTTCTCA	ACTGAAATTG	AAAAAAGGGG	TTCTTATTGC	AGCCATTATT	1260
CGAAAGGGCA	AGACTATTTT	CCCAACTGGG	GAGGATATGT	TGGAAGTTGG	AGACAAGCTC	1320

CTAGTAACAA CCTTGTGCC AAACATCACC AAGATTTATG ACTTGATTGC GAGGTAA

1377

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

AAGCTGGACC	TTCTTCCTTT	ACTGGATCAG	CGTCCTCAGG	ATTTGTCAGG	TGGACAAAAG	60
CAGCGAGTCA	GTCTAGCTGG	TGTCTTGATT	GATGAAAGTC	CGATTCTCTT	GTTTGATGAG	120
CCACTCGCCA	ATCTAGATCC	CAAGTCAGGT	CAGGATATTA	TCGAATTGAT	TGACCAGATT	180
CATAAGGAAG	AGGGGACGAC	GACTCTGATT	ATCGAGCACC	GTTTGGAGGA	CGTTCTGCAT	240
CGCCCTGTGG	ATCGGATTAT	CTTGATAAAC	GATGGTCGTA	TCCTTTTTAA	TGGGAGCCCT	300
GACCACTTGC	TTGCGACTGA	TTTATTGACT	CAAAATGGAA	TTCGAGAACC	CCTTTATCTA	360
ACGACTCTCC	GTCAATTAGG	TGTGGACTTA	GTCAAGGAAG	AACAGTTAGC	GAATCTGGAT	420
AACATGTCTA	TCTCAAAAAG	TCAGGTTTCAG	CTGCAGAAATG	AACTGGCAAA	AGAAACTCCA	480
GAATTGCAGT	CACTCTTTAA	ATTAGAGGAC	GTGCTTTTCT	CTTATGATGA	TAGACCGATT	540
TTAAAATCCC	TACATTTAGA	TATTA AAAAG	GGTGAAAAGA	TTGCTATTGT	CGGAAAAAAT	600
GGAGCAGGGA	AATCAACTCT	AGCCAAGGCT	ATAAGTAGCT	TTATTCAGAC	GGAAGGACGC	660
TATCTTTGGG	AAAAACAGGA	TATAAAAGGC	GATTCTGTTG	CAGAGCGGGC	GGAACGAGTA	720
GGCTATGTGC	TACAAAATCC	TAATCAAATG	ATTTCAACCA	ATATGATTTT	TGATGAGGTG	780
GCTCTAGGGC	TCCGTTTGCG	AGGTGTGGAT	GAGAAGGAAA	TTGANACGAG	AGTCTATGAA	840
ACCTTGAAAA	TCTGTGGACT	TTATGAATTC	CGTAATTGGC	CTATTTCTGC	CCTGTCATTT	900
GGTCAGAAAA	AACGTGTCAC	CATTGCTTCA	ATTTTGGTCT	TAGGAGCTGA	AATTATTTTC	960
CTAGATGAAC	CGACTGCAGG	TCAAGATCAG	AAGAACTATA	CTGAGATTAT	GGAATTTCTC	1020
GAAGAGTTAC	ATCAAAAAGG	GCATACCATT	GTCATGATTA	CCCATGATAT	GCAATTGATG	1080
CTGGATTATT	CAGACCGGGT	CCTTGTCATG	GTGGATGGAG	AATTGATTGC	CGATACTGTT	1140
CCAGCCAGTC	TGTTGAGCGA	TCCTGAGCTG	TTAGTAAAAG	CCAATCTAAA	AGAAACCTCC	1200
ATCTTTAACT	TGGCTAAGAA	ACTAGATGTG	GATCCACTGG	ATTTAACGGC	ATTTTACAAA	1260
GAAAGGAGAG	AGGGATGCAA	GCTAAATTAA				1290

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

GGAGTACATG	AGAGAAGCAT	GATTCAGTCT	ATCACGAGTC	AAGGCTTGGT	GCTTTACAAT	60
CGCAATTTTC	GTGAGGATGA	CAAGCTCGTC	AAAAATTTTA	CAGAGCAGGT	TGGCAAACGC	120
ATGTTTTTTG	TCAAACACGC	TGGTCAGTCT	AAGCTGGCGC	CTGTTATTCA	GCCCTTGGTG	180
CTGGCACGAT	TTCTATTGCG	AATCAATGAT	GACGGACTCA	GTTACATCGA	AGACTATCAT	240
GAGGTCATGA	CTTTTCCCAA	GATTAATAGT	GACCTCTTTG	TCATGGCCTA	TGCGACCTAT	300
GTGGCAGTCT	TTGCAGATGC	TAGTTTGACG	GACAATCAGC	AGGATGCTCC	CTTGTGCTCT	360
TTTTTGCAAA	AGACTTTGGA	GTTGATGGAA	GCAGGCTTGG	ATTATCAGGT	TTTGACCAAT	420
ATTTTTGAAA	TTCAAATTTT	GACTCGATTT	GGAATCAGCC	TCAATTTTAA	TGAGTGTGTC	480
TTCTGCCATC	GGGTTGGTCA	GGCTTTTGAC	TTTTCTTTCA	AATATGGAGC	CTGCCTCTGT	540
CCAGAGCATT	ATCATGAGGA	TAAGAGACGT	TGTCATCTCA	ATCCCAATAT	CCCCTATCTG	600
CTCAATCAAT	TTCAAGCTAT	TGATTTTGAG	ACTTTGGAGA	CCATTTTCGCT	CAAGCCTGGA	660
ATCAAGCAAG	AGCTACGCCA	ATTTATGGAT	CAACTATATG	AAGAGTACGT	TGGGATTAC	720
CTAAAATCAA	AGAAATTTAT	TGATTCCCTA	GCAGACTGGG	GACAATTACT	AAAAGAGGAA	780
AAGAAATGA						789

(2) INFORMATION FOR SEQ ID NO:1214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

TTTCTTAATG	AGAGGGATAT	AACTTCCAGA	CATATCAACA	GTGACGACTT	TAACTTTTTT	60
TCTAGCTTCT	TTCGAGTACT	TGAAGAAATG	ATTTTCGGATG	GTTGTTTGAC	GTCTGTTATC	120
AAGAATGGTC	ATGATTTTCT	TAGTGTGAA	ATCCTGAGCA	ATGAAAGCCA	ATTTCCCTT	180
CTGGTAGGAG	AATTCATCCC	AGGAGAGGAT	TTCAGGCAAA	GTGGTGTAAT	CCTCTTGGA	240

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

AGATATAATG AAGAAAAATC GAGCAAGGAA AAAGAACTGA CAAATTCAAA GTATATTACT	60
TGTTTGAAAC GTTCAGAGGG CCAGTTGTGT GGGATTCAAA AGATGATTGA AGGAGATCGT	120
GACTGTGCTG ATATTGTGAC GCAACTGACA GCAGTGAAAT CTAGTGTAGA GCGCGTGATT	180
GAGATGATAA TTACCGAAAA TCTTACTGAA TGTATCAATC AGCCCCTAGA TGATTCTGAA	240
GCTCAAAAGG AACGCCTAGA AAAGGCTATC CGATACTTGA TTAAACGGAA ATAA	294

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

CTTGAAAATG AAGGTGGGGG TTTTGTNNG NGTTTTTNT TNNTTNNTNN TNNTNNTTT	60
NNNNCCCCGC GNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNCTT TTTACAAAAT	120
AGAGCCACTA TACTGGAGTT TCTATATCGA AATCCAGCAA CATCCCGTAC AGATATTGTT	180

AATGAAACAG	GACTTACTCC	AGCAACAACG	ACTAACATCA	TAAAAGAACT	AAGCGAACAG	240
TCCCTCATAT	ACGAAACTGG	TGATGAATTT	AGCGAGTTTT	CCGGATCTGG	AAGACGTAGA	300
AAAACATTTT	CTATCACAGA	TAATATTCCG	TATGTTGTTG	GAGGTATTGA	AATAAACGTC	360
CTAGGTATCT	TTCTCAGTCT	ATGTGACTTA	CAAGGGAAAA	CTCTTTTCGA	GACAGAAATT	420
TTGAATGAAG	ATTATCCTAT	TTCAGAAATC	AATTCCACCA	TTACCAATAT	GATAAAAACA	480
GCTATAGAGT	ACGTCCCTTT	GGAAACAAAA	TTACTTGGAT	TTGGCTTATC	AATACCTGGA	540
CATTATTACA	AAGACTCCGG	AAGTATCAT	ACAAACAACC	CCATATGGGA	ATCTTTTAAT	600
TTATTAAATG	TAATTAAAA	ATTCAATTTT	CCTTTTATTG	TAAAAAATAA	TATCGATTGT	660
ATGGCTATAG	GACAATACCT	TTTTAATCCA	CACAATACCC	CCGATAACTT	TATTTTCCTA	720
CACGCTGGAT	TAGGTATTTA	CACTTCCTTT	TTCACAAAAG	AAAAAATAGG	AGCCTCTAAA	780
AATCCTTATA	TCGGAGAAAT	TGGACACACC	ATTGTCGAAT	TGAATGGGCA	ATATTGTGAA	840
TGCGGAAAAA	AAGGTTGTTT	ACAAACATAT	ATTTCCGATG	CTTGGTTAAT	CAAACACGCC	900
CAATTATTAT	TTAAAAATC	CCAACCTAAT	GTACTAAAAA	GCCTTGTAAT	GAAGTAAAAA	960
GACATTCAAT	TAGACACCCT	TTTAACGGCT	TATAATTTAG	GCGACTCCGC	TTTACGTCAA	1020
CAAATTGATA	AAGGAGTCAA	TTTATTAGCC	ACTTCTATTG	CAAATCTCCT	CCTCATCAAT	1080
CCTGCTGATA	AAATCTATAT	CAACAGTCAA	TTGCTTAATT	ATCAACCTTT	CACTCATGAA	1140
GTCAGGGATA	AAATCCAAGA	CCAGCTCCAC	TTCGTTCCCT	TTACTCGTAA	TATAGAAATT	1200
GAAATTTTAC	CTTACAACAA	ACATCGTGGA	AGTATAGGAG	CTTGTGCATT	AGCTATCGTC	1260
GCTTTTTTCA	TAGAACATAG	CAATGTATTA	CAAGATATTA	TTTCACCTTA	A	1311

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

AAAAGAAATG	AGTTAGACAT	GTCAAAAGGA	TTTTTTAGTCT	CTCTTGAGGG	ACCAGAGGGA	60
GCAGGCAAGA	CCAGTGTTTT	AGAGGCTCTG	CTACCAATTT	TAGAGGAAAA	AGGAGTAGAG	120
GTGTTGACGA	CCCGTGAACC	TGGCGGAGTC	TTGATTGGGG	AGAAGATTCG	GGAAGTGATT	180
TTGGATCCAA	GTCATACTCA	GATGGATGCT	AAAACAGAGC	TACTTCTCTA	TATTGCCAGT	240
CGCAGACAGC	ATTTGGTGGA	AAAAGTTCTT	CCAGCCCTTG	AAGCTGGCAA	GTTGGTCATC	300
ATGGATCGTT	TTATCGATAG	TTCTGTTGCC	TATCAGGGAT	TTGGTCGTGG	CTTAGATATT	360
GAAGCCATTG	ACTGGCTCAA	TCAGTTTGCG	ACAGATGGCC	TCAAACCCGA	TTTGACACTC	420
TATTTTGACA	TCGAGGTGGA	AGAAGGGCTG	GCTCGTATTG	CTGCTAATAG	TGACCGCGAG	480
GTTAATCGTT	TGGATTTGGA	AGGGTTGGAC	TTGCATAAAA	AAGTTTCGTCA	AGGCTACCTT	540
TCTCTTCTGG	ATAAAGAGGG	AAATCGCAT	GTCAAGATTG	ATGCTAGTCT	CCCTTTGGAG	600
CAAGTTGTGG	AAACTACCAA	GGCTGCTTGG	TTTGACGGAA	TGGGCTTGGC	CAAATGA	657

(2) INFORMATION FOR SEQ ID NO:1218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

GGAGGAAATG ATATGGATAA AAAAGAACGA CAAAAGATTG AACAACAACG TCGAGAGATG	60
GCTCTAACTA ATACTTTTTTT TAATCGATAT CTTCTTCTAC GTTATTCAAT AGCACTCTTC	120
TTTTTTGGGA ATATTTATTG GCTTTTGAAT CAGTTTATTA ATCCCTCGCC TATTATTATT	180
TTCCCCATTA TGCTCATAGT ATTTTCTATT TTAGCAACTG TTGAACAATT TAAACTCTAT	240
GGAAATAGGA AAGAAAAGTT GGGAATAACA CTAATGTTTG TTAGAATACA AATGCTTATT	300
TCAATAGGAT TACTTGTTTT AACTTGGACA AGTTGGTTTA AGAATCTTTT TCCGATTTTT	360
GAAAATAACC AAGTAGCACG TTTATTTGTT TTTGTAGTTC TTCTATTAGG TTTAGTTCTG	420
AGTTTGTTAG ACATTAGAAG AATTAAAAAA ATTTATAAAC GAACAGATAA GGTTTATCAA	480
CAATTTGTCC AATTGGAAAA GAACTCACTT AGTTTATAA	519

(2) INFORMATION FOR SEQ ID NO:1219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

GAAGCGAATG AAGAGAGTAA GATGAAAGAA GCTATAATTG AGTGGAAGGA TTTCTCTTTC	60
CGGTATGAAA CACAACAAGA ACCGACCTTG CAAGGGATAG ACTTGACCAT TTACAAGGGA	120
GAGAAAGTCT TAATTGTTGG ACCATCTGGA TCAGGTAAAT CTACCTTGGG TCAGTGTTTG	180

AATGGGATTA	TTCCCAATAT	TTACAAGGGT	CAGACATATG	GAGAATTTTT	GATAAAGGGT	240
CAAACAGCCT	TTGATATGAG	CATCTATGAT	AAGTCTCATC	TGGTTAGCAC	AGTTTTGCAG	300
GATACAGATG	GGCAGTTTAT	TGGCTTGTCT	GTGGCAGAAG	ATTTGGCGTT	TGCTCTGGAA	360
AATGATGTGA	CAGCCCTAGA	TGAGATGAAA	GGGTCGTGTT	TATAA		405

(2) INFORMATION FOR SEQ ID NO:1220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1131
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

TCTTTTGATG	AAACGAGCAA	GGCAGATACC	AAGACCTTGC	CGAAGGTTTC	TCAGAGTACC	60
TTGACATCTA	TTCTAAGGT	TCAAGCGCAG	ACAGAACACA	AATCAATCAA	AAACCCAAGC	120
CAGGCTGTGA	CAGAGGAAAC	TTACCAACCA	CAAGCACCGA	AAAAACATAG	ATTTAAGATG	180
CGTTACCTGA	TTTTGTGGC	CAGCCTTGTA	TTGGTGGCAG	CTTCTCTTAT	TTGGATACTA	240
TCCAGAACTC	CTGCAACCAT	TGCCATTCCA	GATGTGGCAG	GTCAGACAGT	TGCAGAGGCC	300
AAGGCAACGC	TCAAAAAAGC	CAATTTTGAG	ATTGGTGAGG	AGAAGACAGA	GGCTAGTGAA	360
AAGGTGGAAG	AAGGGCGGAT	TATCCGTACA	GATCCTGGCG	CTGGAACCTGG	TCGAAAAGAA	420
GGAACGAAAA	TCAATCTGGT	TGTCTCATCA	GGCAAACAAT	CCTTCCAAAT	TAGTAATTAT	480
GTCGGCCGGA	AATCTTCTGA	TGTTATCGCG	GAATTAAAAG	AGAAAAAAGT	TCCAGATAAT	540
TTGATTAAAA	TTGAGGAAGA	AGAGTCGAAT	GAGAGTGAGG	CTGGAACGGT	CCTGAAGCAA	600
AGTCTACCAG	AAGGTACGAC	CTATGACTTG	AGCAAGGCAA	CTCAAATTGT	TTTGACAGTA	660
GCTAAAAAAG	CTACGACGAT	TCAATTAGGG	AACTATATTG	GACGGAACCT	TACAGAAGTA	720
ATCTCAGAAC	TCAAGCAGAA	GAAGGTTCCCT	GAGAAATTTGA	TTAAGATAGA	GGAAGAAGAG	780
TCCAGCGAAA	GCGAACAAGG	AACGATTATG	AAACAAAAGTC	CAGGTGCCCG	AACGACTTAT	840
GATGTGAGTA	AACCTACTCA	AATTGTCTTG	ACAGTAGCTA	AAAAAGTTAC	AAGTGTTGCC	900
ATGCCGAGTT	ACATTGGTTC	CAGCTTGGAG	TTTACTAAGA	ACAATTTGAG	TCAAATTGTT	960
GGGATTAAGG	AAGCTAATAT	AGAAGTTGTA	GAAGTGACGA	CAGCGCCTGC	AGGTAGTGTA	1020
GAAGGCATGG	TTGTTGAACA	AAGTCCTAGA	GCAGGTGAAA	AGGTAGACCT	AAATAAGACT	1080
AGAGTCAAGA	TTTCAATCTA	CAAACCTAAA	ACAACCTTCAG	CTACTCCTTA	A	1131

(2) INFORMATION FOR SEQ ID NO:1221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

AAAGGTGATG	AAGAACAAAC	CAAGATTCAA	GCAGGAATTC	CTACTGATAA	TGAAGTAAGT	60
TATGCTCTTA	TTTATCAGCA	GGAAACTCTT	CCTGCAACAG	GTTTCATCAAC	TTCTGCGCTT	120
ACAGCTTTAG	GCCATTAGC	TGTTGGTAGT	TTAGTTCTTT	TGGTTCGGAA	CAGTTTTTTG	180
CTCCCTCTGA	AAAGTCATCA	TTTGATGGCT	TTTTTCTATA	TAGGGTAA		228

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

TTTGTCGATG	ACATCTTCGA	TGGCATTCCA	GTAAATGGCT	TTGTAGTAAG	TTTCCATTTA	60
AAATCTCTTT	CTGTGTTTAG	TATTGCGAAC	TCACAATTAT	TTCTACTTTA	CCATAATTCT	120
ATAGGAGTAT	CGCACAAAAA	GTCGGAAGCC	CGACTTTTAA	AATGTTACAT	AAATTATGTT	180
ATGACATAG						189

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1059 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

ATGAAAGATG	ATCAGAAATA	TTTATTAGCG	GGACTTTATT	CGCTTCTAGT	TGCAATATTT	60
TATTTTCCAT	TGATTGAGTC	CAAGGGGATT	TTTGTAAGTA	TATTGATGGC	GGTTTACTT	120
TTATATTTAA	TATACTTCAT	TGCAACAGTC	ATTCATATTG	TGATAATTAA	GTTTATAAGA	180
AAAAAATCTT	TTAAGTATTT	GGTTCTATAT	CCATTTACTT	ACGATGGGAG	CTGGAGATTT	240
CAACCTATAA	ACTTACTCTA	CTTTCCAGAA	ATGGTGAGAG	ATGTCATTCC	GATTAATTTA	300
GTTCAAGAAT	ATTGCCAAGG	ACAACCTTAC	GGACTGTAA	AAAAGATGCT	GAAAAGAATT	360
CGATTGTCAC	GAGAGATATC	TTTACTCCTG	GCTACCATTA	TCGTCTATTT	TTTTACGCAT	420
AGAATTCTAC	CTCTTTCAGT	ATTTACGTTT	ATATTTTCTT	ACATATTGCT	ATTTGTACAA	480
TCTTATTTGG	GTAGCAATAC	CGCTTGGATT	GGAAATAGAA	GATTAATAAT	AGATGATGAA	540
TTTGAAAAAA	TCTTGCTTTC	AAAAAGTTAT	ATAAAAAGAA	TATCATCTGC	ACGATACTCA	600
GAATACTTGA	CATGTGAATA	CAAAAACCTT	ACACCAATCA	TATTGATAGC	TATTTTGTAA	660
AATTTGCTTG	ACTCCTACTT	GCTTCAGAAT	CAGAGTGAGG	TTGACTTAGA	TATTTTAT	720
AAAGTTTTAC	CTTTGCTTTA	TAAAGAAAAA	TATACTATGG	GATTCAATTA	CTTTGTAAAGT	780
TTAAATTATT	TACTATATAA	GGTTGGATTT	TTGGGAATCA	TTTACGATAA	TGAAGCATT	840
AGAGATTTGT	CAAAACAATA	TTTAAACAAA	AATATTTTCG	AATTACAAGA	TGGTCTTTC	900
GAGGGCGGTA	TACAAGATGC	TGTTGCCTCT	AAACAAATAG	TAGTTATAAA	TGAATTTATA	960
GCTTGTTTAA	ATTCCAGATG	CGTGCCATCC	CAATATGATA	GATTTTTTTA	TAAAGATAGA	1020
CCTTATATTT	TTTCCAGAAA	GAGTCCTATT	AAGGGGTGA			1059

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

AAAGGAGATG	AACTAATGGT	TTTACTTCA	CTTTCCTCAA	AAGATGGCAA	TTACCCCTAT	60
CAGCTCAACA	TTGCCACCT	CTACGGAAAT	CTCATGAATA	CCTACGGGGA	CAATGGAAAC	120

ATCCTCATGC	TCAAGTATGT	GGCTGAAAAA	CTGGGAGCCC	ATGTGACCGT	TGACATCGTT	180
TCTCTCCATG	ATGACTTTGA	TGAAAATCAC	TACGACATCG	CCTTTTTTCGG	TGGTGGTCAA	240
GACTTTGAAC	AAAGTATCAT	TGCAGACGAC	CTACCTGCTA	AAAAAGAGAG	CATTGACAAC	300
TACATCCAAA	ACGACGGTGT	AGTTCTGGCT	ATCTGCGGTG	GTTTCCAAC	ATTGGGTCAA	360
TATTATGTTG	AAGCTTCAGG	AAAACGTATC	GAAGGGCTAG	GGGTCATGGG	ACACTACACG	420
CTCAACCAGA	CCAATAACCG	TTTTATCGGT	GACATCAAGA	TTCACAATGA	AGATTTTCGAT	480
GAAACCTACT	ATGGATTTGA	AAATCACCAA	GGTCGTACCT	TCCTCTCTGA	TGACCAAAAA	540
CCGCTGGGAC	AGGTTGTCTA	TGGAAATGGA	AACAACGAAG	AAAAGGTCGG	TGAAGGGGTT	600
CATTATAAGA	ATGTCTTTGG	TTCCTACTTC	CACGGGCCTA	TCCTCTCTCG	TAATGCCAAT	660
CTGGCTTATC	GCCTAGTTAC	TACTGCCCTC	AAGAAGAAAT	ATGGTCAGGA	CATCCAAC	720
CCTGCCTATG	AGGACATTCT	CAGCCAAGAA	ATCGCTGAAG	AGTACAGTGA	CGTCAAAAGC	780
AAGGCTGACT	TTTCTTAA					798

(2) INFORMATION FOR SEQ ID NO:1225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

AAAAATTGTG	AGGAAAAGAA	AATGGCAAAA	ACAATTCATA	CAGATAAGGC	CCCAAAGGCT	60
ATCGGGCCCT	ATGTTCAAGG	AAAAATCGTT	GGCAACCTTT	TGTTTGCTAG	CGGTCAAGTT	120
CCCCTATCCC	CTGAAACTGG	GGAAATTGTA	GGAGAGAATA	TCCAAGAACA	GACAGAGCAA	180
GTCTTGAAAA	ACATCGGTGC	TATTTTGGCA	GAAGCAGGAA	CAGACTTTGA	CCATGTTGTC	240
AAAACAACTT	GTTTCTTGAG	CGATATGAAC	GACTTTGTTT	CTTTTAATGA	GGTTTACCAA	300
ACGGCCTTCA	AAGAGGAATT	CCCAGCTCGT	TCAGCTGTGG	AGGTAGCTCG	TCTTCCTCGT	360
GATGTAAAAG	TCGAAATTGA	AGTCATCGCA	GAGATTGGAT	AA		402

(2) INFORMATION FOR SEQ ID NO:1226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

AAAGGTTGTG	ATTTTGTGAA	AGATAAACAG	TTTGCTATTC	CAAAAGCTAC	AGCAAAAAGA	60
CTCTCTCTCT	ACTATCGAAT	TTTTAAGAGA	TTTCATGCAG	AAAAGATTGA	ACGTGCCAAC	120
TCTAAGCAAA	TTGCAGAGGC	CATTGGGATT	GATTTCAGCGA	CCGTACGTCG	TGATTTTTCC	180
TATTTTGGTG	AACTTGGTCG	TCGTGGTTTT	GGCTATGATG	TCAAAAAACT	AATGACATTT	240
TTTGCCGATT	TGCTCAATGA	CAACTCTATT	ACCAATGTCA	TGCTGGTTGG	TATTGGAAAT	300
ATGGGCCATG	CCCTTCTCCA	CTACCGCTTC	CACGAACGTA	ACAAGATGAA	GATTATCATG	360
GCCTTTGACC	TAGACGACCA	TCCTGAAGTC	GGTACCCAAA	CTCCTGACGG	GATTCCCATT	420
TACGGGATTT	CTCAGATCAA	GGATAAAATC	AAGGATGCTG	ATGTGAAGAC	TGCTATCCTA	480
ACTGTTCCCA	GCGTCAAGTC	ACAAGAGGTT	GCTAATCTCT	TGGTTGATGC	TGGTGTGAAA	540
GGAATTCTCA	GTTTTTCACC	AGTCCATCTG	CATTTACCAA	AAGACGTGGT	CGTTCAGTAT	600
GTCGATTTGA	CAAGTGAAC	CCAAACCCTC	CTCTACTTCA	TGCGAAAAGA	GGATTAG	657

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GACTGCTGTG	AAACTATGAG	AGTTGCAGCC	CTAAACTCGA	GTATAATTGG	GTCATTCAGG	60
TCTAGAGCGC	CACAGGTGGC	AGACGGCGGC	ACTGGCGCTT	TAAATGTAGT	AAACCGTATA	120
GGGAGATTGG	CCAGACTGAC	AAGTAATGGA	GTTCTACATA	CTAGACATGC	TTTGACGGTA	180
AATGGCCATA	ATGCACAACT	GCGGACATTT	GTATAA			216

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...528
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

TGTAGATGTG	ATAGAATTAG	TGGGGAATTC	ATAATGAGAC	AGTTGAAGCG	AGTTGGAGTA	60
TTTTTATTGC	TTCTTTCTT	TGTTCTAATT	GACGCCCAT	TTAGCCAGCT	TCTGGGCTCA	120
TTTTTCCCC	ATGTACATTT	GGCTAGTCAT	TTTCTTTTTC	TATTTCTCTT	ATTTGAGACG	180
ATAGAAGTAT	CAGAGTATCT	CTACCTAGTC	TATTGTTTTG	TTATAGGCTT	GGTTTATGAT	240
GTTTACTTTT	TCCATCTAAT	AGGGATTACA	ACTCTCTTAT	TTATCTTATT	GGGAGCCTTC	300
CTTCATAAAT	TGAATAGTGT	TATTTTGTTG	AATCGTTGGA	CAAGAATGCT	AGCTATGATT	360
GTGCTGACAT	TCCTGTTTGA	AATGGGTAGT	TATCTTTTGG	CTTTTATGGT	AGGGTTGACA	420
GTAGATAGCA	TGTCGATTTT	TATAGTCTAT	AGCTTGGTAC	CGACGATGAT	TTTAAATTTT	480
TTATGGATTA	CTGTTTTTCA	ATTTATTTTT	GAAAAATATT	ATCTATAA		528

(2) INFORMATION FOR SEQ ID NO:1229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2562 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2562
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

ATATTGTGTG	AAAAAGATAA	ATTCTCTTGT	GAGTTTGCTT	ACTTCAAGAA	TTTTCTATTT	60
TCAC TTGGTA	TTTTATGGGC	TTTGTATCTT	ATGTCTAACA	TTCAAAACAT	GTCCCTGGAG	120
GACATCATGG	GAGAGCGCTT	TGGTCGCTAC	TCCAAGTACA	TTATTCAAGA	CCGGGCTTTG	180
CCAGATATTC	GTGATGGGTT	GAAGCCGGTT	CAGCGCCGTA	TTCTTTATTC	TATGAATAAG	240
GATAGCAATA	CTTTTGACAA	GAGCTACCGT	AAGTCGGCCA	AGTCAGTCGG	GAACATCATG	300
GGGAATTTCC	ACCCACACGG	GGATTCTTCT	ATCTATGATG	CCATGGTTCG	TATGTCACAG	360
AACTGGAAAA	ATCGTGAGAT	TCTAGTTGAA	ATGCACGGTA	ATAACGGTTC	TATGGACGGA	420
GATCCTCCTG	CGGCTATGCG	TTATACTGAG	GCACGTTTGT	CTGAAATTGC	AGGCTACCTT	480

CTTCAGGATA	TCGAGAAAAA	GACAGTTCCT	TTTGCATGGA	ACTTTGACGA	TACGGAGAAA	540
GAACCAACGG	TCTTGCCAGC	AGCCTTTCCA	AACCTCTTGG	TCAATGGTTC	GACTGGGATT	600
TCGGCTGGTT	ATGCCACAGA	CATTCCCTCC	CATAATTTAG	CTGAGGTCAT	AGATGCTGCA	660
GTTTACATGA	TTGACCACCC	AACTGCAAAG	ATTGATAAAC	TCATGGAATT	CTTGCCCTGGA	720
CCAGACTTCC	CTACAGGGGC	TATTATTTCAG	GGTCGTGATG	AAATCAAGAA	AGCTTATGAG	780
ACTGGGAAAAG	GGCGCGTGGT	TGTTTCGTTCC	AAGACTGAAA	TTGAAAAGCT	AAAAGGTGGT	840
AAGGAACAAA	TCGTTATTAC	TGAGATTTCCT	TATGAAATCA	ATAAGGCCAA	TCTAGTCAAG	900
AAAATCGATG	ATGTTCTGT	TAATAACAAG	GTAGCTGGGA	TTGCTGAGGT	TCGTGATGAG	960
TCTGACCGTG	ATGGTCTTCG	TATCGCTATC	GAACCTAAGA	AAGACGCTAA	TACTGAGCTT	1020
GTTCTCAACT	ACTTATTTAA	GTACACCGAC	CTACAAATCA	ACTACAACCT	TAATATGGTG	1080
GCGATTGACA	ATTTACACAC	TCGTCAGGTT	GGGATTGTTC	CAATCCTGTC	TAGCTACATC	1140
GCTCACCGTC	GAGAAGTGAT	TTTGGCGCGT	TCACGCTTTG	ACAAAGAAAA	GGCTGAGAAA	1200
CGTCTCCATA	TCGTCGAAGG	TTTGATTTCGT	GTGATTTCGA	TTTTGGATGA	AGTCATTGCT	1260
CTTATCCGTG	CTTCTGAGAA	TAAGGCGGAC	GCCAAGGAAA	ACCTCAAAGT	TAGCTATGAT	1320
TTTACGGAAAG	AACAGGCTGA	GGCTATCGTA	ACTTTGCAAC	TGTACCGTTT	GACCAATACC	1380
GATGTGGTTG	TCTTGACAGGA	AGAAGAAGCA	GAGCTTTCGTG	AGAAGATTGC	TATGCTGGCG	1440
GCTATTATCG	GTGATGAAAAG	GACTATGTAC	AATCTCATGA	AGAAAAGAACT	TCGTGAGGTC	1500
AAGAAGAAAAT	TTGCAACTCC	TCGTTTGAGT	TCTTTAGAAG	ACACTGCGAA	AGCAATTGAG	1560
ATTGATACAG	CTAGTCTTAT	CGCTGAGGAA	GATACCTACG	TCAGCGTGAC	CAAGGCAGGT	1620
TACATCAAGC	GTACCAGTCC	ACGTTCCCTT	GCGGCTTCCA	CCTTGGAAGA	AATTGGCAAG	1680
CGTGATGATG	ACCGTTTGAT	TTTTGTTCAA	TCTGCCAAGA	CAACCCAGCA	CCTCTTGATG	1740
TTCAACAAGT	TTGGAAATGT	CATCTACAGA	CCAATCCATG	AGTTGGCAGA	TATTCGTTGG	1800
AAGGACATCG	GAGAGCATCT	GAGCCAAACC	ATCACAAACT	TTGAAACGAA	TGAAGAAATC	1860
CTTTATGTGG	AAGTACTGGA	TCAGTTTGAC	GATGCGACAA	CCTACTTTGC	AGTGACTCGC	1920
CTTGGTCAAA	TCAAACGGGT	AGAGCGAAAA	GAATTCACTC	CATGGCGGAC	CTATAGATCT	1980
AAGTCTGTCA	AGTATGCTAA	GCTCAAAGAC	GATACAGATC	AGATTGTAGC	AGTGGCTCCG	2040
ATTAAACTAG	ATGATGTTGT	CTTGGTTAGT	CAAAATGGTT	ATGCCCTGCG	TTTCAATATC	2100
GAAGAGGTTT	CGGTTGTTCG	TGCTAAGGCA	GCAGGTGTCA	AGGCTATGAA	TTTGAAAGAA	2160
GATGATGTCC	TCCAATCTGG	CTTTATCTGT	AATACTTCGT	CCTTCTACCT	CTTGACCCAG	2220
CGTGGAAGCT	TGAAACGTGT	TTCTATTGAG	GAAATTCCTAG	CAACCAGCCG	TGCCAAACGA	2280
GGATTACAAG	TCTTGCGTGA	GTTGAAAAAC	AAACCGCATC	GTGTCTTCTT	GGCAGGAGCA	2340
GTTGCAGAGC	AAGGATTTGT	TGGCGATTTT	TTCAGTACGG	AAGTGGATGT	GAACGACCAA	2400
ACTCTGCTTG	TCCAATCCAA	TAAAGGAACA	ATCTATGAAA	GCCGATTGCA	AGACTTGAAC	2460
TTGTCAGAAC	GCACTAGCAA	TGGAAGCTTC	ATTTCTGACA	CGATTTCAGA	TGAAGAAGTT	2520
TTTGACGCTT	ATCTTCAGGA	AGTAGTTACT	GAAGATAAAT	AA		2562

(2) INFORMATION FOR SEQ ID NO:1230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

GGGACTCGTG	ATACCAGCCG	AAAGGTTCTG	TCTCTCCTCC	AAGATGAAGG	ATTGATCAAG	60
GGGATACCAG	GGCAAGGTTT	TCAAGTCGTC	AAAGAAGAAA	CCGTCCTATTT	CCCTGTATCC	120
AACCTAACCA	GCTACCAAGA	ACTAGTTAAA	GAACTTGGAC	TGCGCTCTAA	AACCAACGTG	180
GTCAGTCTGG	ACAAGATTAT	TATTGATAAA	AAATCCTCGC	TGATAACCGG	TTTCCCAGAG	240
TTTCGGATGG	TTTGGAAGGT	GGTCCGCCAG	CGTGTGGTGG	ATGATCTGGT	ATCCGTTCTG	300
GATACAGACT	ATCTGGATAT	GGAACATAAT	CCAAATCTCA	CTCGCCAAAT	TGCTGAGCAG	360
TCTATCTATT	CTTATATAGA	AAATGGCCTC	AAACTCCTTA	TTGATTATGC	TCAGAAGGAA	420
ATCACCATTG	ACCACTCAAG	CGACCGAGAC	AAGATTCTCA	TGGACATTGG	CAAAGACCCCT	480
TATGTCGTTT	CGATTAAATC	AAAAGTCTAT	CTCCAAGACG	GACGCCAATT	TCAGTTTACC	540
GAAAGTCGCC	ATAAGTTAGA	AAAATTTAGA	TTTGTAGATT	TTGCAAAACG	CAAGAAATAA	600

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

AGTATGCGTG	ATGCCAACCG	TGGTGGATGC	TCTCAGTCAT	GCCGTTGGAA	GTACGACCTT	60
TACGATATGC	CATTTGGGAA	AGAACGTAAG	AGTTTGCAGG	GTGAGATTCC	AGAAGAATTT	120
TCAATGTCAG	CCGTTGACAT	GTCTATGATT	GACCACATTC	CAGATATGAT	TGAAAATGGT	180
GTGGACAGTC	TAAAAATCGA	AGGACGTATG	GAGTCTATT	ACTATGTATT	AACAGTAACC	240
AACTGCTACA	AGGCGGCTGT	GGATGCCTAT	CTTGAAAAGTC	CTGAAAAGTT	TGAAGCTATC	300
AAACAAGACT	TGGTGGACGA	GATGTGGAAG	GTTGCCCAAC	GTGAACTGGC	TACAGGATTT	360
TACTATGGTA	CACCATCTGA	AAATGAGCAG	TTGTTTGGTG	CTCGTCGTAA	AATTCCCTGAG	420
TACAAGTTTG	TCGCTGAAGT	GGTTTCTTAT	GATGATGCGG	CACAAACAGC	AACTATTCGT	480
CAACGAAATG	TCATTAACGA	AGGGGACCAA	GTTGAGTTTT	ATGGTCCAGG	TTTCCGTCAT	540
TTTGAAACCT	ATATTGAAGA	TTTGCATGAT	GCCAAAGGCA	ATAAAATCGA	CCGCGCTCCA	600
AATCCAATGG	AACTATTGAC	TATTAAGGTG	CCTCAACCCG	TTCAATCAGG	AGACATGGTT	660
CGTGCAATTAA	AAGAAGGACT	CATCAATCTT	TATAAGGAAG	ATGGAACCAG	CGTCACAGTT	720
CGTGCTTAA						729

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

AAAATGCGTG AGCATGAGCA TTTACAAAAT CGAAACTCCA TAAAATCACA TCTGCTAGTT	60
CCGCTAACGT TTTTGT TTTT GGAATCTATA TATGTCGGTA GTAACCTTTT TAATTTGACG	120
GAAATGATCC AAGCTTCTAC AGATGCTGGC TTTTCAGCTT CTATTTCTTG TTTTACTAAT	180
TTTAACTGTA GCATTTGA	198

(2) INFORMATION FOR SEQ ID NO:1233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

ACAAAAAGTG ATTCAGCGGT TTTTGACTGC TTTAGTAGGA GAAATCAAAT AATGAGATAT	60
ATTACGGTAG AGGATTGTC CTTCTATTAT GATAAGGAGC CTGTTCTTGA ACATATCAAT	120
TATTGTGTTG ATAGTGGGGA ATTTGTTACC TTGACTGGGG AAAATGGAGC GGCTAAGACG	180
ACGCTCATCA AGGCTAGTCT TGGAAATTCTG CACCCACGCA TTGGAAAGGT GGCTATTTCA	240
AAGACAAATA CGCAAGGTAA GAAATTGAGA ATAGCCTATC TTCCTCAACA TATTGCCAGT	300
TTTAATGCTG GTTTTCAAGT ACGGTCTATG AATTTGTCAA GTCGGGTCGC TATCCGAGAA	360
ATGGCTGGTT CCGTCGTTTG A	381

(2) INFORMATION FOR SEQ ID NO:1234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1149 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1149
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

CAAAAAAGTG	AGGTAAACGC	AATGTGGATG	GAAGAATTGC	CAAATGGCAA	ATTTAAATAT	60
TTTGAGCGAT	ATAAAGATCC	ATATACTGAG	AAATTAAGAA	AAGTTTCAGT	AACCATGGAG	120
AAGAAAACCTC	CCCAGGCAAG	AAATCAAGCT	GCTATCTTGT	TACAAAGAGAA	GATAAAATAAA	180
AAACTCAGCA	CAAAACAAGT	AGAAAAGCATT	ACATTTGAAG	AAATCTATAA	CCTTTTCTAT	240
AAATCATGGG	CGCAAAACAGT	AAAGGAATCA	ACAAAACATA	ATTGTAAATC	AGTTGATAAG	300
AAGATGAAGG	AAGTCATACC	ATCCGATACC	ATACTTGCTA	ATCTTGACAG	GCGTTTCTCT	360
CAAGAGGCTA	TTGAAAAAAT	TATTGAAAGC	AACGGATATA	TTACAGCTAA	AAAAGTACGG	420
CATAGGCTCA	GAGGTATCTT	TAATTACGCT	GTTCAATACT	CTTACATTGA	AAACAACGAG	480
GTCGATTATA	CTACGATTCC	TCAAAAACCA	AAGACTTTAG	AAGAACTGGA	AAAAAAGCGT	540
AACAACCTTC	TCACCATGCA	AGAAATAAAA	GCACTTGTCG	ATGTCCTTAA	TCGTCGAGAA	600
TATCACCAAA	AGTACGCTGA	TATGGTTCCT	GTGCTGACAT	TAACTGGTAT	GAGATATGGT	660
GAGTTAACTG	CCTTACAAC	GAAGAATATA	GACTTCGAAA	ACAACAAAAT	TGAGATCACA	720
GGTAATTTTG	ATTCAAGTAA	CAAAATCAAG	ACGCTACCAA	AGACTACAAA	TTCAATACGG	780
ACAATCAAAG	TATCAGAGAG	TGTCATAGAA	GCTATTCAAA	GACAAATAGT	ACGACTTAGC	840
GAACGTTTCC	AGCCATTGTC	AAGCGATGAT	TATATTTTCT	GTTTTGAAAA	ATGGAATCAA	900
CCTACAACAA	TAGCTTGCTT	CATACAGATA	TTAAAAAAT	ATGGAAAACA	GGCCAAAATA	960
GAAAAAACT	TATCTAGCCA	TATTTTTAGG	CATTCTCATA	TTTCGTTTTT	AGCAGAGTCT	1020
GGCCTCCCAA	TAAAATCAAT	AATGGATCGA	GTTGGGCACT	CAAATGCAAA	AATGACTTTG	1080
GAAATCTATT	CTTCTTTTAC	TGAGGATATG	GAGGATAAAC	TGGTCAATAA	ATTAGATACT	1140
ATTTTTTAA						1149

(2) INFORMATION FOR SEQ ID NO:1235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

TATAGGAGTG	ATGAAATGGT	TGTTTATATT	AGACAAAGTA	AATTACCAAG	TGAGGTTTCA	60
ATTAATAAAT	ACAATGCTCA	AGTAGGTGCC	TACTTACAAG	GAGAAGAAGC	TGTTTTATAT	120
CAATCTTTTT	CTGAAATAAA	AGAGTTAACA	AGTGAAGATA	TAGTTGTAGA	TTATATAATG	180
GAGACTAGAG	CATTACTAAA	AATGATGGGC	TTAAACGTTT	CGGTTTCATG	CTATCCTATT	240
GAGCTTAAAG	AGTTTTATGG	TCGAAAGATT	TATGCTGGTA	TTTTAGGAGA	GATTGTGAAT	300
ATACCTGATA	ATTGGGGAAA	ATTTATTAAG	CCTAAAGCTG	GTTCAAAAGT	CTTTACTGGA	360
AGAGTTGTTA	ATGGAACCCA	TGATTTAATA	GGTATTGGTC	TACCTTTCGA	CTATCCTATA	420
TGGATTAGTG	AGGTTGTAGA	ATTCATAGCT	GAATGGCGTT	GTTTTGTGTT	AGATGGGTCGC	480
GTATTAGATG	TTCGACCCTA	TACAGGTGAT	TATCATGCAC	AATTTGATGC	AAGTGTAATT	540
GATGAAGCGA	TATCATGTTG	GAAAGATGCG	CCAATAGCTT	ATGGACTAGA	TATCGGTGTT	600
ACTCGCGATG	GCAGAACACT	TGTTGTTGAA	GTAAATGATG	GTTATGCATT	GGGAAATTAT	660
GGCCTATCTC	CTTTAAAATC	AATCAATTTT	CATAGAGCTA	GGTGGAAAGA	AATGGTAAAA	720
CCCTATTTTG	AAAAAATGA	AATTTTAAAT	ATCCAACAGG	ATGTTATTTT	CTAA	774

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

GATACTGGTG	ATGCTTATAT	CGTTCCTCAT	GGAGATCATT	ACCATTACAT	TCCTAAGAAT	60
GAGTTATCAG	CTAGCGAGTT	GGCTGCTGCA	GAAGCCTTCC	TATCTGGTCG	GGGAAATCTG	120
TCAAATTCAA	GAACCTATCG	CCGACAAAAT	AGCGATAACA	CTTCAAGAAC	AAACTGGGTA	180
CCTTCTGTAA	GCAATCCAGG	AACTACAAAT	ACTAACACAA	GCAACAACAG	CAACACTAAC	240
AGTCAAGCAA	GTCAAAGTAA	TGAGGATGTT	GATAGCCTTC	TGAAACAAC	TTATGCCTTG	300
CCACTCAGCA	AACGACACGT	AGAATCTGAT	GGCCTTGTCT	TTGATCCAGC	ACAAATCACA	360
AGTCGAACAG	CTAGAGGTGT	TGCAGTGCCA	CACGGAGATC	ATTACCACTT	CATCCCTTAC	420
TCTCAAATGT	CTGAATTGGA	AGAACGAATC	GCTCGTATTA	TTCCCCTTCG	TTATCGTTCA	480
AACCATTTGG	TACCGGATTC	AAGACTAGAA	CAACCAAGTC	TACAACCGAC	TCCGGAACCT	540
AGTCCAGGCC	CGCAACCTGC	ACCAAATCTT	AAAATAGACT	CAAATTCCTC	TTTGGTTAGT	600
CAGCTGGTAC	GAAAAGTTGG	GGAAGGATAT	GTATTCGAAG	AAAAGGGCAT	CTCTCGTTAT	660
GTCTTTGCGA	AAGATTTACC	ATCTGAAACT	GTAAAAAATC	TTGAAAGCAA	GTCATCAAAA	720
CAAGAGAGTG	TTACACACT	TTAA				744

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

GGTAAAGGTG AAAATATGGC TAAATTGATT CCGGGGAAAA TTCGTATCGA AGGTGTTGCC	60
CTTTATGAAA CTGGTAAGGT TGATATCATC AAGGAAAAAA ACAATCGGCT CTACGCTCGC	120
GTTGCAGAAAG AAGAACTGCG CCATAGTTTA GAGGATGATT TGGTTTTTTG TGCCTGTGAT	180
TTTTTTTCAAA AGAGGGGTTA CTGTGTGCAT TTGGCAGCGC TAGAGCATTT TCTGAAAAAT	240
GATGAGCGTG GTCAGGAAAT CTTGTGGAGT CTGGAAGAAG GTCATGAAGA AAAAGAGGCT	300
GTTGAAACCA AGGTGCACCT TGGGTGGCAA GTTTTTGGAT CGAATTTTAT CTCCAAAATC	360
AGAATGCGCC TATGA	375

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

AACGGGGGTG ACCAAGTGAT TGATGGGAAA CGATTATTAT TTAGTTTGAC CATAGTCAGT	60
TATGCCTTGA CGCTAGTAAG TGGAGTTGTG TATCTGTTTA ATAATAATAA TGTTAGCTTA	120

CTTCTACTTT	TATTGTTCTT	GTTGGTTAGT	AGCTTAATTG	CTTGTTGGAA	TGATATCAAG	180
TATTACTTAA	TCCATTTTAT	TTTCTATTTA	ACCATTTTTG	TATTTCTGGT	ATCAAGACCG	240
ACCATTGATT	ATTTTAGGGA	TGGTGCTTTG	GATACCTATC	ATCCAATAGC	CTATCGTTTT	300
GCCTTTATAG	TTGTCATGGT	TTTCGATTCTG	GGCTTGACCA	CAGGAGGCAT	TCTGGCTCGT	360
TACTTCATAG	CTAGGAAGAA	AATAAAAAGTA	GCAAATATAG	GAAATTCTCT	AAAAGAGGTT	420
TATATCAAGC	GGTTACGCTT	TGTATCACTA	TGA			453

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

TTGTTTTGCC	TTCTTCCACT	CTCTGTTTTT	GCCATTGATT	TCAAGATAAA	CTCTTATCAA	60
GGGGATTTGT	ATATTCATGC	AGATAATACG	GCAGAGTTTA	GACAGAAGAT	AGTTTACCAG	120
TTTGAGGAGG	ACTTTAAGGG	CCAAATCGTG	GGACTTGGAC	GTGCTGGTAA	GATGCCTAGC	180
GGGTTTGACA	TTGACCCTCA	TCCAAAGGTT	CAGGCTGCGA	AAAACGGTGC	AGAACTAGCA	240
GATGTGACTA	GCGAAGTAAC	AGAAGAAGCG	GATGGTTATA	CTGTGAGAGT	CTATAATCCA	300
GGTCAGGAGG	GCGACATAGT	TGAAGTTGAC	CTCGTCTGGA	ACTTAAAAAA	TTTACTTTTC	360
CTTTATGATG	ATATCGCTGA	ATTAAATTGG	CAACCTCTGA	CAGATAGTTC	AGAGTCTATT	420
GAAAAGTTTG	AATTTTCATGT	AAGGGGAGAC	AAGGGGGCTG	AAAAACTCTT	TTTCCATACA	480
GGGAACTTTT	TTAGAGAGGG	AACGATTGAA	AAGAGTAACC	TTGATTATAC	TATCCGTTTA	540
GACAATCTTC	CGGCTAAGCG	TGGAGTTGAG	TTGCATGCCT	ATTGGTCTCG	GACCGATTTT	600
GCTAGCGCTA	GGGATCAGGG	CTTGAAAGGG	AATCGTTTAG	AAGAGTTTAA	TAAGATAGAA	660
GACTCGATTG	TTAGAGAAAA	AGATCAGAGT	AAACAACTCG	TTACTTGGGT	CCTCCCTTCG	720
ATACTTTCTA	TCTCCTTGTT	ATTGAGTGTC	TGCTTCTATT	TTATTTATAG	AAGAAAGACC	780
ACTCCTTCAG	TCAAATATGC	CAAAAATCAT	CGTCTCTATG	AACCACCAAT	GGAATTAGAG	840
CCTATGGTTT	TATCAGAAAGC	AGTCTACTCG	ACCTCCTTGG	AGGAAGTGAG	TCCCTTGGTC	900
AAGGGAGCTG	GAAAATTCAC	CTTTGATCAA	CTTATTCAAG	CTACCTTGCT	AGATGTGATA	960
GACCGTGGGA	ATGTCTCTAT	TATTTTCAGAA	GGAGATGCAG	TTGGCTTGAG	ATTGGTGAAA	1020
GAAGATGGTT	TGTCAAGATT	TGAGAGAGAC	TGTCTAAATC	TAGCCTTTTC	AGGCAAAAAA	1080
GAAGCCACTC	TTTCCAATTT	GTTTGCGGAT	TACAAGGTAT	CTGATAGTCT	TTATCGTAGA	1140
GCCAAAGTTT	CTGATGAAAA	ACGGATTCAA	GCAAGAGGGC	TTCAACTCAA	ATCTTCTTTT	1200
GAAGAGGTAT	TGAACCAGAT	GCAAGAAGGA	GTGAGAAAAC	GAGTTTCCTT	CTGGGGGCTC	1260
CCAGATTACT	ATCGTCCTTT	AACTGGTTTG	GAAAAGACTT	TGCAAGTGGG	TATGGGTGTC	1320
TTGACTATCT	TGCCCCTATT	TATCGGATTT	GGTTTGTTCT	TGTACAGTTT	AGACGTTTCAT	1380
GGCTATCTTT	ACCTCCCTTT	GCCAATACTT	GGTTTCTTAG	GGTTAGTTTT	GTCTGTTTTT	1440
TATTATTGGA	AGCTTCGACT	AGATAATCGT	GATGGTGTTT	TAAATGAAGC	GGGAGCTGAG	1500
GTCTACTATC	TCTGGACCAG	TTTTGAAAAA	ATGTTACGTG	AGATTGCACG	ACTGGATAAG	1560
GCTGAATTGG	AAAGTATTGT	TGTTTGGAAT	CGTCTCTTGG	TCTATGCAAC	CTTATTTGGC	1620

TATGCGGACA	AGGTTAGTCA	TTTGATGAAG	GTTCATCAGA	TTCAAGTTGA	AAATCCAGAT	1680
ATCAATCTCT	ATGTAGCTTA	TGGCTGGCAC	AGTATGTTTT	ATCATTCAAG	CGCGCAAATG	1740
AGCCATTATG	CTAGTGTGCG	AAATACAGCA	AGTACCTACT	CCGTATCTTC	TGGAAGTGGA	1800
AGTTCTGGCG	GTGGCTTCTC	TGGAGGCGGA	GGTGGCGGCA	GTATCGGAGC	CTTTTAA	1857

(2) INFORMATION FOR SEQ ID NO:1240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

ACAAAAATCG	AACTATATAT	AGGAGAAATC	ATGAACAAAA	CAACATTTAT	GGCTAAACCA	60
GGCCAAGTTG	AACGTAAATG	GTACGTAGTT	GACGCAACTG	ATGTACCACT	TGGACGTCTT	120
TCTGCAGTAG	TTGCTAGCGT	ACTTCGCGGA	AAAAACGACC	CCACATTTAC	ACCTCATACA	180
GCAGCGTCGT	TCTCAACAAG	TTCGCCCCAC	CCA			213

(2) INFORMATION FOR SEQ ID NO:1241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

TCNTTCGTCG	AGATGTTCTG	CGGCGTGGGC	GCTTCCCGTG	TCCGCGACAT	GTTCGANCA	60
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GCCAAGAAGC	ATGCGCCGTG	CATCATCTTC	ATCGACGAGA	TTGACGCCGT	CGGCCGCCAT	120
CGCGGCGCCG	GCCTGGGCGG	TGGTCACGAC	GAGCGCGAGC	AGACCCTCAA	CCAGTTGCTG	180
GTGGAGATGG	ATGGCTTCGA	GATGAACGAT	GGCATCATCG	TCATCGCTGC	CACCAACCGT	240
CCGGACGTTN	TGGACCCGGC	GCTGCTGCGT	CCGGGCCGCT	TCGACCGCCA	GGTGGTGGTC	300
GGCTTGCCGG	ATATCCGCGG	GCGCGAACAG	ATCCTCAAGG	TGCACATGCG	TAAGGTGCCG	360
CTGGGCGACC	ATGTCGATCC	TGCCGTCATC	GCCCCGCGTA	CGCCCGGTTT	CTCCGGCGCT	420
GATGGCCCN	GGTCTNTTTT	TNNAANTGCC	AANNAGCTNA	ANNNAAGG	GCCC	474

(2) INFORMATION FOR SEQ ID NO:1242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

CAATACGTCG	AAGACACCGT	CACCCAATTC	AAGGATAGAG	ACGTCGAATG	TACCACCACC	60
AAGGTCAAAT	ACCAAGATTT	TTTCTTCTTT	GTCAGTCTTG	TCCAAACCAT	AAGCAAGAGC	120
TGCTGCAGTT	GGTTCGTTAA	CAATACGTTT	TACTTCAAGA	CCAGCAATTT	TACCAGCGTC	180
TTTTGTTGCT	TGACGTTGAG	CGTCGTTGAA	GTAAGCCGGA	ACTGTGATAA	CAGCTTTGGT	240
TACTTTCTCA	CCAAGGTAGT	CTTCAGCGTA	GCCTTTCAAG	TATTGAAGGA	TCATAGCTGA	300

(2) INFORMATION FOR SEQ ID NO:1243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432